

Solving the genetic specimen sample size problem for
DNA barcoding with a local search optimization
algorithm

Supplementary Information

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Figures

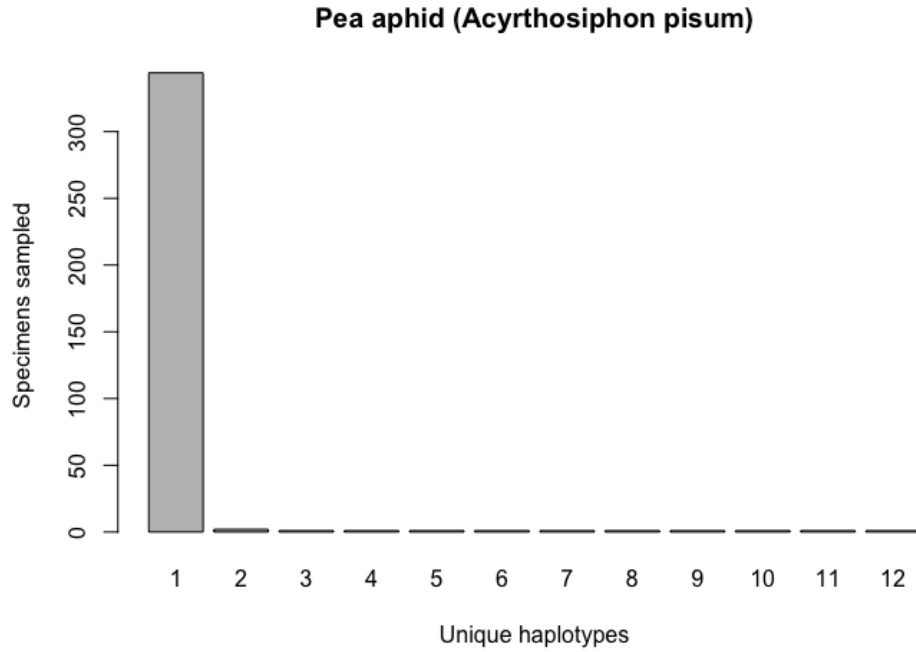


Figure 1: Initial haplotype frequency distribution for $N = 356$ high-quality Pea aphid (*Acyrtosiphon pisum*) COI barcode sequences obtained from BOLD. This species displays a highly-skewed pattern of observed haplotype variation, Haplotype 1 accounts for *c.* 96.6% (344/356) of all sampled records.

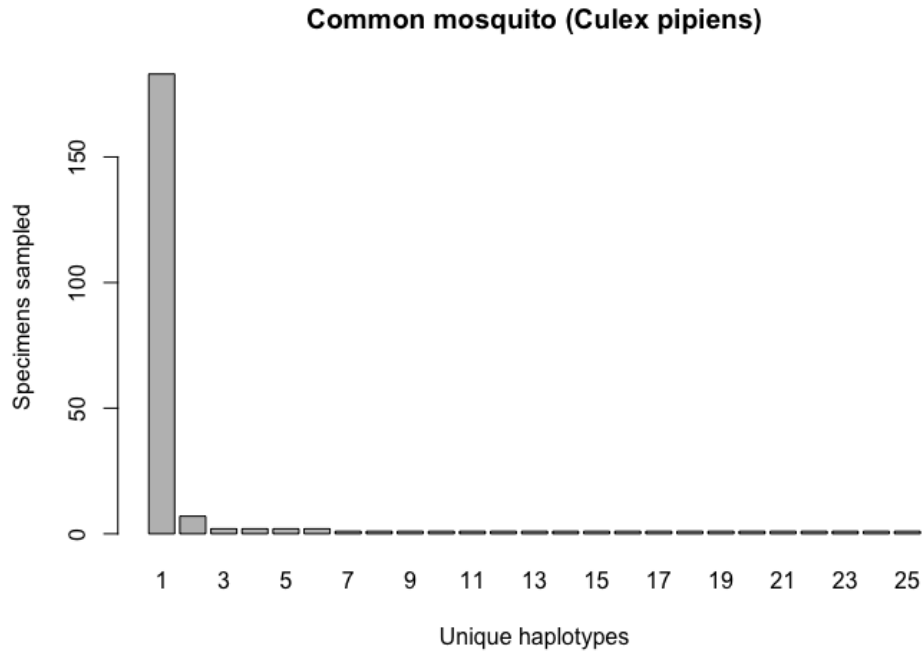


Figure 2: Initial haplotype frequency distribution for $N = 217$ high-quality Common mosquito (*Culex pipiens*) COI barcode sequences obtained from BOLD. In this species, Haplotype 1 accounts for *c.* 84.3% (183/217) of all sampled records.

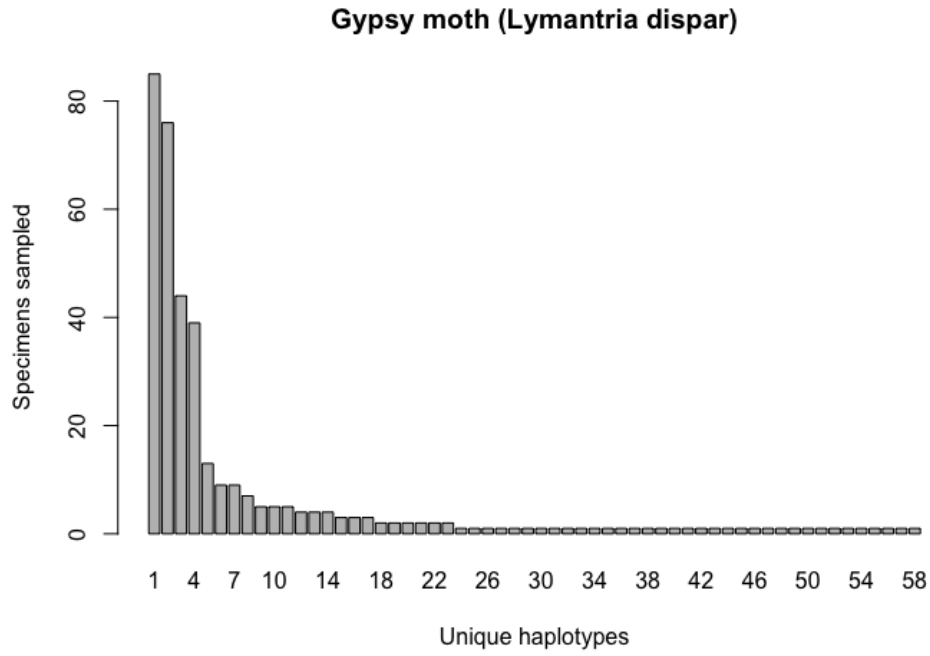


Figure 3: Initial haplotype frequency distribution for $N = 365$ high-quality Gypsy moth (*Lymantria dispar*) COI barcode sequences obtained from BOLD. In this species, Haplotypes 1-5 account for *c.* 70.4% (257/365) of all sampled records.

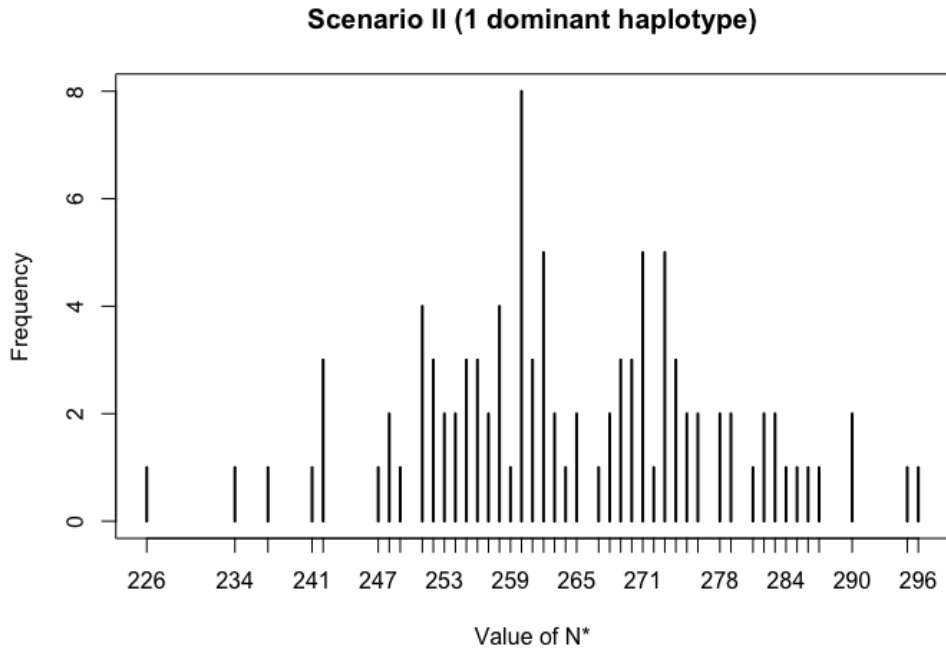


Figure 4: Frequency plot showing all located local optima and the number of times each was found by HACSim for Scenario II (1 dominant haplotype).

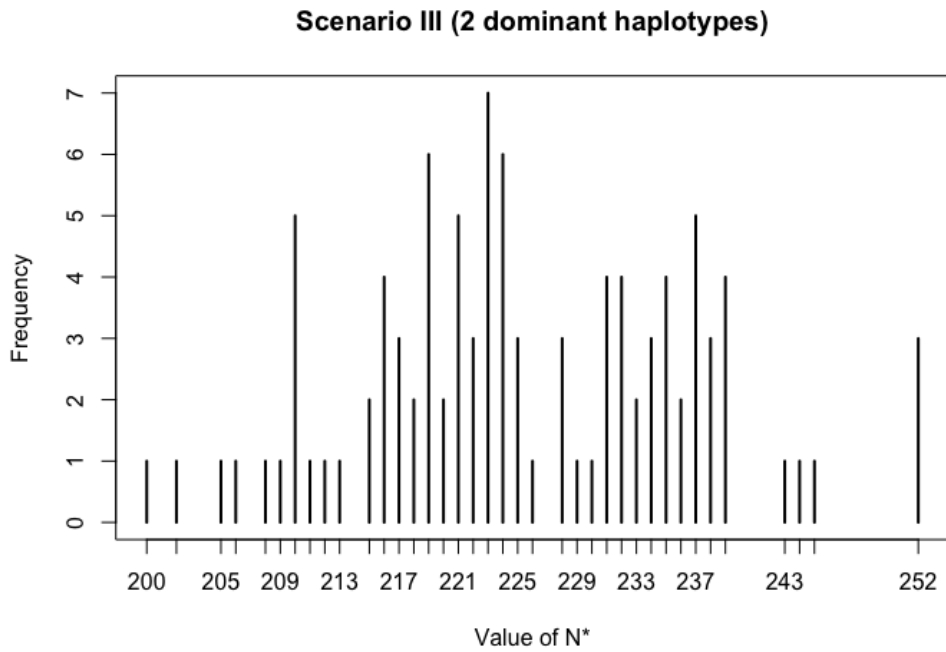


Figure 5: Frequency plot showing all located local optima and the number of times each was found by HACSim for Scenario III (2 dominant haplotypes).

