Demography
Why model demographic history?

- Understand population history
  Bottlenecks, gene flow, etc.
Excoffier
Allele Frequency Spectrum

Demography DISTORTS genealogies

Schraiber and Akey (2015) Nat Rev Genet

Ryan Gutenkunst
Joint SFS (2D-SFS)

Model of Isolation with migration (IM)

Excoffier
Using estimates of theta

\[ E(\pi) = \theta \]
\[ E(S) = \theta \sum_{i=1}^{n-1} \frac{1}{i} \]

Tajima (1989)

Tajima’s D = \( \frac{\pi - \theta_w}{\text{stdev}(\pi - \theta_w)} \)
Modeling workflow

Compare simulations with data.

Choose candidate parameter values, simulate data.

Update parameters to (hopefully) fit data better.

Converged output model

Ryan Gutenkunst
<table>
<thead>
<tr>
<th>Name</th>
<th>Data type</th>
<th>Inference</th>
<th>Notes</th>
<th>Refs</th>
</tr>
</thead>
<tbody>
<tr>
<td>STRUCTURE</td>
<td>Unlinked multi-allelic genotypes</td>
<td>Population structure, admixture</td>
<td>User-friendly GUI can be computationally demanding</td>
<td>32</td>
</tr>
<tr>
<td>FRAPPE</td>
<td>Unlinked bi-allelic SNVs</td>
<td>Population structure, admixture</td>
<td>Alexander et al. argue that convergence is not guaranteed</td>
<td>40</td>
</tr>
<tr>
<td>ADMIXTURE</td>
<td>Unlinked bi-allelic SNVs</td>
<td>Population structure, admixture</td>
<td>Estimates the number of populations via cross-validation error</td>
<td>41</td>
</tr>
<tr>
<td>fastSTRUCTURE</td>
<td>Unlinked bi-allelic SNVs</td>
<td>Population structure, admixture</td>
<td>Obtains variational Bayesian estimates of posterior probability distribution</td>
<td>42</td>
</tr>
<tr>
<td>Structurama</td>
<td>Unlinked multi-allelic genotypes</td>
<td>Population structure, admixture</td>
<td>Uses a Dirichlet process to estimate the number of populations</td>
<td>43</td>
</tr>
<tr>
<td>HAPMIX</td>
<td>Phaseled haplotypes; reference panel</td>
<td>Chromosome painting</td>
<td>Requires populations to be specified a priori</td>
<td>48</td>
</tr>
<tr>
<td>fineSTRUCTURE</td>
<td>Phaseled haplotypes</td>
<td>Population structure, admixture, chromosome painting</td>
<td>Can be used to identify the number and identity of populations</td>
<td>49</td>
</tr>
<tr>
<td>GLOBETROTTER</td>
<td>Phaseled haplotypes</td>
<td>Population structure, admixture, chromosome painting</td>
<td>Extends the fineSTRUCTURE approach to estimate unsampled ancestral populations and admixture times</td>
<td>7</td>
</tr>
<tr>
<td>LAMP</td>
<td>Phaseled haplotypes; reference panel</td>
<td>Chromosome painting</td>
<td>Identifies local ancestry in windows, rather than using an HMM, so is more discrete than other approaches</td>
<td>52</td>
</tr>
<tr>
<td>PCAdmixture</td>
<td>Phaseled haplotypes</td>
<td>Chromosome painting</td>
<td>Uses PCA in small chunks followed by an HMM to estimate local ancestry</td>
<td>53</td>
</tr>
<tr>
<td>doslf</td>
<td>Frequency spectrum of unlinked bi-allelic SNVs</td>
<td>Demographic history</td>
<td>Requires some Python-coding skills; applicable to up to three populations</td>
<td>60</td>
</tr>
<tr>
<td>fastSimcoal2</td>
<td>Frequency spectrum of unlinked bi-allelic SNVs</td>
