**SUPPLEMENTARY MATERIALS**

Table S1. Representation on survey blocks, urban indices, and trait values for focal species. “Urban index” refers to the correlation coefficient of the species’ nesting status on each survey block (0–2, n=173) and the percent urban cover on that block, as measured by a Spearman’s Rank test. Note: several of the species listed in Table S1 have undergone name changes, and are included here by the “old” names which are found in the datasets utilized, including the phylogenetic materials (e.g., Jetz et al., 2012). We include newer names in parentheses. Note that migratory status includes short-distance migrants as well as species that see a consistent influx of individuals from outside the region in fall/winter.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Latin binomial** | **English name** | **# blocks recorded (early)** | **# blocks recorded (late)** | **Urban index (early)** | **Urban index (late)** | **Body mass** | **Nest height (Low)** | **Forage ground** | **Migrat-ory status** | **Cavity nest** | **Struct-ures** | **HB** | **DB** |
| *Accipiter cooperii* | Cooper’s Hawk | 112 | 135 | -0.341 | 0.150 | 452 | 35 | 0 | 0 | 0 | 0 | 1 | 1 |
| *Aphelocoma californica* | California scrub-jay | 168 | 162 | -0.304 | -0.230 | 82.75 | 3 | 0 | 0 | 0 | 0 | 3 | 4 |
| *Archilochus alexandri* | Black-chinned Hummingbird | 105 | 115 | -0.141 | -0.139 | 3.45 | 4 | 0 | 1 | 0 | 0 | 1 | 2 |
| *Baeolophus inornatus* | Oak Titmouse | 96 | 105 | -0.628 | -0.443 | 16.26 | 3 | 0 | 0 | 1 | 0 | 1 | 4 |
| *Buteo jamaicensis* | Red-tailed Hawk | 154 | 155 | -0.357 | -0.141 | 1126 | 15 | 0 | 0 | 0 | 1 | 2 | 2 |
| *Buteo lineatus* | Red-shouldered Hawk | 99 | 109 | -0.195 | -0.026 | 616 | 20 | 0 | 0 | 0 | 0 | 1 | 2 |
| *Callipepla californica* | California Quail | 103 | 105 | -0.513 | -0.484 | 171.5 | 0 | 1 | 0 | 0 | 0 | 2 | 2 |
| *Calypte anna* | Anna’s Hummingbird | 167 | 168 | -0.182 | 0.067 | 4.4 | 1.5 | 0 | 0 | 0 | 0 | 2 | 2 |
| *Calypte costae* | Costa’s Hummingbird | 85 | 58 | -0.576 | -0.262 | 3.12 | 3 | 0 | 0 | 0 | 0 | 1 | 2 |
| *Carduelis (Spinus) psaltria* | Lesser Goldfinch | 136 | 159 | -0.465 | -0.160 | 9.12 | 2 | 0 | 0 | 0 | 0 | 3 | 3 |
| *Carduelis (Spinus) tristis* | American Goldfinch | 48 | 111 | 0.050 | 0.137 | 12.8 | 1 | 0 | 0 | 0 | 0 | 1 | 4 |
| *Carpodacus (Haemorhous) mexicanus* | House Finch | 173 | 166 | 0.089 | 0.103 | 21.4 | 5 | 0 | 0 | 0 | 1 | 3 | 3 |
| *Carpodacus (Haemorhous) purpureus* | Purple Finch | 35 | 63 | -0.571 | -0.144 | 25.23 | 6 | 0 | 1 | 0 | 0 | 1 | 4 |
| *Chamaea fasciata* | Wrentit | 102 | 110 | -0.632 | -0.541 | 14.7 | 1 | 0 | 0 | 0 | 0 | 1 | 3 |
| *Colaptes auratus* | Northern Flicker | 92 | 103 | -0.612 | -0.371 | 130.67 | 6 | 0 | 1 | 1 | 0 | 1 | 3 |
| *Corvus corax* | Common Raven | 138 | 167 | -0.498 | -0.185 | 1097 | 0 | 0 | 0 | 0 | 1 | 3 | 6 |
| *Empidonax difficilis* | Pacific-slope Flycatcher | 101 | 82 | -0.583 | -0.313 | 10.85 | 0 | 0 | 1 | 0 | 1 | 1 | 3 |
| *Euphagus cyanocephalus* | Brewer’s Blackbird | 140 | 103 | 0.432 | 0.302 | 62.65 | 0 | 0 | 0 | 0 | 1 | 1 | 4 |
| *Falco sparverius* | American Kestrel | 120 | 90 | 0.205 | 0.157 | 115.5 | 12 | 0 | 0 | 1 | 1 | 2 | 2 |
| *Icterus bullockii* | Bullock’s Oriole | 135 | 112 | -0.294 | -0.127 | 35.23 | 15 | 0 | 1 | 0 | 0 | 1 | 3 |
| *Icterus cucullatus* | Hooded Oriole | 132 | 135 | -0.154 | 0.155 | 24.3 | 12 | 0 | 1 | 0 | 0 | 1 | 3 |