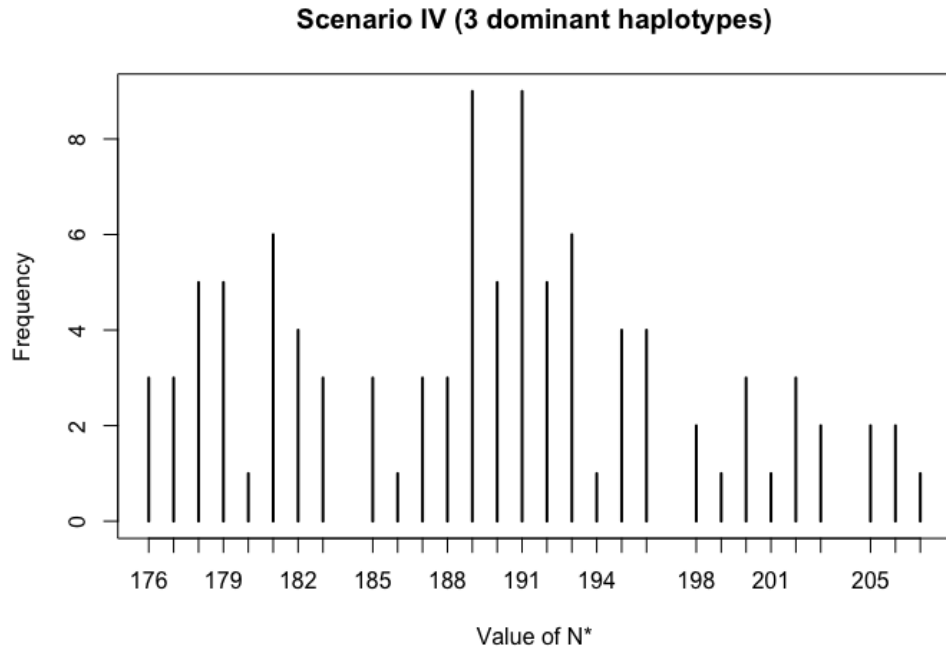


Figure 6: Frequency plot showing all located local optima and the number of times each was found by HACSim for Scenario IV (3 dominant haplotypes).

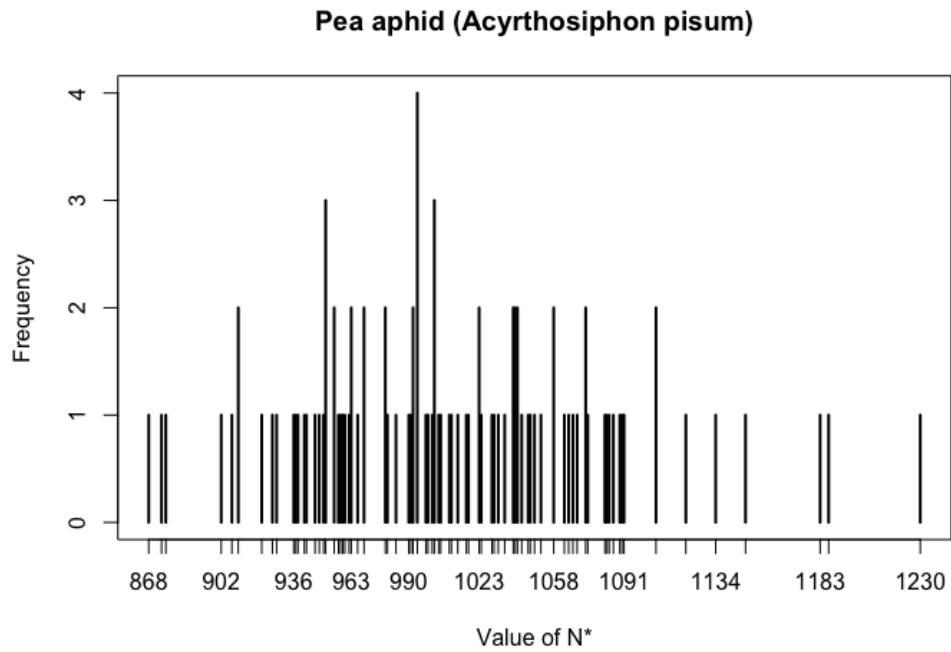


Figure 7: Frequency plot showing all located local optima and the number of times each was found by HACSim for Pea aphid (*Acyrtosiphon pisum*).

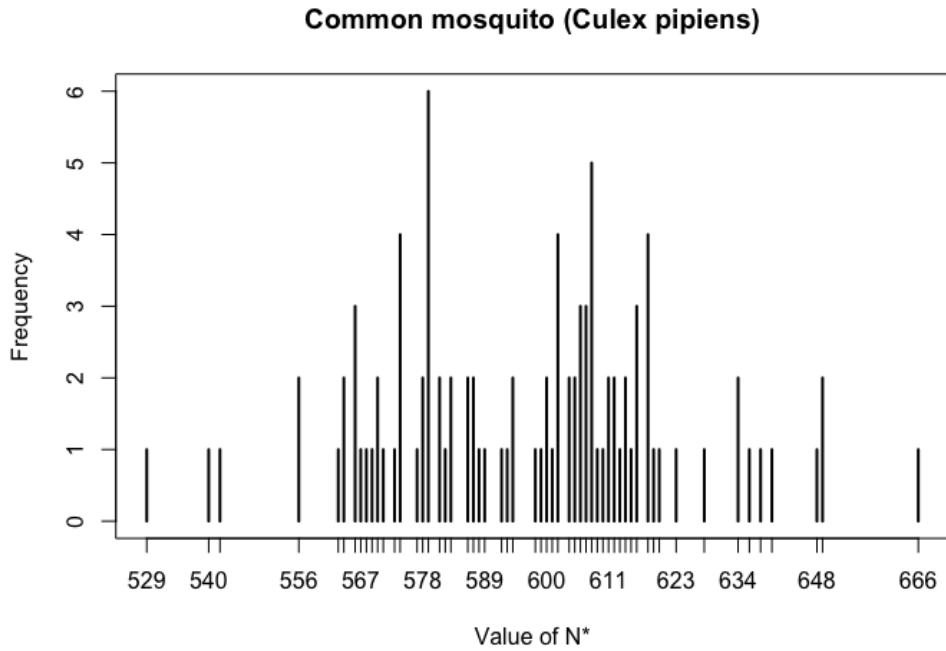


Figure 8: Frequency plot showing all located local optima and the number of times each was found by HACSim for Common mosquito (*Culex pipiens*).

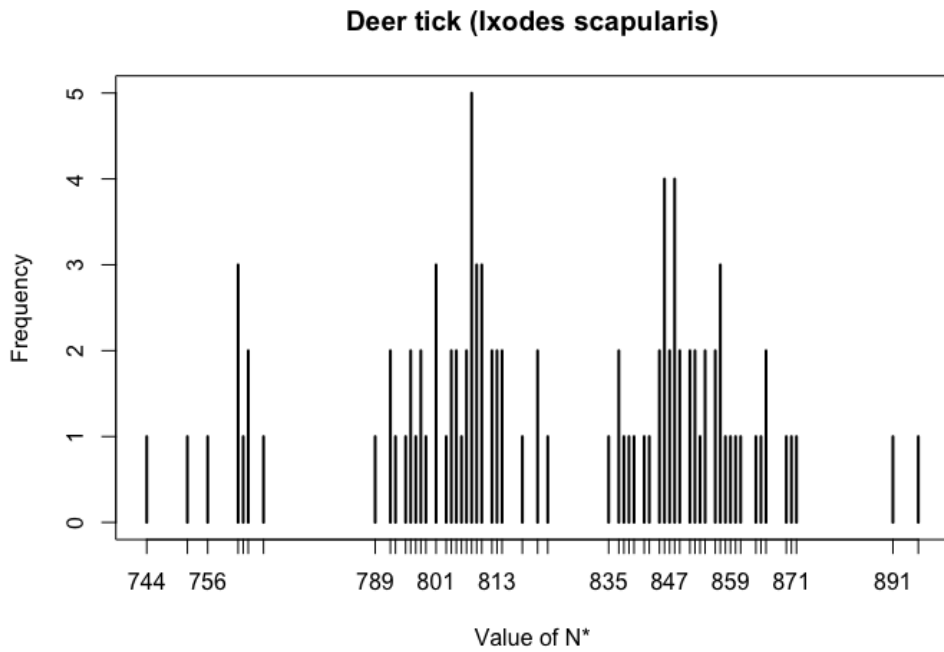


Figure 9: Frequency plot showing all located local optima and the number of times each was found by HACSim for Deer tick (*Ixodes scapularis*).

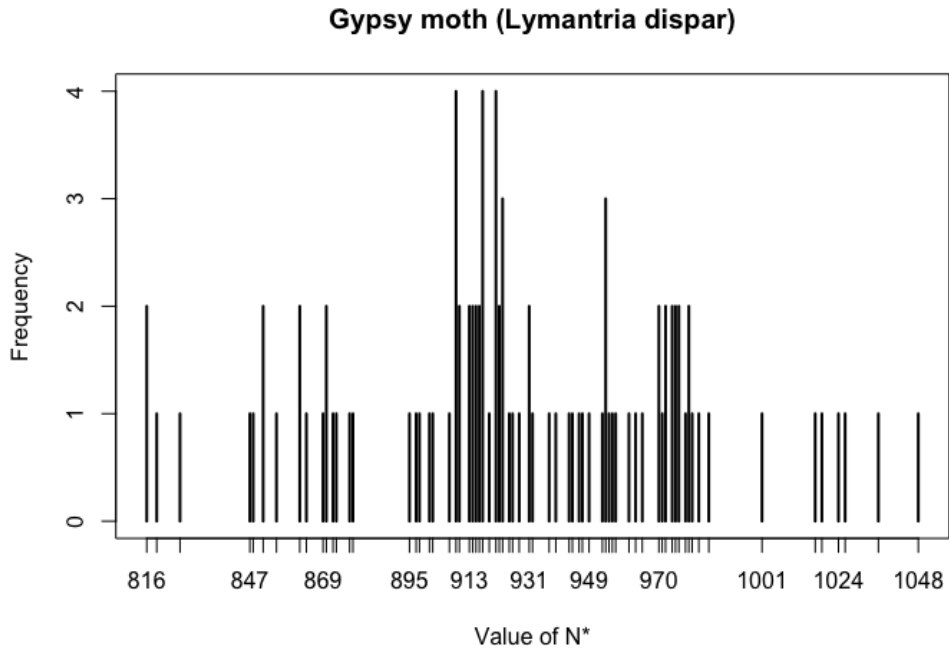


Figure 10: Frequency plot showing all located local optima and the number of times each was found by HACSim for Gypsy moth (*Lymantria dispar*).