<td>Demographic history</td>
<td>Can also be used to simulate data under the SMC</td>
<td>62,63</td>
</tr>
<tr>
<td>Treemix</td>
<td>Frequencies of unlinked bi-allelic SNVs</td>
<td>Admixture graph</td>
<td>Highly multimodal likelihood surface and heuristic search; reoff inference from many starting points</td>
<td>64</td>
</tr>
<tr>
<td>fastNeutrino</td>
<td>Frequency spectrum of unlinked bi-allelic SNVs</td>
<td>Demographic history</td>
<td>Applicable only to a single population; designed specifically for extremely large sample sizes</td>
<td>65</td>
</tr>
<tr>
<td>DeoSIS</td>
<td>Lengths of IBD blocks between pairs of individuals</td>
<td>Demographic history</td>
<td>IBD must be inferred (for example, using Beagle or GERMLINE); specification of lower cut-off minimizes false-negative IBD tracts</td>
<td>71,72</td>
</tr>
<tr>
<td>IBS tract inference</td>
<td>Lengths of IBS blocks between pairs of individuals</td>
<td>Demographic history</td>
<td>IBS can easily be confounded by missing data and/or sequencing errors</td>
<td>76</td>
</tr>
<tr>
<td>PSMC</td>
<td>Diploid genotypes from one individual</td>
<td>Demographic history</td>
<td>Best used in PSMC's PSMC mode, which uses the SMC to more accurately model recombination than the original PSMC; applicable to a single population</td>
<td>78</td>
</tr>
<tr>
<td>MSMC</td>
<td>Whole genome, phased haplotypes</td>
<td>Demographic history</td>
<td>Requires large amounts of RAM; cross-coalescence rate should not be interpreted as migration rate</td>
<td>82</td>
</tr>
<tr>
<td>CoalHMM</td>
<td>Whole genome, phased haplotypes</td>
<td>Demographic history</td>
<td>Multiple applications, including inference of population sizes, migration rates and incomplete lineage sorting</td>
<td>83–87</td>
</tr>
<tr>
<td>dCal</td>
<td>Medium-length, phased haplotypes</td>
<td>Demographic history</td>
<td>Uses shorter sequences than MSMC, but can be applied to multiple individuals in complex demographic models; infers explicit population genetic parameters for migration rates</td>
<td>89,92</td>
</tr>
<tr>
<td>LAMARC</td>
<td>Short, phased haplotypes</td>
<td>Demographic history</td>
<td>Requires Monte Carlo sampling of coalescent genealogies; very flexible</td>
<td>93</td>
</tr>
<tr>
<td>BEAST</td>
<td>Short, phased haplotypes</td>
<td>Species trees, effective population sizes</td>
<td>Used mainly as a method of phylogenetic inference. Can also infer population size history</td>
<td>94</td>
</tr>
<tr>
<td>MCMCcoal</td>
<td>Short, phased haplotypes</td>
<td>Divergence times between populations</td>
<td>Now incorporated into the software BPP (iii)</td>
<td>95</td>
</tr>
<tr>
<td>G-PhoCS</td>
<td>Short, unphased haplotypes</td>
<td>Demographic history</td>
<td>Incorporates migration into the MCMCcoal framework. Averages over unphased haplotypes</td>
<td>96</td>
</tr>
<tr>
<td>Exact likelihoods using generating functions</td>
<td>Short, phased haplotypes</td>
<td>Demographic history</td>
<td>Implemented in Mathematica; applicable only to specific classes of multi-population models</td>
<td>97,98</td>
</tr>
</tbody>
</table>