| *Junco hyemalis* | Dark-eyed Junco | 31 | 98 | -0.560 | -0.150 | 19.48 | 0 | 1 | 1 | 0 | 1 | 1 | 2 |
| *\*Lonchura punctulata* | Scaly-breasted Munia | 9 | 51 | 0.056 | 0.140 | 14 | 1 | 0 | 0 | 0 | 0 | 0 | 3 |
| *Melanerpes formicivorus* | Acorn Woodpecker | 87 | 96 | -0.496 | -0.332 | 79.05 | 20 | 0 | 0 | 1 | 0 | 1 | 6 |
| *Melospiza melodia* | Song Sparrow | 135 | 145 | -0.407 | -0.133 | 23.35 | 0 | 1 | 0 | 0 | 0 | 1 | 3 |
| *Mimus polyglottos* | Northern Mockingbird | 160 | 156 | 0.399 | 0.404 | 48.5 | 3 | 0 | 0 | 0 | 0 | 2 | 3 |
| *Molothrus ater* | Brown-headed Cowbird | 149 | 125 | -0.286 | -0.046 | 42.55 | 0 | 0 | 0 | 0 | 0 | 1 | 2 |
| *Myiarchus cinerascens* | Ash-throated Flycatcher | 125 | 118 | -0.556 | -0.367 | 28.2 | 3 | 0 | 1 | 1 | 1 | 3 | 3 |
| *\*Passer domesticus* | House Sparrow | 160 | 143 | 0.468 | 0.526 | 27.7 | 0 | 0 | 0 | 0 | 1 | 0 | 4 |
| *Phainopepla nitens* | Phainopepla | 113 | 105 | -0.499 | -0.430 | 22.55 | 4 | 0 | 1 | 0 | 0 | 2 | 2 |
| *Picoides nuttallii* | Nuttall’s Woodpecker | 116 | 137 | -0.512 | -0.290 | 38 | 2.5 | 0 | 0 | 1 | 0 | 1 | 4 |
| *Picoides pubescens* | Downy Woodpecker | 58 | 112 | -0.010 | 0.166 | 27.5 | 3 | 0 | 0 | 1 | 0 | 1 | 4 |
| *Pipilo crissalis* | California Towhee | 148 | 166 | -0.349 | -0.252 | 47 | 4 | 1 | 0 | 0 | 0 | 1 | 4 |
| *Pipilo maculatus* | Spotted Towhee | 119 | 130 | -0.591 | -0.549 | 39.85 | 0 | 1 | 0 | 0 | 0 | 2 | 3 |
| *Polioptila caerulea* | Blue-gray Gnatcatcher | 50 | 72 | -0.621 | -0.366 | 6.13 | 2 | 0 | 1 | 0 | 0 | 2 | 1 |
| *Psaltriparus minimus* | Bushtit | 171 | 166 | 0.044 | -0.019 | 5.3 | 4 | 0 | 0 | 0 | 0 | 2 | 3 |
| *\*Pycnonotus jocosus* | Red-whiskered Bulbul | 7 | 34 | 0.089 | 0.061 | 27.7 | 5 | 0 | 0 | 0 | 0 | 0 | 4 |
| *Sayornis nigricans* | Black Phoebe | 171 | 161 | -0.039 | 0.172 | 18.25 | 0 | 0 | 0 | 0 | 1 | 0 | 3 |
| *Sayornis saya* | Say’s Phoebe | 23 | 93 | 0.000 | 0.041 | 21 | 0 | 0 | 0 | 0 | 1 | 1 | 2 |
| *Selasphorus sasin* | Allen’s Hummingbird | 94 | 151 | 0.099 | 0.238 | 3.17 | 1 | 0 | 0 | 0 | 0 | 2 | 2 |
| *Sialia mexicana* | Western Bluebird | 65 | 130 | -0.333 | -0.063 | 27.05 | 2 | 1 | 0 | 1 | 0 | 2 | 2 |
| *Sitta carolinensis* | White-breasted Nuthatch | 27 | 71 | -0.493 | -0.344 | 21 | 10 | 0 | 0 | 1 | 0 | 1 | 3 |
| *\*Sturnus vulgaris* | European Starling | 167 | 148 | 0.287 | 0.278 | 77.68 | 10 | 0 | 0 | 1 | 1 | 1 | 6 |
| *Thryomanes bewickii* | Bewick’s Wren | 123 | 120 | -0.448 | -0.397 | 9.9 | 0 | 0 | 0 | 1 | 1 | 1 | 2 |
| *Toxostoma redivivum* | California Thrasher | 107 | 108 | -0.564 | -0.424 | 84.4 | 2 | 1 | 0 | 0 | 0 | 1 | 3 |
| *Troglodytes aedon* | House Wren | 107 | 123 | -0.546 | -0.425 | 11 | 0 | 0 | 0 | 1 | 1 | 2 | 1 |
| *Turdus migratorius* | American Robin | 126 | 108 | -0.211 | 0.056 | 78.78 | 10 | 1 | 1 | 0 | 0 | 1 | 2 |
| *Tyrannus verticalis* | Western Kingbird | 74 | 97 | 0.057 | 0.101 | 39.6 | 15 | 0 | 1 | 0 | 1 | 2 | 2 |
| *Tyrannus vociferans* | Cassin’s Kingbird | 28 | 115 | 0.101 | 0.214 | 44.65 | 20 | 0 | 0 | 0 | 1 | 2 | 4 |
| *Vermivora (Leiothlypis) celata* | Orange-crowned Warbler | 83 | 123 | -0.651 | -0.101 | 9.2 | 0 | 0 | 0 | 0 | 0 | 2 | 1 |
| *Vireo huttoni* | Hutton’s Vireo | 75 | 101 | -0.586 | -0.317 | 11.3 | 6 | 0 | 0 | 0 | 0 | 1 | 2 |
| *Zenaida macroura* | Mourning Dove | 173 | 169 | 0.064 | 0.086 | 119 | 0 | 1 | 0 | 0 | 1 | 3 | 3 |