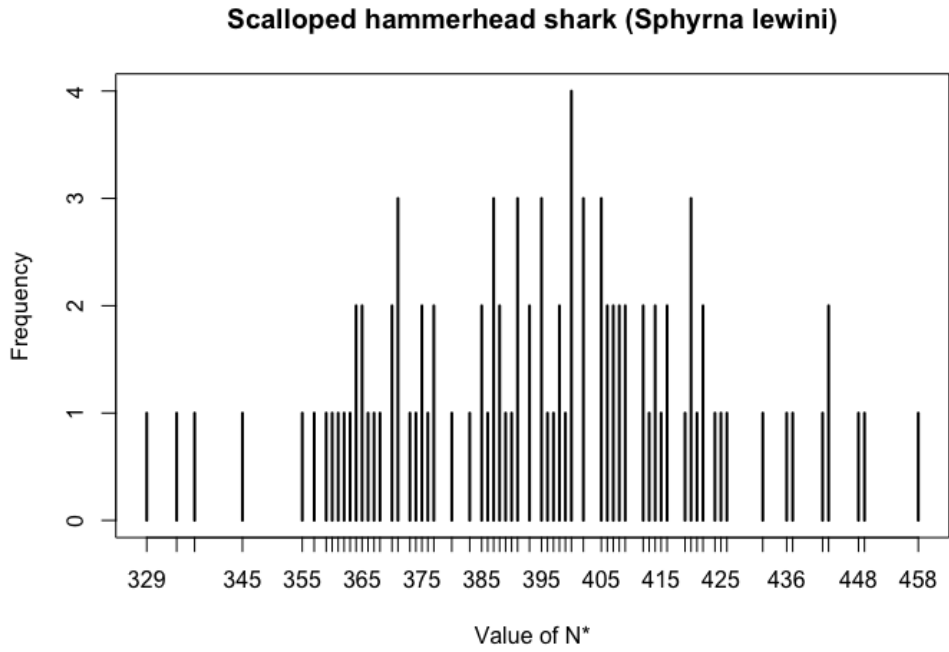


Figure 11: Frequency plot showing all located local optima and the number of times each was found by HACSim for Scalloped hammerhead shark (*Sphyrna lewini*).

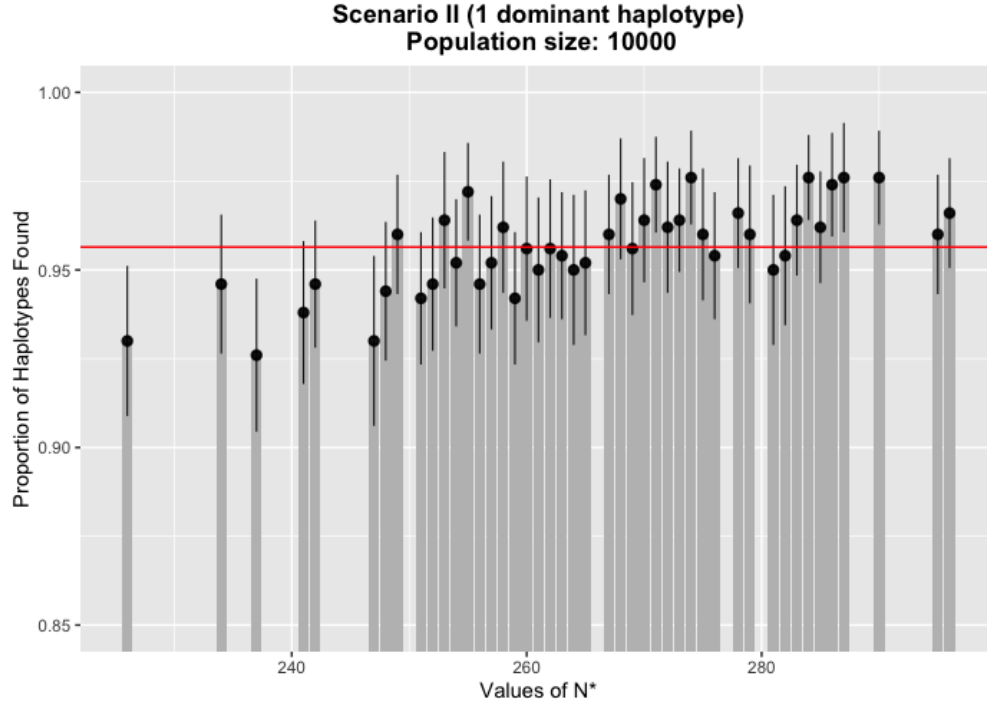


Figure 12: Plot showing all located local optima and the proportion of observed haplotypes captured for Scenario II (1 dominant haplotype) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` based on the number of local optima and holds no additional meaning in the context of this study.

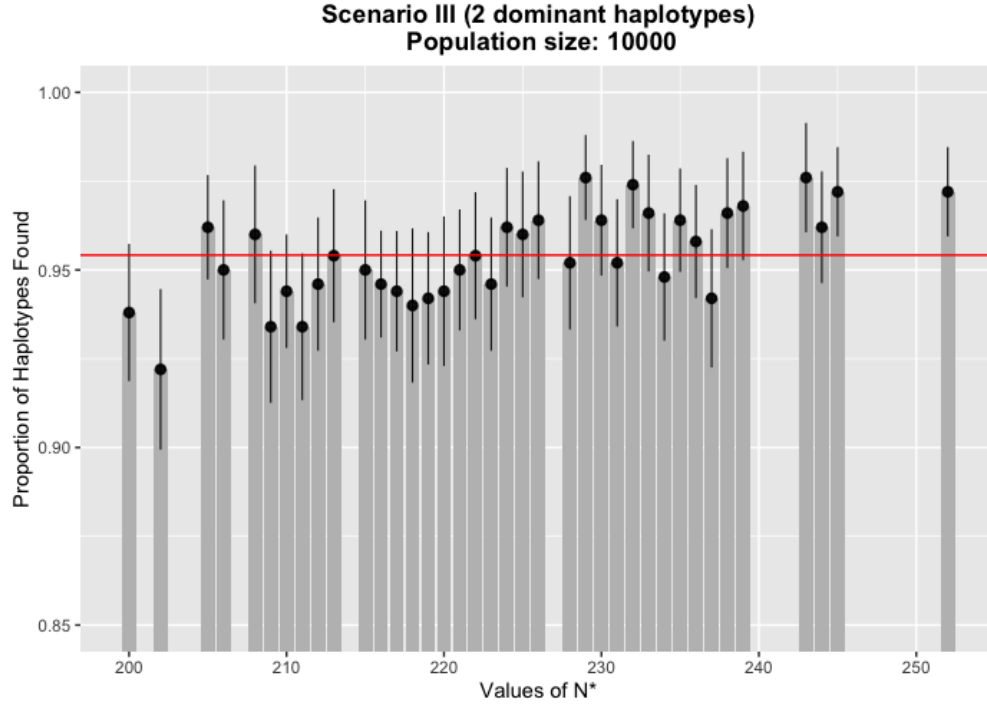


Figure 13: Plot showing all located local optima and the proportion of observed haplotypes captured for Scenario III (2 dominant haplotypes) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` based on the number of local optima and holds no additional meaning in the context of this study.

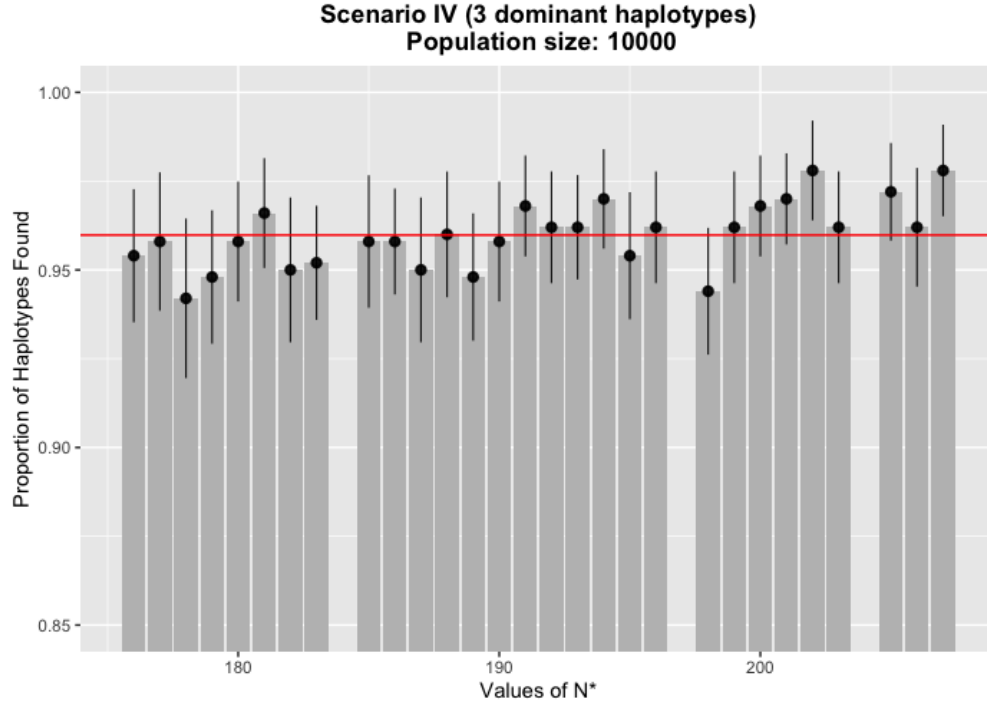


Figure 14: Plot showing all located local optima and the proportion of observed haplotypes captured for Scenario IV (3 dominant haplotypes) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` based on the number of local optima and holds no additional meaning in the context of this study.

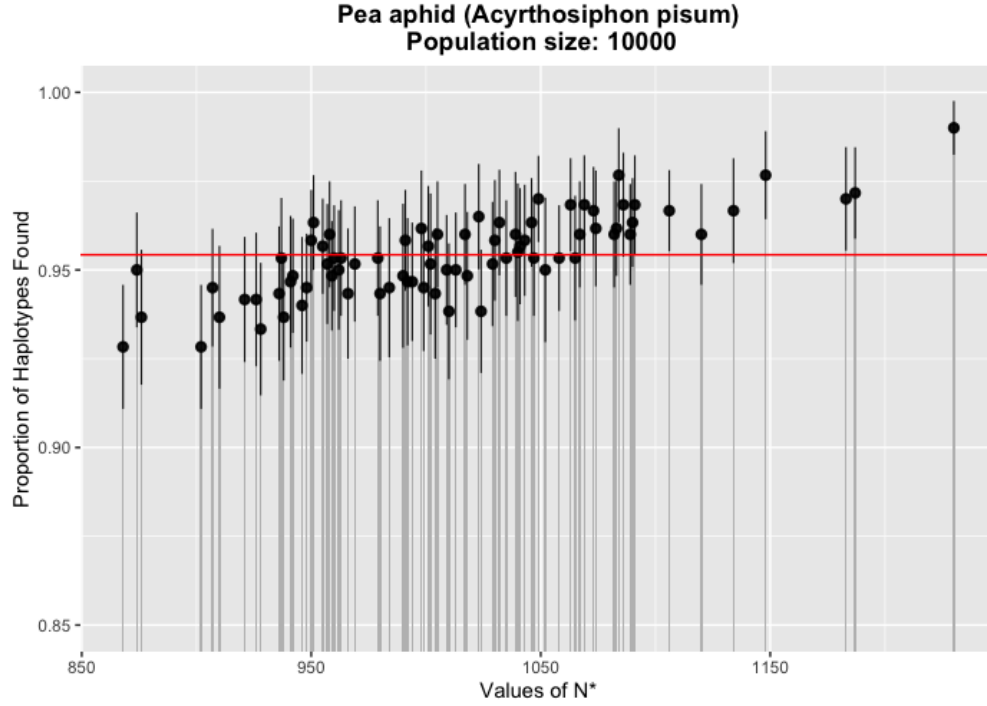


Figure 15: Plot showing all located local optima and the proportion of observed haplotypes captured for Pea aphid (*A. pisum*) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` based on the number of local optima and holds no additional meaning in the context of this study.