Ryan Gutenkunst
**IM/IMa/IMa2**

- Uses coalescent simulation to calculate the full likelihood of the data given the model, for non-recombining regions (mitochondria, Y chromosome, small autosomal regions).
- Bayesian inference based on MCMC walk through parameter space, can be computationally expensive.
- Handles arbitrary number of populations.

Hey and Nielsen (2004) Genetics

Ryan Gutenkunst
Estimate pairwise joint frequency spectra using coalescent simulations.

Scales to arbitrary number of populations.

Estimate parameters by maximum composite likelihood.

Optimization may be more robust than \( \partial a \partial t \).

Excoffier et al.  
\textit{dadi}: Diffusion Approximations for Demographic Inference

- Up to three interacting populations, with arbitrary parameter time courses
- 1 pop, 20 samples, \( \sim 3 \) params: \( \sim 1 \) minute to fit
  2 pops, 20 samples each, \( \sim 6 \) params: \( \sim 10 \) minutes to fit
  3 pops, 20 samples each, \( \sim 12 \) params: \( \sim 3 \) hours to fit
- Computational cost independent of SNP count, but exponential in number of populations.

Gutenkunft et al. 
Demographic History of *Drosophila melanogaster*
What is the demographic history of East African *D. melanogaster*?
Approach: Data collection

- Sample: 20 strains from Uganda
- Target Region: 2 Mb X chromosome region
- Sequencing strategy: Illumina
  - Barcoded genomic library preparation
  - Multiplex selective enrichment
    - Nimblegen chip-capture
    - 385,000 oligo array
  - Single end (86 bp reads)
    - 2.5 million reads/strain
Approach: Bioinformatics

• Reads mapped with BWA
  – ~72% reads map uniquely
    • ~90% map to target

• Alignments processed in SAMtools
  – Final coverage: 32.4X
  – ~89% sites with ≥2X

• SNP calls:
Approach: Bioinformatics

• Reads mapped with BWA
  – ~72% reads map uniquely
    • ~90% map to target
• Alignments processed in SAMtools
  – Final coverage: 32.4X
  – ~89% sites with > 2X
• SNP calls: Joint Genotyper for Inbred Lines
  – Simultaneously considers all reads (per site) across lines
  – Assumes shared error profile across lines
  – Line genotypes depend on population frequency, error
Demographic modeling: dadi

- Restrict to third codon positions
Demographic modeling: dadi

- Restrict to third codon positions
- Polarize polymorphisms (*D. simulans*)

![Genetic Tree Diagram]

- **G** -> **A**
  - *D. melanogaster*       **A/G**
  - *D. simulans*           **G**
Demographic modeling: dadi

• Restrict to third codon positions
• Polarize polymorphisms (*D. simulans*)
• Five models
  – Neutral
  – Two epoch
  – Growth
  – Bottlegrowth
  – Three Epoch
Demographic modeling: dadi

• Restrict to third codon positions
• Polarize polymorphisms (*D. simulans*)
• Five models
  – Neutral
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  – Bottlegrowth
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Demographic modeling: dadi

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  - Neutral
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  - Growth
  - Bottlegrowth
  - Three Epoch
Demographic modeling: dadi

- Restrict to third codon positions
- Polarize polymorphisms (*D. simulans*)
- Five models
  - Neutral
  - Two epoch
  - Growth
  - Bottlegrowth
  - Three epoch
Results: Demography

Neutral; LL = -206.63

Two Epoch; LL = -116.00

Growth; LL = -116.00

BottleGrowth; LL = -76.64

Three Epoch; LL = -79.89
Results: Demography

- Bottle Growth; LL = -76.64
- Three Epoch; LL = -79.89
Results: Demography

\[ N_B/N_A = 0.016 - 0.064 \]

\[ N_C/N_A = 0.47 - 0.76 \]

\[ T_R = 0.14 \ (\sim 28,000 \ ybp) \]
Summary: *D. melanogaster*

- Population genetic data from ancestral population
  - Next-generation sequencing
  - Targeted enrichment
  - JGIL

- Nonequilibrium demography in Uganda
  - Population contraction followed by expansion
Demography in *Drosophila suzukii*
D. suzukii

• Native to Southeast Asia
D. suzukii

- Native to Southeast Asia
- Closely related to *D. melanogaster*
D. suzukii

- Native to Southeast Asia
- Closely related to *D. melanogaster*
- Pest of soft-skinned fruits
Female morphology