Table S2. Model Results

Early/BBA dataset

**PGLS (Brownian)**

pgls\_BBAa <- gls(BBAUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, correlation=corBrownian(1,consensus\_tree\_pruned), na.action=na.exclude)

Generalized least squares fit by REML

Model: BBAUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

93.72421 111.3362 -36.8621

Correlation Structure: corBrownian

Formula: ~1

Parameter estimate(s): numeric(0)

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.2394915 0.4844684 -0.4943388 0.6236

log(adult\_body\_mass\_g) 0.0004281 0.0815598 0.0052487 0.9958

NestHt\_low 0.0003431 0.0106545 0.0322067 0.9745

Forage\_ground\_only1 -0.3716588 0.1955043 -1.9010263 0.0640

Migratory1 -0.1769778 0.1099194 -1.6100689 0.1147

Cavity\_nest1 -0.2977074 0.1912812 -1.5563861 0.1269

Structures1 0.2177579 0.1340784 1.6241088 0.1117

DB 0.0677306 0.0612375 1.1060304 0.2749

HB -0.0249060 0.0605202 -0.4115322 0.6827

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.486

NestHt\_low -0.005 -0.185

Forage\_ground\_only1 -0.068 -0.235 0.209

Migratory1 -0.116 -0.034 -0.159 0.009

Cavity\_nest1 -0.106 0.128 0.063 0.054 0.010

Structures1 0.142 -0.269 0.304 0.120 -0.086 -0.118

DB -0.100 -0.365 -0.211 0.101 0.308 -0.195 -0.176

HB -0.211 -0.154 0.028 0.063 0.156 -0.127 -0.149 0.348

Standardized residuals:

Min Q1 Med Q3 Max

-1.0556525 -0.3140120 -0.1245639 0.1300914 0.6347966

Residual standard error: 0.7683028

Degrees of freedom: 52 total; 43 residual

**PGLS (O-U)**

pgls\_BBAb <- gls(BBAUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, correlation=corMartins(1,consensus\_tree\_pruned, fixed = TRUE), na.action=na.exclude)

Generalized least squares fit by REML

Model: BBAUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

66.98784 84.59984 -23.49392

Correlation Structure: corMartins

Formula: ~1

Parameter estimate(s): alpha 1

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.23980965 0.16065437 -1.4927054 0.1428