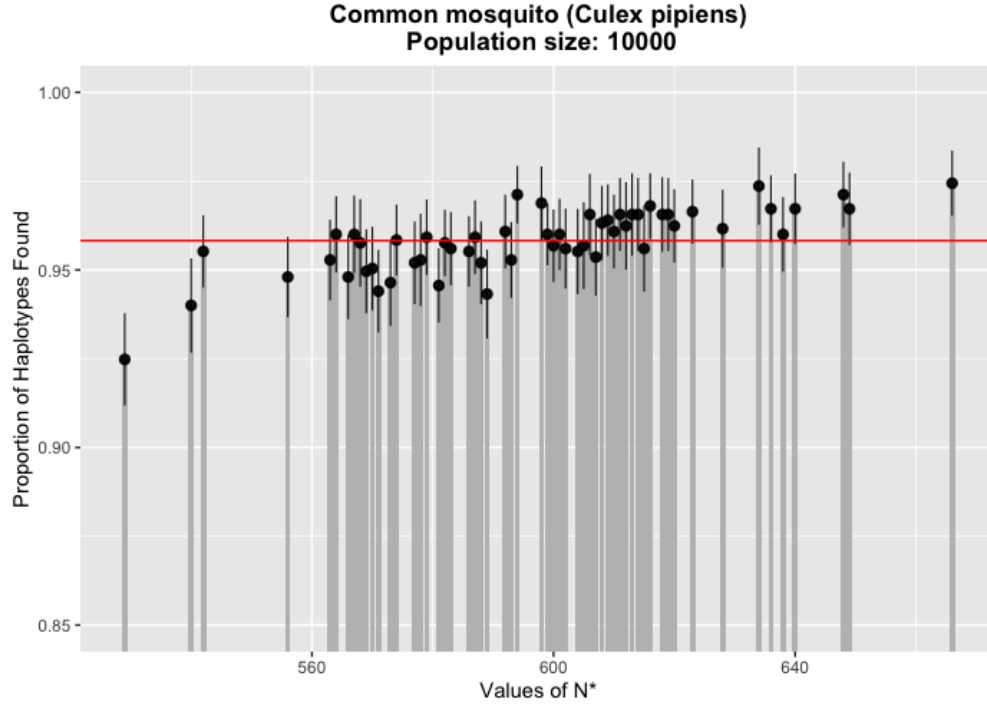


Figure 16: Plot showing all located local optima and the proportion of observed haplotypes captured for Common mosquito (*C. pipiens*) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` based on the number of local optima and holds no additional meaning in the context of this study.

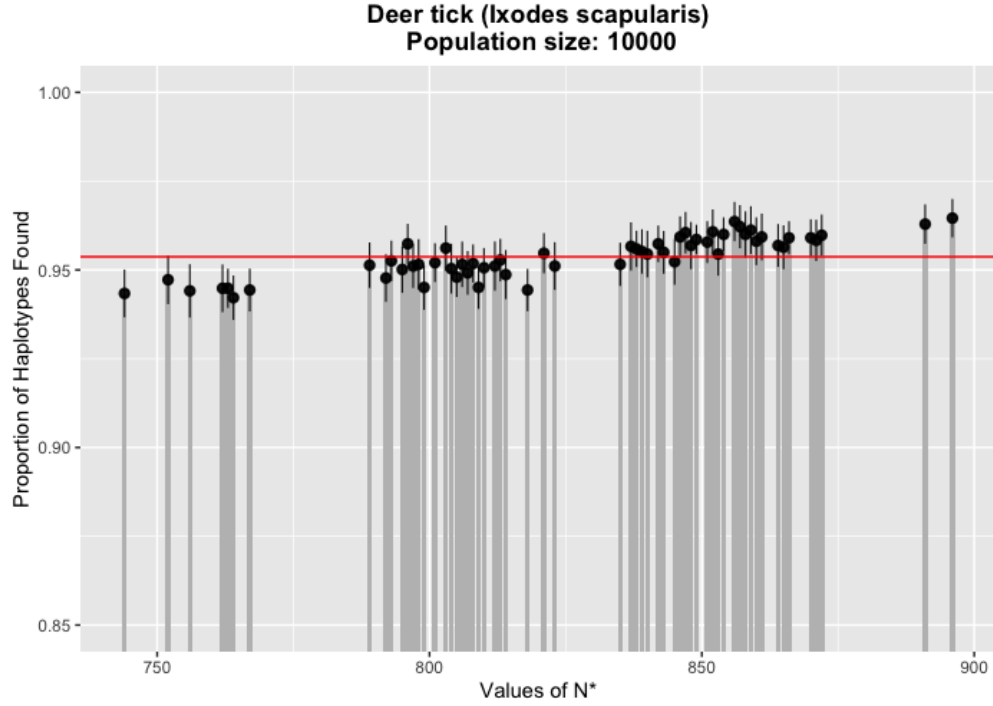


Figure 17: Plot showing all located local optima and the proportion of observed haplotypes captured for Deer tick (*I. scapularis*) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` based on the number of local optima and holds no additional meaning in the context of this study.

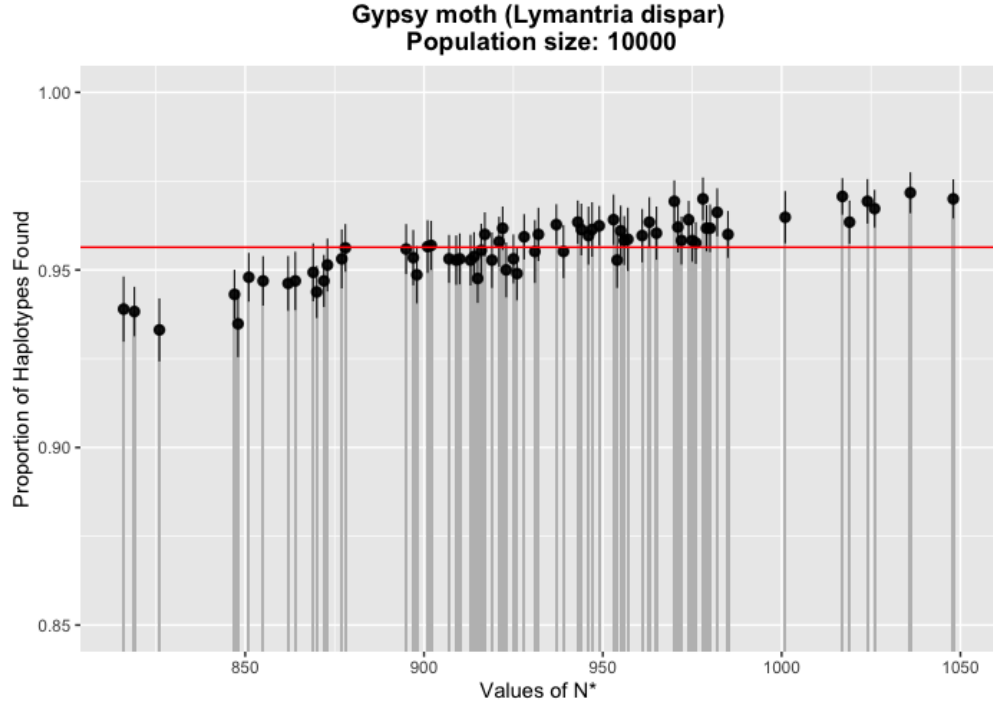


Figure 18: Plot showing all located local optima and the proportion of observed haplotypes captured for Gypsy moth (*L. dispar*) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` and thus holds no additional meaning in the context of this study.

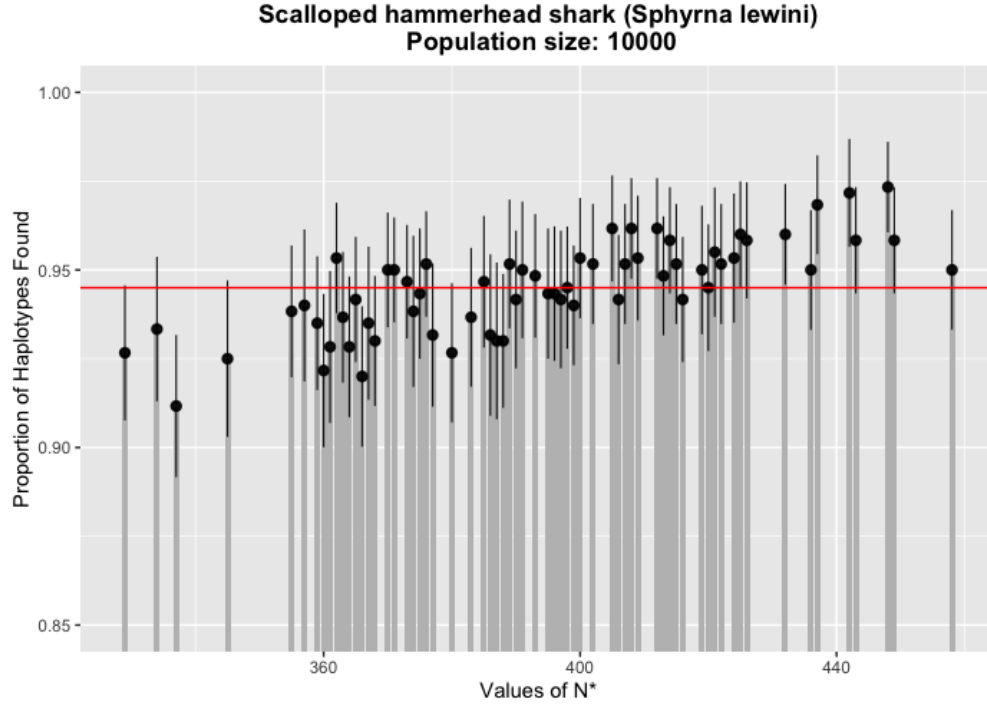


Figure 19: Plot showing all located local optima and the proportion of observed haplotypes captured for Scalloped hammerhead shark (*S. lewini*) with 95% confidence intervals for a population size of 10000. The mean proportion across 50 replications is depicted as a black dot. The mean proportion across all located local optima is displayed as a solid red horizontal line. The thickness of displayed grey error bars is a construct of `ggplot2` and thus holds no additional meaning in the context of this study.