Photos courtesy of H. Burrack

Hauser 2011
# Economic impact: West Coast

<table>
<thead>
<tr>
<th><strong>Table 1. Revenue Losses Due to SWD: 20% Yield Loss, 2008 Value of Production</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
</tr>
<tr>
<td><strong>Strawberries</strong></td>
</tr>
<tr>
<td>Total farmgate value ($Million) 1,544.7 Oregon 16.8 Washington 10.1 Three-state Total 1,571.5</td>
</tr>
<tr>
<td>Share of U.S. production (%) 82 Oregon 1 Washington 1 Three-state Total 83</td>
</tr>
<tr>
<td>Total losses ($Million) 308.9 Oregon 3.4 Washington 2.0 Three-state Total 314.3</td>
</tr>
<tr>
<td><strong>Blueberries (cultivated)</strong></td>
</tr>
<tr>
<td>Total farmgate value ($Million) 49.1 Oregon 49.4 Washington 43.4 Total 141.9</td>
</tr>
<tr>
<td>Share of U.S. production (%) 9 Oregon 9 Washington 8 Three-state Total 26</td>
</tr>
<tr>
<td>Total losses ($Million) 9.8 Oregon 9.9 Washington 8.7 Three-state Total 28.4</td>
</tr>
<tr>
<td><strong>Raspberries and Blackberries</strong></td>
</tr>
<tr>
<td>Total farmgate value ($Million) 179.5 Oregon 41.7 Washington 92.1 Total 313.3</td>
</tr>
<tr>
<td>Share of U.S. production (%) 57 Oregon 13 Washington 29 Three-state Total 100</td>
</tr>
<tr>
<td>Total losses ($Million) 35.9 Oregon 8.3 Washington 18.4 Three-state Total 62.7</td>
</tr>
<tr>
<td><strong>Cherries</strong></td>
</tr>
<tr>
<td>Total farmgate value ($Million) 194.5 Oregon 58.7 Washington 297.1 Total 550.3</td>
</tr>
<tr>
<td>Share of U.S. production (%) 30 Oregon 9 Washington 45 Three-state Total 84</td>
</tr>
<tr>
<td>Total losses ($Million) 38.3 Oregon 9.9 Washington 57.8 Three-state Total 105.9</td>
</tr>
<tr>
<td><strong>ALL CROPS</strong></td>
</tr>
<tr>
<td>Total farmgate value ($Million) 1,967.9 Oregon 166.5 Washington 442.6 Total 2,577.0</td>
</tr>
<tr>
<td>Share of U.S. production (%) 58 Oregon 5 Washington 13 Three-state Total 76</td>
</tr>
<tr>
<td>Total losses ($Million) 393.0 Oregon 31.4 Washington 86.9 Three-state Total 511.3</td>
</tr>
</tbody>
</table>

*Source: Authors’ calculations based on data from the National Agricultural Statistics Service (NASS), 2009.*
## Economic impact: East Coast

<table>
<thead>
<tr>
<th>Crop</th>
<th>Total Farmgate Value ($1,000s)</th>
<th>Potential Yield Loss (%)</th>
<th>Potential Losses ($1,000s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blueberries</td>
<td>192,859</td>
<td>40</td>
<td>77,144</td>
</tr>
<tr>
<td>Caneberries</td>
<td>4,395</td>
<td>50</td>
<td>2,198</td>
</tr>
<tr>
<td>Peaches</td>
<td>144,005</td>
<td>20?</td>
<td>28,801</td>
</tr>
<tr>
<td>Fresh Strawberries</td>
<td>386,332</td>
<td>0?</td>
<td>0</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>727,591</strong></td>
<td></td>
<td><strong>108,143</strong></td>
</tr>
</tbody>
</table>

Courtesy of H. Burrack
What is the invasion history of *D. suzukii*?
Samples
Markers

- Draft genome provided by M. B. Eisen
- *D. melanogaster* annotations
  - Gene location
  - Gene model
- 6 X-linked gene fragments
  - Evenly spaced
  - 700 bp (coding + noncoding)
Methods

- Single male DNA extraction
- PCR
- Sanger sequencing
Results: Nucleotide diversity

Locus 1

Locus 2

Locus 3
Results: Haplotype diversity

Locus 1

Locus 2

Locus 3
Results: Haplotype network
Results: Haplotype network
Results: Haplotype network
Results: Haplotype network
Fig. 2. Change in haplotype diversity at each locus in each population relative to Japan as estimated by the following equation:

\[ \frac{Hd_{\text{sample}} - Hd_{\text{Japan}}}{Hd_{\text{Japan}}} \].
<table>
<thead>
<tr>
<th>Population</th>
<th>JP</th>
<th>HI</th>
<th>ST</th>
<th>SD</th>
<th>FL</th>
<th>GA</th>
<th>MA</th>
<th>MI</th>
<th>NC</th>
<th>SC</th>
<th>WV</th>
</tr>
</thead>
<tbody>
<tr>
<td>HI</td>
<td>0.23*</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>ST</td>
<td>0.112*</td>
<td>0.042</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>SD</td>
<td>0.113*</td>
<td>0.118*</td>
<td>0.011</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>FL</td>
<td>0.032</td>
<td>0.199*</td>
<td>—0.097</td>
<td>—0.352</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>GA</td>
<td>0.076*</td>
<td>0.195*</td>
<td>0.058</td>
<td>0.037</td>
<td>—0.025</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>MA</td>
<td>0.027</td>
<td>0.177*</td>
<td>0.05</td>
<td>—0.012</td>
<td>—0.151</td>
<td>0.017</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>MI</td>
<td>0.036</td>
<td>0.177*</td>
<td>0.075*</td>
<td>0.047</td>
<td>—0.129</td>
<td>—0.028</td>
<td>—0.019</td>
<td>—</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>NC</td>
<td>0.061*</td>
<td>0.265*</td>
<td>0.13*</td>
<td>0.061</td>
<td>0.008</td>
<td>0.02</td>
<td>0.042</td>
<td>—0.022</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>SC</td>
<td>0.111*</td>
<td>0.219*</td>
<td>0.14*</td>
<td>0.02</td>
<td>—0.313</td>
<td>0.061</td>
<td>—0.073</td>
<td>0.052</td>
<td>0.097*</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>WV</td>
<td>0.076*</td>
<td>0.242*</td>
<td>0.128*</td>
<td>0.021</td>
<td>—0.153</td>
<td>0.024</td>
<td>0.001</td>
<td>0.024</td>
<td>0.006</td>
<td>0.032</td>
<td>—</td>
</tr>
<tr>
<td>SP</td>
<td>0.287*</td>
<td>0.491*</td>
<td>0.379*</td>
<td>0.472*</td>
<td>0.535*</td>
<td>0.319*</td>
<td>0.42*</td>
<td>0.285*</td>
<td>0.395*</td>
<td>0.383*</td>
<td>0.363*</td>
</tr>
</tbody>
</table>

**Note.**—Asterisks denote values significant at P < 0.05 (permutation test, see Materials and Methods).
Fig. 4. Invasion models for *Drosophila suzukii*. We denote as ASIA the unsampled source population of the invasions and JP, HI, WUS, EUS, SP the Japanese, Hawaii, Western United States, Eastern United States, and Spanish populations for which we have samples. For Model 1, we assumed independent colonization of all continents from Japan. For Model 2, we assumed that EUS was colonized from WUS. For Model 3, we assumed that both the SP and EUS populations were colonized from WUS. The arrows between ASIA and JP denote migration between those populations at a rate equal to 2Nm.
Table 3. Model Choice Results.

<table>
<thead>
<tr>
<th>Colonization History Models</th>
<th>Posterior Probability</th>
<th>Observed $P$ Value</th>
<th>Tukey Depth</th>
<th>Tukey $P$ Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.4181</td>
<td>0.999</td>
<td>0.227</td>
<td>0.999</td>
</tr>
<tr>
<td>2</td>
<td>0.2770</td>
<td>0.960</td>
<td>0.098</td>
<td>0.958</td>
</tr>
<tr>
<td>3</td>
<td>0.3049</td>
<td>0.943</td>
<td>0.105</td>
<td>0.937</td>
</tr>
</tbody>
</table>