log(adult\_body\_mass\_g) -0.04086456 0.04142664 -0.9864320 0.3294

NestHt\_low 0.00886671 0.00741171 1.1963122 0.2381

Forage\_ground\_only1 -0.07000813 0.11988942 -0.5839392 0.5623

Migratory1 -0.20130709 0.09860903 -2.0414670 0.0474

Cavity\_nest1 -0.20820453 0.09804350 -2.1235933 0.0395

Structures1 0.26437880 0.09190021 2.8768032 0.0062

DB 0.05799259 0.03812181 1.5212445 0.1355

HB -0.04904998 0.05250183 -0.9342528 0.3554

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.358

NestHt\_low 0.028 -0.612

Forage\_ground\_only1 -0.042 -0.402 0.396

Migratory1 -0.317 0.170 -0.175 -0.061

Cavity\_nest1 -0.046 0.052 -0.069 0.066 0.065

Structures1 0.065 -0.285 0.227 0.210 -0.087 -0.094

DB -0.543 -0.329 0.216 0.185 0.113 -0.179 0.012

HB -0.440 -0.177 0.144 0.015 0.006 -0.003 -0.133 0.166

Standardized residuals:

Min Q1 Med Q3 Max

-1.51989762 -0.75611756 -0.00926871 0.77797215 2.41407152

Residual standard error: 0.2878099

Degrees of freedom: 52 total; 43 residual

**PGLS (Pagel’s Lambda)**

pgls\_BBAc <- gls(BBAUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, correlation=corPagel(1,consensus\_tree\_pruned), na.action=na.exclude)

Generalized least squares fit by REML

Model: BBAUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

68.61922 87.99242 -23.30961

Correlation Structure: corPagel

Formula: ~1

Parameter estimate(s): lambda -0.04736847

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.22240390 0.15268934 -1.4565777 0.1525

log(adult\_body\_mass\_g) -0.04346284 0.04028499 -1.0788844 0.2867

NestHt\_low 0.00905482 0.00730652 1.2392797 0.2220

Forage\_ground\_only1 -0.06876456 0.11844267 -0.5805725 0.5646

Migratory1 -0.21018889 0.09802815 -2.1441686 0.0377

Cavity\_nest1 -0.20950448 0.09480851 -2.2097645 0.0325

Structures1 0.25640838 0.08888883 2.8845960 0.0061

DB 0.05606823 0.03735947 1.5007768 0.1407

HB -0.05005208 0.05196068 -0.9632684 0.3408

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.343

NestHt\_low 0.035 -0.632

Forage\_ground\_only1 -0.055 -0.407 0.412

Migratory1 -0.347 0.184 -0.175 -0.065

Cavity\_nest1 -0.028 0.039 -0.073 0.080 0.069

Structures1 0.059 -0.282 0.220 0.223 -0.099 -0.078

DB -0.593 -0.329 0.238 0.182 0.106 -0.179 0.020

HB -0.456 -0.178 0.145 0.020 0.011 0.004 -0.135 0.170

Standardized residuals:

Min Q1 Med Q3 Max

-1.4964582323 -0.7729040871 -0.0009894507 0.7824656215 2.4668518957

Residual standard error: 0.2816084

Degrees of freedom: 52 total; 43 residual

**GLS (Non-phylogenetic)**

gls\_BBAd <- gls(BBAUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, na.action=na.exclude)

summary(gls\_BBAd)

Generalized least squares fit by REML

Model: BBAUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

66.97885 84.59085 -23.48942

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.23992583 0.16054716 -1.4944258 0.1424

log(adult\_body\_mass\_g) -0.04082956 0.04140534 -0.9860941 0.3296

NestHt\_low 0.00886667 0.00741053 1.1964953 0.2381

Forage\_ground\_only1 -0.06996365 0.11987308 -0.5836477 0.5625

Migratory1 -0.20124424 0.09857937 -2.0414438 0.0474

Cavity\_nest1 -0.20816585 0.09802507 -2.1235980 0.0395

Structures1 0.26443014 0.09188648 2.8777917 0.0062

DB 0.05799982 0.03811583 1.5216728 0.1354

HB -0.04912449 0.05249651 -0.9357669 0.3546

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.358

NestHt\_low 0.028 -0.612

Forage\_ground\_only1 -0.042 -0.402 0.396

Migratory1 -0.316 0.169 -0.175 -0.061

Cavity\_nest1 -0.046 0.052 -0.069 0.066 0.065

Structures1 0.065 -0.285 0.227 0.210 -0.087 -0.094

DB -0.543 -0.330 0.216 0.185 0.113 -0.179 0.012

HB -0.441 -0.177 0.143 0.015 0.006 -0.003 -0.133 0.166

Standardized residuals:

Min Q1 Med Q3 Max

-1.520095718 -0.756222944 -0.008952661 0.778086630 2.414760849

Residual standard error: 0.2877724

Degrees of freedom: 52 total; 43 residual

Late/eBird dataset

**PGLS (Brownian)**

Generalized least squares fit by REML

Model: EBUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

71.68451 89.29651 -25.84226

Correlation Structure: corBrownian

Formula: ~1

Parameter estimate(s): numeric(0)