Tables

p = 0.80

Table 1: Mean proportion of observed unique haplotypes found over 50 replications of the simulation study for hypothetical species. In all cases, **HACSim** was run 100 times. Estimates correspond to the solid red horizontal lines depicted in confidence interval plots found within and **Supplemental Information** accompanying the present article.

| Scenario | Pop. size | <i>R</i> Mean | <i>R</i> Range | <i>R</i> Std. dev. |
|----------|-----------|---------------|----------------|--------------------|
| II | 1000 | 0.878 | 0.840-0.932 | 0.03148935 |
| II | 10000 | 0.8648 | 0.812-0.910 | 0.02980922 |
| II | 100000 | 0.8424 | 0.798-0.900 | 0.03256475 |
| II | 10000000 | 0.8396 | 0.794-0.894 | 0.0341304 |
| III | 1000 | 0.8493333 | 0.764-0.886 | 0.03029951 |
| III | 10000 | 0.851 | 0.770-0.892 | 0.03328663 |
| III | 100000 | 0.8441667 | 0.768-0.864 | 0.0269202 |
| III | 10000000 | 0.8365 | 0.784-0.868 | 0.02419805 |
| IV | 1000 | 0.822 | 0.822-0.822 | N/A |
| IV | 10000 | 0.858 | 0.858-0.858 | N/A |
| IV | 100000 | 0.814 | 0.814-0.814 | N/A |
| IV | 10000000 | 0.858 | 0.858-0.858 | N/A |

Table 2: Mean proportion of observed unique haplotypes found over 50 replications of the simulation study for real species. In all cases, HACSIm was run 100 times. Estimates correspond to the solid red horizontal lines depicted in confidence interval plots found within the **Supplemental Information** accompanying the present article.

| Species | Pop. size | R Mean | R Range | R Std. dev. |
|--|-----------|-----------|---------------------|-------------|
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 1000 | 0.8965344 | 0.8366667-0.96 | 0.03823655 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 10000 | 0.8317196 | 0.765-0.895 | 0.03675206 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 100000 | 0.8342857 | 0.7616667-0.8933333 | 0.03595436 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 1000000 | 0.8315873 | 0.7733333-0.8966667 | 0.03537615 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 1000 | 0.8322963 | 0.7840000-0.8906667 | 0.03074708 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 10000 | 0.8249259 | 0.7853333-0.8746667 | 0.02958819 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 100000 | 0.8384074 | 0.7973333-0.8946667 | 0.03157306 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 1000000 | 0.8373333 | 0.7773333-0.8973333 | 0.03067412 |
| Common mosquito (<i>Culex pipiens</i>) | 1000 | 0.8189943 | 0.7816-0.8592 | 0.0270726 |
| Common mosquito (<i>Culex pipiens</i>) | 10000 | 0.8341943 | 0.7816-0.8856 | 0.03253051 |
| Common mosquito (<i>Culex pipiens</i>) | 100000 | 0.83312 | 0.7816-0.8864 | 0.02916385 |
| Common mosquito (<i>Culex pipiens</i>) | 1000000 | 0.8349714 | 0.7928-0.8792 | 0.02954371 |
| Deer tick (<i>Ixodes scapularis</i>) | 1000 | 0.8416466 | 0.7857831-0.8525301 | 0.01804434 |
| Deer tick (<i>Ixodes scapularis</i>) | 10000 | 0.8518875 | 0.8084337-0.8612048 | 0.0146289 |
| Deer tick (<i>Ixodes scapularis</i>) | 100000 | 0.8463052 | 0.8028916-0.8575904 | 0.01411039 |
| Deer tick (<i>Ixodes scapularis</i>) | 1000000 | 0.8440964 | 0.8033735-0.8590361 | 0.01460819 |
| Gypsy moth (<i>Lymantria dispar</i>) | 1000 | 0.8401799 | 0.8289655-0.8551724 | 0.007725896 |
| Gypsy moth (<i>Lymantria dispar</i>) | 10000 | 0.8029085 | 0.7906897-0.8172414 | 0.007518086 |
| Gypsy moth (<i>Lymantria dispar</i>) | 100000 | 0.8253523 | 0.8075862 0.84 | 0.008070782 |
| Gypsy moth (<i>Lymantria dispar</i>) | 1000000 | 0.8274363 | 0.8151724-0.8444828 | 0.006767465 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 1000 | 0.8033333 | 0.7683333-0.8266667 | 0.02232962 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 10000 | 0.8456667 | 0.8116667-0.8633333 | 0.02046676 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 100000 | 0.8386667 | 0.8083333-0.865 | 0.02283395 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 1000000 | 0.9314815 | 0.90-0.96 | 0.01565895 |

Table 3: Bonferroni-corrected Dunn’s post-hoc test results at the 3.33% significance level for comparison of population size *versus* haplotype frequency distribution in hypothetical species. **Note:** KW test statistics, p -values and statistical significance for Scenario I could not be calculated.

| Scenario | Pop. size pairing | Test statistic | p -value | Significant? |
|----------|-------------------|----------------|------------|--------------|
| II | 1000/10000 | 1.126447 | 0.7799 | No |
| II | 1000/100000 | 3.025414 | 0.0074 | Yes |
| II | 1000/10000000 | 3.239814 | 0.0036 | Yes |
| II | 10000/100000 | 1.898966 | 0.1727 | No |
| II | 10000/10000000 | 2.113366 | 0.1037 | No |
| II | 100000/10000000 | 0.214399 | 1 | No |
| III | 1000/10000 | -0.167851 | 1 | No |
| III | 1000/100000 | 0.634915 | 1 | No |
| III | 1000/10000000 | 1.517958 | 0.3871 | No |
| III | 10000/100000 | 0.802766 | 1 | No |
| III | 10000/10000000 | 1.685809 | 0.2755 | No |
| III | 100000/10000000 | 0.883043 | 1 | No |
| IV | 1000/10000 | -0.866025 | 1 | No |
| IV | 1000/100000 | 0.577350 | 1 | No |
| IV | 1000/10000000 | -0.866025 | 1 | No |
| IV | 10000/100000 | 1.443375 | 0.4467 | No |
| IV | 10000/10000000 | 0 | 1 | No |
| IV | 100000/10000000 | -1.443375 | 0.4467 | No |

Table 4: Bonferroni-corrected Dunn’s post-hoc test results at the 3.33% significance level for comparison of population size *versus* haplotype frequency distribution in real species.

| Species | Pop. size pairing | Test statistic | <i>p</i> -value | Significant? |
|------------------------|-------------------|----------------|-----------------|--------------|
| <i>A. pisum</i> | 1000/10000 | 7.084884 | 0 | Yes |
| <i>A. pisum</i> | 1000/100000 | 6.743842 | 0 | Yes |
| <i>A. pisum</i> | 1000/10000000 | 7.127668 | 0 | Yes |
| <i>A. pisum</i> | 10000/100000 | -0.341042 | 1 | No |
| <i>A. pisum</i> | 10000/10000000 | 0.042783 | 1 | No |
| <i>A. pisum</i> | 100000/10000000 | 0.383825 | 1 | No |
| <i>C. clupeaformis</i> | 1000/10000 | 1.250438 | 0.6334 | No |
| <i>C. clupeaformis</i> | 1000/100000 | -0.873187 | 1 | No |
| <i>C. clupeaformis</i> | 1000/10000000 | -0.897207 | 1 | No |
| <i>C. clupeaformis</i> | 10000/100000 | -2.123625 | 0.1011 | No |
| <i>C. clupeaformis</i> | 10000/10000000 | -2.147645 | 0.0952 | No |
| <i>C. clupeaformis</i> | 100000/10000000 | -0.024019 | 1 | No |
| <i>C. pipiens</i> | 1000/10000 | -2.667296 | 0.0229 | Yes |
| <i>C. pipiens</i> | 1000/100000 | -2.577403 | 0.0299 | Yes |
| <i>C. pipiens</i> | 1000/10000000 | -2.830870 | 0.0139 | Yes |
| <i>C. pipiens</i> | 10000/100000 | 0.089892 | 1 | No |
| <i>C. pipiens</i> | 10000/10000000 | -0.163574 | 1 | No |
| <i>C. pipiens</i> | 100000/10000000 | -0.253466 | 1 | No |
| <i>I. scapularis</i> | 1000/10000 | -2.895996 | 0.0113 | Yes |
| <i>I. scapularis</i> | 1000/100000 | -1.196331 | 0.6947 | No |
| <i>I. scapularis</i> | 1000/10000000 | -0.372029 | 1 | No |
| <i>I. scapularis</i> | 10000/100000 | 1.699665 | 0.2676 | No |
| <i>I. scapularis</i> | 10000/10000000 | 2.523967 | 0.0348 | No |
| <i>I. scapularis</i> | 100000/10000000 | 0.824301 | 1 | No |
| <i>L. dispar</i> | 1000/10000 | 8.129073 | 0 | Yes |
| <i>L. dispar</i> | 1000/100000 | 3.854682 | 0.0003 | Yes |
| <i>L. dispar</i> | 1000/10000000 | 3.446020 | 0.0017 | Yes |
| <i>L. dispar</i> | 10000/100000 | -4.274390 | 0.0001 | Yes |
| <i>L. dispar</i> | 10000/10000000 | -4.683053 | 0 | Yes |
| <i>L. dispar</i> | 100000/10000000 | -0.408662 | 1 | No |
| <i>S. lewini</i> | 1000/10000 | -2.008237 | 0.1339 | No |
| <i>S. lewini</i> | 1000/100000 | -1.606590 | 0.3244 | No |
| <i>S. lewini</i> | 1000/10000000 | -2.811532 | 0.0148 | Yes |
| <i>S. lewini</i> | 10000/100000 | 0.401647 | 1 | No |
| <i>S. lewini</i> | 10000/10000000 | -0.803295 | 1 | No |
| <i>S. lewini</i> | 100000/10000000 | -1.204942 | 0.6847 | No |

Table 5: Characteristics of local optima found by HACSIm for hypothetical species.

| Scenario | No. optima | N^* range | N^* std. dev. | Highest mode(s) | Highest mode freq. |
|----------|------------|-------------|-----------------|-----------------|--------------------|
| II | 20 | 137-182 | 10.94328 | 143 | 18 |
| III | 12 | 100-136 | 3.620927 | 130 | 22 |
| IV | 1 | 100-100 | 0 | 100 | 100 |

Table 6: Characteristics of local optima found by HACSIm for real species. For some species, distinct optima were located for different population sizes.

| Species | No. optima | N^* range | N^* std. dev. | Highest mode(s) | Highest mode freq. |
|-------------------------|------------|-------------|-----------------|-----------------|--------------------|
| <i>A. pisum</i> | 63 | 499-708 | 66.0065 | 647 | 4 |
| <i>C. clupearformis</i> | 36 | 309-418 | 29.27554 | 325 | 12 |
| <i>C. pipiens</i> | 35 | 301-399 | 32.30498 | 314 | 8 |
| <i>I. scapularis</i> | 12 | 349-447 | 34.61179 | 439 | 18 |
| <i>L. dispar</i> | 23 | 468-492 | 5.241212 | 486 | 10 |
| <i>S. lewini</i> | 5 | 171-217 | 13.83943 | 171 | 89 |