Note.—Reported are the posterior probabilities for models of the colonization history of *Drosophila suzukii*. The model with the highest probability is shown in italic. The $P$ value for the observed data and the Tukey depth and the $P$ value for a Tukey test are reported.
Table 4. Priors and Weighted Posterior Estimates for Parameters of the Three Models of Colonization for *Drosophila suzukii*.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Population (/j)</th>
<th>Prior</th>
<th>Mode</th>
<th>Mean</th>
<th>Median</th>
<th>Q5%</th>
<th>Q95%</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\text{Log}_{10}(N_j)$</td>
<td>Asia</td>
<td>$U[4, 8]^{a}$</td>
<td>6.27</td>
<td>6.26</td>
<td>6.26</td>
<td>5.94</td>
<td>6.56</td>
</tr>
<tr>
<td></td>
<td>Japan (JP)</td>
<td>$U[2, 6]^{a}$</td>
<td>5.64</td>
<td>5.31</td>
<td>5.40</td>
<td>3.46</td>
<td>6.88</td>
</tr>
<tr>
<td></td>
<td>Hawaii (HI)</td>
<td></td>
<td>5.18</td>
<td>4.32</td>
<td>4.37</td>
<td>2.78</td>
<td>5.77</td>
</tr>
<tr>
<td></td>
<td>Western United States (WUS)</td>
<td></td>
<td>5.37</td>
<td>4.66</td>
<td>4.77</td>
<td>3.12</td>
<td>5.84</td>
</tr>
<tr>
<td></td>
<td>Eastern United States</td>
<td></td>
<td>3.66</td>
<td>4.25</td>
<td>4.24</td>
<td>2.76</td>
<td>5.74</td>
</tr>
<tr>
<td></td>
<td>Spain</td>
<td></td>
<td>3.03</td>
<td>4.04</td>
<td>3.98</td>
<td>2.68</td>
<td>5.61</td>
</tr>
<tr>
<td>$\text{Log}_{10}(j)$</td>
<td>Hawaii</td>
<td>$U[0.6, 3]^{a}$</td>
<td>2.30</td>
<td>2.10</td>
<td>2.14</td>
<td>1.23</td>
<td>2.84</td>
</tr>
<tr>
<td></td>
<td>Western United States</td>
<td></td>
<td>2.52</td>
<td>2.14</td>
<td>2.25</td>
<td>1.00</td>
<td>2.89</td>
</tr>
<tr>
<td></td>
<td>Eastern United States (EUS)</td>
<td></td>
<td>1.81</td>
<td>1.79</td>
<td>1.79</td>
<td>0.95</td>
<td>2.63</td>
</tr>
<tr>
<td></td>
<td>Spain (SP)</td>
<td></td>
<td>0.87</td>
<td>1.03</td>
<td>0.98</td>
<td>0.65</td>
<td>1.56</td>
</tr>
<tr>
<td>$\tau_j$</td>
<td>Hawaii (HI)</td>
<td>$U[100, 750]^{a}$</td>
<td>421</td>
<td>431</td>
<td>434</td>
<td>147</td>
<td>704</td>
</tr>
<tr>
<td></td>
<td>Western United States (WUS)</td>
<td>$U[10, 100]^{b}$</td>
<td>88</td>
<td>75</td>
<td>78</td>
<td>42</td>
<td>97</td>
</tr>
<tr>
<td></td>
<td>Eastern United States (EUS)</td>
<td>$\tau_{HI} &gt; \tau_{WUS} &gt; \tau_{SP} &gt; \tau_{ELS}$</td>
<td>21</td>
<td>32</td>
<td>29</td>
<td>12</td>
<td>62</td>
</tr>
<tr>
<td></td>
<td>Spain (SP)</td>
<td></td>
<td>60</td>
<td>58</td>
<td>58</td>
<td>24</td>
<td>90</td>
</tr>
<tr>
<td>$\text{Log}_{10}(Nm)$</td>
<td>—</td>
<td>$U[-2, 2]^{a}$</td>
<td>—27</td>
<td>—21</td>
<td>—23</td>
<td>—105</td>
<td>0.69</td>
</tr>
<tr>
<td>$\mu \times 10^9$</td>
<td>—</td>
<td>$N(3.46, 0.28)^c$</td>
<td>3.49</td>
<td>3.49</td>
<td>3.49</td>
<td>2.46</td>
<td>4.52</td>
</tr>
</tbody>
</table>
Fig. 6. The posterior probability of the parameters of the three colonization models for *D. suzukii* weighted by the posterior probability of each model, where *N* is the current population size, *f* is the number of founding individuals, *τ* is the colonization time for each population (in generations), and *Nm* is the migration rate among demes in the structured Japan population model. Note that the posterior distribution of *τ* was plotted separately from the remaining *τ* estimates due to its unique prior range.
Summary: *D. suzukii*

- Interested in US colonization history
- Sampled worldwide populations
- Used X-linked loci to probe population structure
- Preliminary data inconsistent with one US invasion
- No clear founding population for US invasion
- Europe may reflect single invasion