**Appendix I. Population genetic analyses of *Scotonycteris* populations under migrate-n**

**Estimates of population sizes (*Θ*) and migration rates (*Nem*) between four populations of *Scotonycteris*.**

|  |  |  |
| --- | --- | --- |
| **Parameter** | **Mode** | **95% credibility interval** |
| *Θ*1 | 0.0016 | [0.0000–0.0032] |
| *Θ*2 | 0.0024 | [0.0004–0.0042] |
| *Θ*3 | 0.0013 | [0.0000–0.0030] |
| *Θ*4 | 0.0007 | [0.0000–0.0025] |
| *Nem* 2→1 | 0.020 | [0.000–0.161] |
| *Nem* 3→1 | 0.009 | [0.000–0.117] |
| *Nem* 4→1 | 0.008 | [0.000–0.147] |
| *Nem* 1→2 | 0.020 | [0.000–0.205] |
| *Nem* 3→2 | 0.017 | [0.000–0.141] |
| *Nem* 4→2 | 0.501 | [0.027–1.036] |
| *Nem* 1→3 | 0.017 | [0.000–0.200] |
| *Nem* 2→3 | 0.019 | [0.000–0.245] |
| *Nem* 4→3 | 0.012 | [0.000–0.179] |
| *Nem* 1→4 | 0.006 | [0.000–0.103] |
| *Nem* 2→4 | 0.014 | [0.000–0.253] |
| *Nem* 3→4 | 0.003 | [0.000–0.078] |

1: Cameroon; 2: eastern Democratic Republic of the Congo;

3: Upper Guinea; 4: western Equatorial Africa.

**Model selection between eastern DRC and western Equatorial Africa (WEA) populations of *Scotonycteris* (method as described in Beerli & Palczewski, 2010).**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Bezier approximation score** | **log Bayes Factors** | **Model choice** | **Model probability** |
| Full (4 param.) | –13,681.82 | –32.09 | 3 | 0.00 |
| Same population (1 param.) | –13,682.74 | –33.01 | 4 | 0.00 |
| Migration from DRC to WEA (3 param.) | –13,657.31 | –7.58 | 2 | 0.00 |
| Migration from WEA to DRC (3 param.) | –13,649.73 | 0 | 1 | 1.00 |