Table 7: Coverage probabilities and 95% Clopper-Pearson confidence intervals for hypothetical species for $p = 0.80$ across all assessed population sizes. Calculated probabilities are based on the number of observed local optima found using **HACSim**. * Scenario IV comprised only a single local optimum.

| Scenario | Pop. size | Coverage prob. | 95% Exact binomial CI | Coverage type |
|----------|-----------|----------------|-----------------------|---------------|
| II | 1000 | 1 | (0.8315665, 1) | conservative |
| II | 10000 | 1 | (0.8315665, 1) | conservative |
| II | 100000 | 1 | (0.8315665, 1) | conservative |
| II | 10000000 | 1 | (0.8315665, 1) | conservative |
| III | 1000 | 1 | (0.7353515, 1) | conservative |
| III | 10000 | 1 | (0.7353515, 1) | conservative |
| III | 100000 | 1 | (0.7353515, 1) | conservative |
| III | 10000000 | 1 | (0.7353515, 1) | conservative |
| IV* | 1000 | 1 | (0.025, 1) | conservative |
| IV | 10000 | 1 | (0.025, 1) | conservative |
| IV | 100000 | 1 | (0.025, 1) | conservative |
| IV | 10000000 | 1 | (0.025, 1) | conservative |

Table 8: Coverage probabilities and 95% Clopper-Pearson confidence intervals for real species for $p = 0.80$ across all assessed population sizes. Calculated probabilities are based on the number of observed local optima found using **HACSim**.

| Species | Pop. size | Coverage prob. | 95% Exact binomial CI | Coverage type |
|-------------------------|-----------|----------------|-----------------------|---------------|
| <i>A. pisum</i> | 1000 | 1 | (0.9431276, 1) | conservative |
| <i>A. pisum</i> | 10000 | 1 | (0.9431276, 1) | conservative |
| <i>A. pisum</i> | 100000 | 1 | (0.9431276, 1) | conservative |
| <i>A. pisum</i> | 10000000 | 1 | (0.9431276, 1) | conservative |
| <i>C. clupearformis</i> | 1000 | 1 | (0.9026062, 1) | conservative |
| <i>C. clupearformis</i> | 10000 | 1 | (0.9026062, 1) | conservative |
| <i>C. clupearformis</i> | 100000 | 1 | (0.9026062, 1) | conservative |
| <i>C. clupearformis</i> | 10000000 | 1 | (0.9026062, 1) | conservative |
| <i>C. pipiens</i> | 1000 | 1 | (0.8999676, 1) | conservative |
| <i>C. pipiens</i> | 10000 | 1 | (0.8999676, 1) | conservative |
| <i>C. pipiens</i> | 100000 | 1 | (0.8999676, 1) | conservative |
| <i>C. pipiens</i> | 10000000 | 1 | (0.8999676, 1) | conservative |
| <i>I. scapularis</i> | 1000 | 1 | (0.7353515, 1) | conservative |
| <i>I. scapularis</i> | 10000 | 1 | (0.7353515, 1) | conservative |
| <i>I. scapularis</i> | 100000 | 1 | (0.7353515, 1) | conservative |
| <i>I. scapularis</i> | 10000000 | 1 | (0.7353515, 1) | conservative |
| <i>L. dispar</i> | 1000 | 1 | (0.8518149, 1) | conservative |
| <i>L. dispar</i> | 10000 | 1 | (0.8518149, 1) | conservative |
| <i>L. dispar</i> | 100000 | 1 | (0.8518149, 1) | conservative |
| <i>L. dispar</i> | 10000000 | 1 | (0.8518149, 1) | conservative |
| <i>S. lewini</i> | 1000 | 1 | (0.4781762, 1) | conservative |
| <i>S. lewini</i> | 10000 | 1 | (0.4781762, 1) | conservative |
| <i>S. lewini</i> | 100000 | 1 | (0.4781762, 1) | conservative |
| <i>S. lewini</i> | 10000000 | 1 | (0.4781762, 1) | conservative |

p = 0.90

Table 9: Mean proportion of observed unique haplotypes found over 50 replications of the simulation study for hypothetical species. In all cases, **HACSim** was run 100 times. Estimates correspond to the solid red horizontal lines depicted in confidence interval plots found within **Supplemental Information** accompanying the present article.

| Scenario | Pop. size | <i>R</i> Mean | <i>R</i> Range | <i>R</i> Std. dev. |
|-----------------|------------------|----------------------|-----------------------|---------------------------|
| II | 1000 | 0.9053333 | 0.852-0.948 | 0.01919418 |
| II | 10000 | 0.9193939 | 0.870-0.962 | 0.02000303 |
| II | 100000 | 0.9129091 | 0.864-0.946 | 0.01890166 |
| II | 10000000 | 0.9130303 | 0.864-0.940 | 0.01763605 |
| III | 1000 | 0.9468333 | 0.918-0.964 | 0.01410417 |
| III | 10000 | 0.9144167 | 0.874-0.950 | 0.02036176 |
| III | 100000 | 0.9148333 | 0.876-0.950 | 0.01983336 |
| III | 10000000 | 0.9115833 | 0.862-0.944 | 0.02228651 |
| IV | 1000 | 0.8660909 | 0.822-0.900 | 0.02006159 |
| IV | 10000 | 0.9093636 | 0.874-0.930 | 0.01783935 |
| IV | 100000 | 0.9183636 | 0.896-0.950 | 0.01355955 |
| IV | 10000000 | 0.9133636 | 0.866-0.940 | 0.01685102 |

Table 10: Mean proportion of observed unique haplotypes found over 50 replications of the simulation study for real species. In all cases, HACSIm was run 100 times. Estimates correspond to the solid red horizontal lines depicted in confidence interval plots found within the **Supplemental Information** accompanying the present article.

| Species | Pop. size | R Mean | R Range | R Std. dev. |
|--|-----------|-----------|---------------------|-------------|
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 1000 | 0.8937446 | 0.850-0.915 | 0.01309869 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 10000 | 0.8947836 | 0.8266667-0.9466667 | 0.02516662 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 100000 | 0.9008658 | 0.8283333-0.9466667 | 0.02355101 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 1000000 | 0.9051732 | 0.8316667-0.9466667 | 0.02243506 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 1000 | 0.9493771 | 0.9093333-0.9746667 | 0.01565928 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 10000 | 0.9177268 | 0.8760000-0.9506667 | 0.01989952 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 100000 | 0.9018798 | 0.8466667-0.9426667 | 0.02272721 |
| Lake whitefish (<i>Coregonus clupeaformis</i>) | 1000000 | 0.9094645 | 0.860-0.944 | 0.01890594 |
| Common mosquito (<i>Culex pipiens</i>) | 1000 | 0.9339833 | 0.9032-0.9592 | 0.01333865 |
| Common mosquito (<i>Culex pipiens</i>) | 10000 | 0.9128167 | 0.8832-0.9456 | 0.01534088 |
| Common mosquito (<i>Culex pipiens</i>) | 100000 | 0.9114667 | 0.8896-0.9416 | 0.01427876 |
| Common mosquito (<i>Culex pipiens</i>) | 1000000 | 0.9107833 | 0.8744-0.9448 | 0.01589668 |
| Deer tick (<i>Ixodes scapularis</i>) | 1000 | 0.9436145 | 0.9327711-0.9583133 | 0.008038651 |
| Deer tick (<i>Ixodes scapularis</i>) | 10000 | 0.9142972 | 0.9007229-0.9310843 | 0.008461128 |
| Deer tick (<i>Ixodes scapularis</i>) | 100000 | 0.9112115 | 0.8971084-0.9281928 | 0.00893221 |
| Deer tick (<i>Ixodes scapularis</i>) | 1000000 | 0.9110375 | 0.8978313-0.9265060 | 0.00824903 |
| Gypsy moth (<i>Lymantria dispar</i>) | 1000 | 0.9213282 | 0.9017241-0.94 | 0.01130016 |
| Gypsy moth (<i>Lymantria dispar</i>) | 10000 | 0.909387 | 0.8865517-0.9313793 | 0.01087714 |
| Gypsy moth (<i>Lymantria dispar</i>) | 100000 | 0.9100894 | 0.8903448-0.9320690 | 0.01193619 |
| Gypsy moth (<i>Lymantria dispar</i>) | 1000000 | 0.9108174 | 0.8868966-0.9306897 | 0.01150925 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 1000 | 0.935754 | 0.8966667-0.96 | 0.01433344 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 10000 | 0.8940873 | 0.8566667-0.9366667 | 0.01773106 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 100000 | 0.9107937 | 0.86-0.95 | 0.02057848 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 1000000 | 0.9073016 | 0.8533333-0.9483333 | 0.01848955 |

Table 11: Bonferroni-corrected Dunn’s post-hoc test results at the 1.67% significance level for comparison of population size *versus* haplotype frequency distribution in hypothetical species. **Note:** KW test statistics, p -values and statistical significance for Scenario I could not be calculated.

| Scenario | Pop. size pairing | Test statistic | p -value | Significant? |
|----------|-------------------|----------------|------------|--------------|
| II | 1000/10000 | -3.091851 | 0.0060 | Yes |
| II | 1000/100000 | -1.849633 | 0.1931 | No |
| II | 1000/10000000 | -1.703015 | 0.2657 | No |
| II | 10000/100000 | 1.242218 | 0.6425 | No |
| II | 10000/10000000 | 1.388835 | 0.4946 | No |
| II | 100000/10000000 | 0.146617 | 1 | No |
| III | 1000/10000 | 4.826797 | 0 | Yes |
| III | 1000/100000 | 4.803466 | 0 | Yes |
| III | 1000/10000000 | 5.104169 | 0 | Yes |
| III | 10000/100000 | -0.023330 | 1 | No |
| III | 10000/10000000 | 0.277372 | 1 | No |
| III | 100000/10000000 | 0.300702 | 1 | No |
| IV | 1000/10000 | -4.830426 | 0 | Yes |
| IV | 1000/100000 | -6.043938 | 0 | Yes |
| IV | 1000/10000000 | -5.317602 | 0 | Yes |
| IV | 10000/100000 | -1.213511 | 0.6748 | No |
| IV | 10000/10000000 | -0.487176 | 1 | No |
| IV | 100000/10000000 | 0.726335 | 1 | No |

Table 12: Bonferroni-corrected Dunn’s post-hoc test results at the 1.67% significance level for comparison of population size *versus* haplotype frequency distribution in real species.

