Table 1: Methods for the genetic inference of dispersal. Classification according to the dispersal parameter that can be estimated. The parameters are defined in text (Section 2).

<table>
<thead>
<tr>
<th>Method</th>
<th>Parameter</th>
<th>Population structure</th>
<th>Time scale</th>
<th>Data</th>
<th>Assumptions</th>
<th>Sampling scheme</th>
<th>Software</th>
<th>Ref.</th>
</tr>
</thead>
<tbody>
<tr>
<td>F-statistics</td>
<td>$N_m e$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes, Haplotypes</td>
<td>$\mu$ known or $&lt;&lt;m_c$, Island model, LE</td>
<td>Sample of individuals in a set of populations, One sampling event, After dispersal</td>
<td></td>
<td>1-3</td>
</tr>
<tr>
<td>Rare alleles</td>
<td>$N, m_c$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes, Haplotypes</td>
<td>$&lt;&lt;m_c$, Island or 2D isolation by distance, LE</td>
<td>Sample of individuals in a set of populations, One sampling event, After dispersal</td>
<td></td>
<td>4, 5</td>
</tr>
<tr>
<td>Coalescence</td>
<td>$N, m_c$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Haplotypes</td>
<td>Island model, Infinite sites model of mutation</td>
<td>Sample of individuals in a set of populations, One sampling event</td>
<td>Upon request</td>
<td>6</td>
</tr>
<tr>
<td>Effective number of migrants</td>
<td>$N, m_c$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus biallelic genotypes</td>
<td>No selection, No mutation, Constant and equal $N_e$, Symmetric migration, LE</td>
<td>Sample of individuals in two populations, One sampling event</td>
<td></td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>$N, m_c$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes, Haplotypes</td>
<td>Simulations of the data possible under the investigated model</td>
<td>Sample of individuals in one or a set of populations, One sampling event</td>
<td></td>
<td>8-11</td>
</tr>
<tr>
<td>Method</td>
<td>Parameter</td>
<td>Population structure</td>
<td>Time scale</td>
<td>Data</td>
<td>Assumptions</td>
<td>Sampling scheme</td>
<td>Software</td>
<td>Ref.</td>
</tr>
<tr>
<td>--------</td>
<td>-----------</td>
<td>----------------------</td>
<td>------------</td>
<td>------</td>
<td>-------------</td>
<td>----------------</td>
<td>----------</td>
<td>------</td>
</tr>
<tr>
<td>F-statistics and derivatives</td>
<td>$m_e^{ij}$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus biallelic genotypes</td>
<td>No selection Low mutation rate and low immigration from unsampled populations $N_e$ of each population known and constant LE, Panmixia</td>
<td>Sample of individuals in a set of populations One sampling event After dispersal</td>
<td></td>
<td>12, 13</td>
</tr>
<tr>
<td>Parentage</td>
<td>$m_e^i$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes</td>
<td>No selection IAM or KAM $\mu &lt;&lt; m_e^i$ Immigrants come with equal probability from all other populations Panmixia</td>
<td>Sample of individuals in a set of populations One sampling event After dispersal</td>
<td>ESTIM</td>
<td>14</td>
</tr>
<tr>
<td>Parentage</td>
<td>$m_e$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes</td>
<td>Island model without selfing LE</td>
<td>Sample of individuals in a set of populations One sampling event Before dispersal</td>
<td></td>
<td>15</td>
</tr>
<tr>
<td>Parentage</td>
<td>$m_e^i$</td>
<td>Discrete</td>
<td>Single to a few generations</td>
<td>Multilocus genotypes</td>
<td>No selection and no mutation during the sampling interval LE</td>
<td>Sample of individuals in the focal population and from all potential source populations $\geq 2$ sampling events in the focal population; and one or $\geq 2$ sampling events in the source populations Before dispersal</td>
<td>MLNE</td>
<td>16</td>
</tr>
<tr>
<td>Parentage</td>
<td>$m_e^i$ (pollen)</td>
<td>Discrete or continuous</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>No mutation between parental and offspring's genotypes</td>
<td>Sample of mother plants, associated seeds and all potential fathers in focal population. One sampling event. Before seed dispersal</td>
<td></td>
<td>17, 18</td>
</tr>
<tr>
<td>Coalescence</td>
<td>$m_e^{ij}$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Haplotypes</td>
<td>No selection IAM</td>
<td>Sample of individuals in a set of populations One sampling event</td>
<td>GENETREE</td>
<td>23</td>
</tr>
<tr>
<td>Coalescence</td>
<td>$m_e^{ij}$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes</td>
<td>No selection $\mu$ is known, valid molecular clock Constant $N_e$ of each population LE, Panmixia</td>
<td>Sample of individuals in all populations (see 24, 25) One sampling event</td>
<td>MIGRATE</td>
<td>26, 27</td>
</tr>
<tr>
<td>Coalescence</td>
<td>$m_e^{ij}$ (divergence model)</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes</td>
<td>No selection Infinite sites, finite sites (see 28) or stepwise (see 29) model of mutation $\mu$ or $N_e$ is known Constant $N_e$ of each population LE, Panmixia</td>
<td>Sample of individuals in two populations One sampling event</td>
<td>MDIV</td>
<td>30, 31</td>
</tr>
<tr>
<td>Coalescence</td>
<td>$m_e^{ij}$</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Haplotypes</td>
<td>No selection Applies to Measurably Evolving Populations (i.e. high $\mu$, see 32), GTR Constant $N_e$ between two sampling events Immigrants come with equal probability from all other populations Valid molecular clock</td>
<td>Sample of individuals in a set of populations $\geq 2$ sampling events</td>
<td>BEAST</td>
<td>33, 34</td>
</tr>
<tr>
<td>Method</td>
<td>Parameter</td>
<td>Population structure</td>
<td>Time scale</td>
<td>Data</td>
<td>Assumptions</td>
<td>Sampling scheme</td>
<td>Software</td>
<td>Ref.</td>
</tr>
<tr>
<td>--------</td>
<td>-----------</td>
<td>----------------------</td>
<td>------------</td>
<td>------</td>
<td>-------------</td>
<td>----------------</td>
<td>----------</td>
<td>------</td>
</tr>
<tr>
<td>F-statistics and derivatives</td>
<td>$m$</td>
<td>Discrete (hierarchical structure allowed)</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>No selection Island migration model LE Panmixia</td>
<td>Sample of individuals in a set of populations Pre- and post-dispersal sampling within a generation</td>
<td>Many softwares available (see 37-42)</td>
<td>35, 36</td>
</tr>
<tr>
<td>Assignment and mixture analysis</td>
<td>$m^g$</td>
<td>Discrete</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>LE Panmixia</td>
<td>Sample of individuals in a set of populations After dispersal</td>
<td>BayesAss 43, 44</td>
<td>37-42</td>
</tr>
<tr>
<td>Estimating non-effective migration rate $m$</td>
<td>$m^g$</td>
<td>Discrete</td>
<td>1-3 generations</td>
<td>Multilocus genotypes</td>
<td>No selection No drift over 1-3 generations Low $m^g$ LE</td>
<td>Sample of individuals from all populations exchanging migrants. After dispersal</td>
<td>BIMr 45</td>
<td>43, 44, 45</td>
</tr>
<tr>
<td></td>
<td>$m^g$</td>
<td>Discrete</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>No selection LE</td>
<td>Sample of individuals from all populations exchanging migrants. Before dispersal</td>
<td></td>
<td>46</td>
</tr>
<tr>
<td></td>
<td>$m^g$</td>
<td>Discrete</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>No selection LE</td>
<td>Pre- and post-dispersal sampling of individuals from all populations exchanging migrants.</td>
<td>Upon request 46</td>
<td>46</td>
</tr>
<tr>
<td>Method</td>
<td>Parameter</td>
<td>Population structure(a)</td>
<td>Time scale(b)</td>
<td>Data(c)</td>
<td>Assumptions(d)</td>
<td>Sampling scheme(e)</td>
<td>Software(f)</td>
<td>Ref.(g)</td>
</tr>
<tr>
<td>------------------------</td>
<td>--------------------</td>
<td>-----------------------------</td>
<td>-----------------</td>
<td>-----------------------------</td>
<td>----------------------------------------------------------------------------------</td>
<td>---------------------------------------------------------------------------------</td>
<td>---------------------------------------------------------------</td>
<td>-----------</td>
</tr>
<tr>
<td>Marker allele</td>
<td>Discrete distances</td>
<td>Discrete or continuous</td>
<td>Single generation</td>
<td>Multilocus genotypes Haplotype</td>
<td>No selection Rare allele(s) can be used as marker and introduced</td>
<td>Sample of individuals in the surroundings of introduction spot One sampling event after the introduction After dispersal</td>
<td>SNM + Many softwares available for parentage analysis(h)</td>
<td>47(i)</td>
</tr>
<tr>
<td>Parentage</td>
<td>Discrete distances or kernel (pollen and/or seeds)</td>
<td>Discrete or continuous</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>No mutation between parental and offspring's genotypes</td>
<td>Sample of seeds or seedlings and all potential parents in focal population. One sampling event</td>
<td>Upon request</td>
<td>20, 48-52</td>
</tr>
<tr>
<td>Two-Gener</td>
<td>(\sigma^2) or kernel</td>
<td>Continuous</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>No selection (\mu) is negligible Density homogeneous and known (LE)</td>
<td>Sample of mother plants and associated seeds One sampling event</td>
<td>Upon request</td>
<td>53-56</td>
</tr>
<tr>
<td>Distribution of lineages</td>
<td>(\sigma^2)</td>
<td>Discrete or continuous</td>
<td>Equilibrium</td>
<td>Haplotype</td>
<td>No selection Valid molecular clock</td>
<td>Sample of individuals in one or a set of populations One sampling event</td>
<td>Upon request</td>
<td>57(i)</td>
</tr>
<tr>
<td>Isolation by distance</td>
<td>(\sigma^2)</td>
<td>Discrete or continuous</td>
<td>Equilibrium</td>
<td>Multilocus genotypes</td>
<td>No selection (\mu) is negligible Density homogeneous and known (LE)</td>
<td>Sample of individuals in one or a set of populations One sampling event</td>
<td>GENEPOP SPAGEDI(h)</td>
<td>2, 58-62</td>
</tr>
<tr>
<td>Clines</td>
<td>(\sigma^2)</td>
<td>Discrete</td>
<td>Equilibrium</td>
<td>Multilocus genotypes</td>
<td>Loci under selection or linked to selected genes Recombination rate known</td>
<td>Sample of individuals in a set of populations One sampling event</td>
<td>63-65</td>
<td></td>
</tr>
<tr>
<td>Parentage</td>
<td>Discrete distances</td>
<td>Continuous</td>
<td>Single generation</td>
<td>Multilocus genotypes</td>
<td>Sample of individuals in focal population One sampling event After dispersal</td>
<td>Many softwares available for parentage analysis(l)</td>
<td>66-69</td>
<td></td>
</tr>
</tbody>
</table>