| Species | Pop. size pairing | Test statistic | <i>p</i> -value | Significant? |
|------------------------|-------------------|----------------|-----------------|--------------|
| <i>A. pisum</i> | 1000/10000 | -1.031040 | 0.9076 | No |
| <i>A. pisum</i> | 1000/100000 | -2.658617 | 0.0235 | No |
| <i>A. pisum</i> | 1000/10000000 | -3.600946 | 0.0010 | Yes |
| <i>A. pisum</i> | 10000/100000 | -1.627577 | 0.3108 | No |
| <i>A. pisum</i> | 10000/10000000 | -2.569906 | 0.0305 | No |
| <i>A. pisum</i> | 100000/10000000 | -0.942329 | 1 | No |
| <i>C. clupeaformis</i> | 1000/10000 | 6.719296 | 0 | Yes |
| <i>C. clupeaformis</i> | 1000/100000 | 9.849622 | 0 | Yes |
| <i>C. clupeaformis</i> | 1000/10000000 | 8.381319 | 0 | Yes |
| <i>C. clupeaformis</i> | 10000/100000 | 3.130326 | 0.0052 | Yes |
| <i>C. clupeaformis</i> | 10000/10000000 | 1.662023 | 0.2895 | No |
| <i>C. clupeaformis</i> | 100000/10000000 | -1.468302 | 0.4261 | No |
| <i>C. pipiens</i> | 1000/10000 | 5.671734 | 0 | Yes |
| <i>C. pipiens</i> | 1000/100000 | 6.183339 | 0 | Yes |
| <i>C. pipiens</i> | 1000/10000000 | 6.301825 | 0 | Yes |
| <i>C. pipiens</i> | 10000/100000 | 0.511604 | 1 | No |
| <i>C. pipiens</i> | 10000/10000000 | 0.630090 | 1 | No |
| <i>C. pipiens</i> | 100000/10000000 | 0.118486 | 1 | No |
| <i>I. scapularis</i> | 1000/10000 | 6.461802 | 0 | Yes |
| <i>I. scapularis</i> | 1000/100000 | 7.737492 | 0 | Yes |
| <i>I. scapularis</i> | 1000/10000000 | 7.771397 | 0 | Yes |
| <i>I. scapularis</i> | 10000/100000 | 1.275690 | 0.6062 | No |
| <i>I. scapularis</i> | 10000/10000000 | 1.309595 | 0.5710 | No |
| <i>I. scapularis</i> | 100000/10000000 | 0.033905 | 1 | No |
| <i>L. dispar</i> | 1000/10000 | 4.818699 | 0 | Yes |
| <i>L. dispar</i> | 1000/100000 | 4.442226 | 0 | Yes |
| <i>L. dispar</i> | 1000/10000000 | 4.101167 | 0.0001 | Yes |
| <i>L. dispar</i> | 10000/100000 | -0.376472 | 1 | No |
| <i>L. dispar</i> | 10000/10000000 | -0.717531 | 1 | No |
| <i>L. dispar</i> | 100000/10000000 | -0.341058 | 1 | No |
| <i>S. lewini</i> | 1000/10000 | 8.326225 | 0 | Yes |
| <i>S. lewini</i> | 1000/100000 | 4.978232 | 0 | Yes |
| <i>S. lewini</i> | 1000/10000000 | 5.778205 | 0 | Yes |
| <i>S. lewini</i> | 10000/100000 | -3.347993 | 0.0024 | Yes |
| <i>S. lewini</i> | 10000/10000000 | -2.548020 | 0.0325 | No |
| <i>S. lewini</i> | 100000/10000000 | 0.799972 | 1 | No |

Table 13: Characteristics of local optima found by HACSIm for hypothetical species.

| Scenario | No. optima | N^* range | N^* std. dev. | Highest mode(s) | Highest mode freq. |
|----------|------------|-------------|-----------------|-----------------|--------------------|
| II | 33 | 181-231 | 11.72283 | 202 | 10 |
| III | 24 | 155-199 | 7.704361 | 175 | 17 |
| IV | 22 | 123-158 | 7.886339 | 139 | 11 |

Table 14: Characteristics of local optima found by HACSIm for real species. For some species, distinct optima were located for different population sizes.

| Species | No. optima | N* range | N* std. dev. | Highest mode(s) | Highest mode freq. |
|------------------------|------------|----------|--------------|-----------------|--------------------|
| <i>A. pisum</i> | 77 | 623-962 | 65.23966 | 777/788/837 | 3 |
| <i>C. chupeaformis</i> | 61 | 383-542 | 34.27441 | 462 | 5 |
| <i>C. pipiens</i> | 48 | 424-549 | 27.83662 | 446 | 8 |
| <i>I. scapularis</i> | 36 | 574-665 | 25.14735 | 588 | 11 |
| <i>L. dispar</i> | 54 | 651-765 | 39.27425 | 672 | 5 |
| <i>S. lewini</i> | 42 | 244-343 | 19.29278 | 279 | 9 |

Table 15: Coverage probabilities and 95% Clopper-Pearson confidence intervals for hypothetical species for $p = 0.90$ across all assessed population sizes. Calculated probabilities are based on the number of observed local optima found using **HACSim**.

| Scenario | Pop. size | Coverage prob. | 95% Exact binomial CI | Coverage type |
|----------|-----------|----------------|------------------------|---------------|
| II | 1000 | 1 | (0.8942372, 1) | conservative |
| II | 10000 | 1 | (0.8942372, 1) | conservative |
| II | 100000 | 1 | (0.8942372, 1) | conservative |
| II | 10000000 | 0.969697 | (0.8424060, 0.9992331) | conservative |
| III | 1000 | 1 | (0.8575264, 1) | conservative |
| III | 10000 | 1 | (0.8575264, 1) | conservative |
| III | 100000 | 1 | (0.8575264, 1) | conservative |
| III | 10000000 | 0.9166667 | (0.7300272, 0.9897437) | conservative |
| IV | 1000 | 1 | (0.8456275, 1) | conservative |
| IV | 10000 | 1 | (0.8456275, 1) | conservative |
| IV | 100000 | 1 | (0.8456275, 1) | conservative |
| IV | 10000000 | 1 | (0.7715556, 0.9988499) | conservative |

Table 16: Coverage probabilities and 95% Clopper-Pearson confidence intervals for real species for $p = 0.90$ across all assessed population sizes. Calculated probabilities are based on the number of observed local optima found using **HACSim**.

| Species | Pop. size | Coverage prob. | 95% Exact binomial CI | Coverage type |
|-------------------------|-----------|----------------|------------------------|---------------|
| <i>A. pisum</i> | 1000 | 1 | (0.9532219, 1) | conservative |
| <i>A. pisum</i> | 10000 | 1 | (0.9532219, 1) | conservative |
| <i>A. pisum</i> | 100000 | 1 | (0.9532219, 1) | conservative |
| <i>A. pisum</i> | 10000000 | 0.9220779 | (0.8380736, 0.9708670) | conservative |
| <i>C. clupearformis</i> | 1000 | 1 | (0.9413188, 1) | conservative |
| <i>C. clupearformis</i> | 10000 | 1 | (0.9413188, 1) | conservative |
| <i>C. clupearformis</i> | 100000 | 1 | (0.9413188, 1) | conservative |
| <i>C. clupearformis</i> | 10000000 | 0.9016393 | (0.7981038, 0.9630400) | conservative |
| <i>C. pipiens</i> | 1000 | 1 | (0.9260272, 1) | conservative |
| <i>C. pipiens</i> | 10000 | 1 | (0.9260272, 1) | conservative |
| <i>C. pipiens</i> | 100000 | 1 | (0.9260272, 1) | conservative |
| <i>C. pipiens</i> | 10000000 | 0.9583333 | (0.8574590, 0.9949135) | conservative |
| <i>I. scapularis</i> | 1000 | 1 | (0.9026062, 1) | conservative |
| <i>I. scapularis</i> | 10000 | 1 | (0.9026062, 1) | conservative |
| <i>I. scapularis</i> | 100000 | 1 | (0.9026062, 1) | conservative |
| <i>I. scapularis</i> | 10000000 | 1 | (0.9026062, 1) | conservative |
| <i>L. dispar</i> | 1000 | 1 | (0.9339685, 1) | conservative |
| <i>L. dispar</i> | 10000 | 1 | (0.9339685, 1) | conservative |
| <i>L. dispar</i> | 100000 | 1 | (0.9339685, 1) | conservative |
| <i>L. dispar</i> | 10000000 | 0.962963 | (0.8725282, 0.9954827) | conservative |
| <i>S. lewini</i> | 1000 | 1 | (0.9159161, 1) | conservative |
| <i>S. lewini</i> | 10000 | 1 | (0.9159161, 1) | conservative |
| <i>S. lewini</i> | 100000 | 1 | (0.9159161, 1) | conservative |
| <i>S. lewini</i> | 10000000 | 0.9761905 | (0.8743414, 0.9993974) | conservative |

p = 0.95

Table 17: Mean proportion of observed unique haplotypes found over 50 replications of the simulation study for hypothetical species. In all cases, **HACSim** was run 100 times. Estimates correspond to the solid red horizontal lines depicted in confidence interval plots found within **Figures 13-15** and **Supplemental Information** accompanying this paper.

| Scenario | Pop. size | <i>R</i> Mean | <i>R</i> Range | <i>R</i> Std. dev. |
|----------|-----------|---------------|----------------|--------------------|
| II | 1000 | 0.962 | 0.936-0.980 | 0.009999 |
| II | 10000 | 0.956 | 0.926-0.976 | 0.0126 |
| II | 100000 | 0.953 | 0.914-0.978 | 0.0152 |
| II | 10000000 | 0.954 | 0.918-0.978 | 0.0125 |
| III | 1000 | 0.934 | 0.886-0.970 | 0.0148 |
| III | 10000 | 0.954 | 0.922-0.976 | 0.0130 |
| III | 100000 | 0.951 | 0.924-0.978 | 0.0137 |
| III | 10000000 | 0.955 | 0.930-0.970 | 0.0102 |
| IV | 1000 | 0.965 | 0.940-0.988 | 0.0117 |
| IV | 10000 | 0.960 | 0.942-0.978 | 0.00926 |
| IV | 100000 | 0.954 | 0.930-0.978 | 0.0117 |
| IV | 10000000 | 0.954 | 0.936-0.980 | 0.0128 |

Table 18: Mean proportion of observed unique haplotypes found over 50 replications of the simulation study for real species. In all cases, HACSIm was run 100 times. Estimates correspond to the solid red horizontal lines depicted in confidence interval plots found within **Figures 14-21** and **Supplemental Information** accompanying this paper.