\(a\) Method parameter

\(b\) Time scale

\(c\) Data

\(d\) Assumptions

\(e\) Sampling scheme

\(f\) Software

\(g\) Ref.
Footnotes

a- divergence models were developed to assess whether shared polymorphism results from gene flow among recently diverged species or populations, or from conserved ancestral polymorphism. They are all restricted to the analysis of two populations only.
b- Equilibrium means here that dispersal parameters are assumed to be constant through time (although other parameters may be allowed to vary). These methods therefore deliver estimates that integrate migration movements over a large number of generations and may not depict current dispersal patterns if the equilibrium assumption is violated. By contrast, single- or few generations refer to methods delivering dispersal estimates that are valid only for the sampled generations.
c- Multilocus genotypes are classically obtained from unlinked codominant genetic markers (e.g. microsatellites, SNPs). Listed references indicate whether dominant markers (e.g. AFLPs, RAPDs) may be used in some cases (refer to original references for information on the best choice of genetic markers). Haplotypes are obtained by sequencing clonally inherited DNA (e.g. chloroplastic or mitochondrial DNA, Y and Z chromosomes). Further assumptions regarding selection or mutation model are listed in the "Assumptions" column.
d- Island model includes: constant and equally-sized panmictic populations made of N diploid hermaphrodites, immigrants come with equal probability from all other populations, no selection; Island migration model refers only to constant and equal $m_r$ for each population, with immigrants coming with equal probability from all other populations; $s = \text{selection coefficient}; \mu = \text{mutation rate}; \text{LE} = \text{linkage equilibrium between loci within populations}, \text{IAM} = \text{infinite alleles or infinite sites model}, \text{KAM} = \text{K-allele model}, \text{GTR} = \text{general time reversible substitution model}$
e- The timing of sampling regarding the life-cycle of the species (i.e. pre- vs. post-dispersal sampling) is indicated when relevant.
f- non-exhaustive list of softwares. Additional information may be found in 70. Upon request means that relevant softwares are available directly from the authors of described methods.
g- non-exhaustive list of references. Additional references will be found in relevant sections of the text.
h- Many other softwares (partly reviewed in 70) which allow performing regression analyses and Mantel tests may be used.
i- see 71 for a review
j- Method not presented in the main text