| Species | Pop. size | R Mean | R Range | R Std. dev. |
|--|-----------|--------|-------------|-------------|
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 1000 | 0.999 | 0.992-1 | 0.00212 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 10000 | 0.954 | 0.928-0.990 | 0.0114 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 100000 | 0.955 | 0.920-0.980 | 0.0118 |
| Pea aphid (<i>Acyrtosiphon pisum</i>) | 1000000 | 0.951 | 0.920-0.977 | 0.0130 |
| Common mosquito (<i>Culex pipiens</i>) | 1000 | 0.956 | 0.926-0.974 | 0.00913 |
| Common mosquito (<i>Culex pipiens</i>) | 10000 | 0.958 | 0.925-0.974 | 0.00903 |
| Common mosquito (<i>Culex pipiens</i>) | 100000 | 0.951 | 0.934-0.972 | 0.00780 |
| Common mosquito (<i>Culex pipiens</i>) | 1000000 | 0.952 | 0.931-0.968 | 0.00824 |
| Deer tick (<i>Ixodes scapularis</i>) | 1000 | 0.940 | 0.926-0.953 | 0.00622 |
| Deer tick (<i>Ixodes scapularis</i>) | 10000 | 0.954 | 0.942-0.965 | 0.00579 |
| Deer tick (<i>Ixodes scapularis</i>) | 100000 | 0.954 | 0.936-0.965 | 0.00620 |
| Deer tick (<i>Ixodes scapularis</i>) | 1000000 | 0.954 | 0.938-0.970 | 0.00595 |
| Gypsy moth (<i>Lymantria dispar</i>) | 1000 | 0.937 | 0.918-0.947 | 0.00658 |
| Gypsy moth (<i>Lymantria dispar</i>) | 10000 | 0.956 | 0.933-0.972 | 0.00844 |
| Gypsy moth (<i>Lymantria dispar</i>) | 100000 | 0.952 | 0.934-0.968 | 0.00762 |
| Gypsy moth (<i>Lymantria dispar</i>) | 1000000 | 0.952 | 0.932-0.966 | 0.00814 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 1000 | 0.965 | 0.938-0.988 | 0.00981 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 10000 | 0.945 | 0.912-0.973 | 0.0128 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 100000 | 0.949 | 0.917-0.975 | 0.0148 |
| Scalloped hammerhead shark (<i>Sphyrna lewini</i>) | 1000000 | 0.949 | 0.923-0.972 | 0.0127 |

Table 19: Bonferroni-corrected Dunn’s post-hoc test results at the 0.83% significance level for comparison of population size *versus* haplotype frequency distribution in hypothetical species. **Note:** KW test statistics, p -values and statistical significance for Scenario I could not be calculated.

| Scenario | Pop. size pairing | Test statistic | p -value | Significant? |
|----------|-------------------|----------------|------------|--------------|
| II | 1000/10000 | 2.322 | 0.061 | No |
| II | 1000/100000 | 3.270 | 0.00320 | Yes |
| II | 1000/10000000 | 3.22 | 0.00380 | Yes |
| II | 10000/100000 | 0.948 | 1 | No |
| II | 10000/10000000 | 0.900 | 1 | No |
| II | 100000/10000000 | -0.0486 | 1 | No |
| III | 1000/10000 | -5.396 | 0 | Yes |
| III | 1000/100000 | -4.307 | 0 | Yes |
| III | 1000/10000000 | -5.698 | 0 | Yes |
| III | 10000/100000 | 1.089 | 0.828 | No |
| III | 10000/10000000 | -0.303 | 1 | No |
| III | 100000/10000000 | -1.392 | 0.492 | No |
| IV | 1000/10000 | 1.666 | 0.287 | No |
| IV | 1000/100000 | 3.358 | 0.00240 | Yes |
| IV | 1000/10000000 | 3.159 | 0.00480 | Yes |
| IV | 10000/100000 | 1.692 | 0.272 | No |
| IV | 10000/10000000 | 1.492 | 0.407 | No |
| IV | 100000/10000000 | -0.1995 | 1 | No |

Table 20: Bonferroni-corrected Dunn’s post-hoc test results at the 0.83% significance level for comparison of population size *versus* haplotype frequency distribution in real species.

| Species | Pop. size pairing | Test statistic | <i>p</i> -value | Significant? |
|----------------------|-------------------|----------------|-----------------|--------------|
| <i>A. pisum</i> | 1000/10000 | 8.506 | 0 | Yes |
| <i>A. pisum</i> | 1000/100000 | 8.018 | 0 | Yes |
| <i>A. pisum</i> | 1000/10000000 | 9.348 | 0 | Yes |
| <i>A. pisum</i> | 10000/100000 | -0.619 | 1 | No |
| <i>A. pisum</i> | 10000/10000000 | 1.068 | 0.8560 | No |
| <i>A. pisum</i> | 100000/10000000 | 1.688 | 0.275 | No |
| <i>C. pipiens</i> | 1000/10000 | -1.341 | 0.540 | No |
| <i>C. pipiens</i> | 1000/100000 | 3.475 | 0.00150 | Yes |
| <i>C. pipiens</i> | 1000/10000000 | 2.841 | 0.0135 | No |
| <i>C. pipiens</i> | 10000/100000 | 4.816 | 0 | Yes |
| <i>C. pipiens</i> | 10000/10000000 | 4.182 | 0.000100 | Yes |
| <i>C. pipiens</i> | 100000/10000000 | -0.634 | 1 | No |
| <i>I. scapularis</i> | 1000/10000 | -8.204 | 0 | Yes |
| <i>I. scapularis</i> | 1000/100000 | -8.856 | 0 | Yes |
| <i>I. scapularis</i> | 1000/10000000 | -8.050 | 0 | Yes |
| <i>I. scapularis</i> | 10000/100000 | -0.649 | 1 | No |
| <i>I. scapularis</i> | 10000/10000000 | 0.154 | 1 | No |
| <i>I. scapularis</i> | 100000/10000000 | 0.803 | 1 | No |
| <i>L. dispar</i> | 1000/10000 | -10.411 | 0 | Yes |
| <i>L. dispar</i> | 1000/100000 | -7.584 | 0 | Yes |
| <i>L. dispar</i> | 1000/10000000 | -7.928 | 0 | Yes |
| <i>L. dispar</i> | 10000/100000 | 2.905 | 0.011 | No |
| <i>L. dispar</i> | 10000/10000000 | 2.551 | 0.0322 | No |
| <i>L. dispar</i> | 100000/10000000 | -0.354 | 1 | No |
| <i>S. lewini</i> | 1000/10000 | 7.901 | 0 | Yes |
| <i>S. lewini</i> | 1000/100000 | 5.983 | 0 | Yes |
| <i>S. lewini</i> | 1000/10000000 | 6.409 | 0 | Yes |
| <i>S. lewini</i> | 10000/100000 | -1.918 | 0.165 | No |
| <i>S. lewini</i> | 10000/10000000 | -1.492 | 0.407 | No |
| <i>S. lewini</i> | 100000/10000000 | 0.426 | 1 | No |

Table 21: Characteristics of local optima found by HACSIm for hypothetical species.

| Scenario | No. optima | N^* range | N^* | Std. dev. | Highest mode(s) | Highest mode freq. |
|----------|------------|-------------|-------|-----------|-----------------|--------------------|
| II | 45 | 226-296 | | 13.469 | 260 | 8 |
| III | 38 | 200-252 | | 11.009 | 223 | 7 |
| IV | 29 | 176-207 | | 8.104 | 189/191 | 9 |

Table 22: Characteristics of local optima found by HACSIm for real species. For some species, distinct optima were located for different population sizes. * corresponds to a population size of 1000 and ** to population sizes of 10000, 100000 and 1000000.

| Species | No. optima | N* range | N* Std. dev. | Highest mode(s) | Highest mode freq. |
|----------------------|------------|---------------------|------------------|-----------------|--------------------|
| <i>A. pisum</i> | 36*/80** | 868-999*/868-1230** | 33.677*/68.380** | 994 | 4 |
| <i>C. pipiens</i> | 57 | 529-666 | 25.128 | 579 | 6 |
| <i>I. scapularis</i> | 60 | 744-896 | 32.939 | 808 | 5 |
| <i>L. dispar</i> | 63*/70** | 816-985*/816-1048** | 42.434*/48.938** | 909/917/921 | 4 |
| <i>S. lewini</i> | 65 | 329-458 | 26.395 | 400 | 4 |

Table 23: Coverage probabilities and 95% Clopper-Pearson confidence intervals for hypothetical species across all assessed population sizes. Calculated probabilities are based on the number of observed local optima found using **HACSim**.

| Scenario | Pop. size | Coverage prob. | 95% Exact binomial CI | Coverage type |
|----------|-----------|----------------|-----------------------|---------------|
| II | 1000 | 1 | (0.921, 1) | conservative |
| II | 10000 | 0.978 | (0.882, 0.999) | conservative |
| II | 100000 | 0.956 | (0.849, 0.995) | conservative |
| II | 10000000 | 0.956 | (0.849, 0.995) | conservative |
| III | 1000 | 0.658 | (0.486, 0.804) | permissive |
| III | 10000 | 0.974 | (0.862, 0.999) | conservative |
| III | 100000 | 0.974 | (0.862, 0.999) | conservative |
| III | 10000000 | 0.974 | (0.862, 0.999) | conservative |
| IV | 1000 | 1 | (0.881, 1) | conservative |
| IV | 10000 | 1 | (0.881, 1) | conservative |
| IV | 100000 | 1 | (0.881, 1) | conservative |
| IV | 10000000 | 1 | (0.881, 1) | conservative |

Table 24: Coverage probabilities and 95% Clopper-Pearson confidence intervals for real species across all assessed population sizes. Calculated probabilities are based on the number of observed local optima found using HACSim.

| Species | Pop. size | Coverage prob. | 95% Exact binomial CI | Coverage type |
|----------------------|-----------|----------------|-----------------------|---------------|
| <i>A. pisum</i> | 1000 | 1 | (0.903, 1) | conservative |
| <i>A. pisum</i> | 10000 | 0.975 | (0.913, 0.997) | conservative |
| <i>A. pisum</i> | 100000 | 0.975 | (0.913, 0.997) | conservative |
| <i>A. pisum</i> | 10000000 | 0.925 | (0.844, 0.972) | permissive |
| <i>C. pipiens</i> | 1000 | 0.965 | (0.879, 0.996) | conservative |
| <i>C. pipiens</i> | 10000 | 0.982 | (0.906, 1) | conservative |
| <i>C. pipiens</i> | 100000 | 0.930 | (0.830, 0.981) | permissive |
| <i>C. pipiens</i> | 10000000 | 0.965 | (0.879, 0.996) | conservative |
| <i>I. scapularis</i> | 1000 | 0.150 | (0.0710, 0.266) | permissive |
| <i>I. scapularis</i> | 10000 | 0.983 | (0.911, 1) | conservative |
| <i>I. scapularis</i> | 100000 | 0.900 | (0.795, 0.962) | permissive |
| <i>I. scapularis</i> | 10000000 | 0.950 | (0.861, 0.990) | exact |
| <i>L. dispar</i> | 1000 | 0 | (0, 0.0569) | permissive |
| <i>L. dispar</i> | 10000 | 0.943 | (0.860, 0.984) | permissive |
| <i>L. dispar</i> | 100000 | 0.900 | (0.805, 0.959) | permissive |
| <i>L. dispar</i> | 10000000 | 0.843 | (0.736, 0.919) | permissive |
| <i>S. lewini</i> | 1000 | 1 | (0.945, 1) | conservative |
| <i>S. lewini</i> | 10000 | 0.846 | (0.735, 0.924) | permissive |
| <i>S. lewini</i> | 100000 | 0.877 | (0.772, 0.945) | permissive |
| <i>S. lewini</i> | 10000000 | 0.908 | (0.810, 0.965) | permissive |