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.0030582 0.3749440 -0.0081563 0.9935

log(adult\_body\_mass\_g) -0.0122038 0.0631215 -0.1933388 0.8476

NestHt\_low 0.0027825 0.0082458 0.3374391 0.7374

Forage\_ground\_only1 -0.3168070 0.1513064 -2.0938115 0.0422

Migratory1 -0.1388215 0.0850698 -1.6318544 0.1100

Cavity\_nest1 -0.2512182 0.1480380 -1.6969845 0.0969

Structures1 0.1634093 0.1037671 1.5747694 0.1226

DB 0.0285505 0.0473935 0.6024140 0.5501

HB -0.0254231 0.0468383 -0.5427840 0.5901

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.486

NestHt\_low -0.005 -0.185

Forage\_ground\_only1 -0.068 -0.235 0.209

Migratory1 -0.116 -0.034 -0.159 0.009

Cavity\_nest1 -0.106 0.128 0.063 0.054 0.010

Structures1 0.142 -0.269 0.304 0.120 -0.086 -0.118

DB -0.100 -0.365 -0.211 0.101 0.308 -0.195 -0.176

HB -0.211 -0.154 0.028 0.063 0.156 -0.127 -0.149 0.348

Standardized residuals:

Min Q1 Med Q3 Max

-0.95593996 -0.32616378 -0.06725772 0.18383027 0.90148453

Residual standard error: 0.5946116

Degrees of freedom: 52 total; 43 residual

**PGLS (O-U)**

pgls\_EBb <- gls(EBUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, correlation=corMartins(1,consensus\_tree\_pruned), na.action=na.exclude) # deleted Fixed = TRUE

Generalized least squares fit by REML

Model: EBUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

51.69454 71.06774 -14.84727

Correlation Structure: corMartins

Formula: ~1

Parameter estimate(s): alpha 3.901947

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.03812067 0.13131611 -0.2902970 0.7730

log(adult\_body\_mass\_g) -0.03053409 0.03386661 -0.9015987 0.3723

NestHt\_low 0.01040714 0.00606129 1.7169848 0.0932

Forage\_ground\_only1 -0.07134329 0.09804761 -0.7276393 0.4708

Migratory1 -0.13364434 0.08063088 -1.6574833 0.1047

Cavity\_nest1 -0.20608938 0.08017750 -2.5704139 0.0137

Structures1 0.19168921 0.07515657 2.5505316 0.0144

DB 0.03263487 0.03117602 1.0467937 0.3010

HB -0.05140388 0.04293839 -1.1971544 0.2378

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.358

NestHt\_low 0.028 -0.612

Forage\_ground\_only1 -0.042 -0.402 0.396

Migratory1 -0.316 0.169 -0.175 -0.061

Cavity\_nest1 -0.046 0.052 -0.069 0.066 0.065

Structures1 0.065 -0.285 0.227 0.210 -0.087 -0.094

DB -0.543 -0.330 0.216 0.185 0.113 -0.179 0.012

HB -0.441 -0.177 0.143 0.015 0.006 -0.003 -0.133 0.166

Standardized residuals:

Min Q1 Med Q3 Max

-2.03069137 -0.70659589 -0.06128047 0.65200608 2.27033384

Residual standard error: 0.2353772

Degrees of freedom: 52 total; 43 residual

**PGLS (Pagel’s Lambda)**

pgls\_EBc <- gls(EBUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, correlation=corPagel(1,consensus\_tree\_pruned), na.action=na.exclude)

summary(pgls\_EBc)

Generalized least squares fit by REML

Model: EBUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

51.52206 70.89526 -14.76103

Correlation Structure: corPagel

Formula: ~1

Parameter estimate(s): lambda -0.05449779

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.03115667 0.12748744 -0.2443901 0.8081

log(adult\_body\_mass\_g) -0.03090361 0.03326725 -0.9289499 0.3581

NestHt\_low 0.01037400 0.00598425 1.7335494 0.0902

Forage\_ground\_only1 -0.05238588 0.09898367 -0.5292376 0.5994

Migratory1 -0.13694163 0.08029542 -1.7054726 0.0953

Cavity\_nest1 -0.20583717 0.07722623 -2.6653788 0.0108

Structures1 0.18443043 0.07330945 2.5157797 0.0157

DB 0.03288493 0.03041916 1.0810596 0.2857

HB -0.05329785 0.04224065 -1.2617670 0.2138

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.354

NestHt\_low 0.053 -0.641

Forage\_ground\_only1 -0.020 -0.404 0.417

Migratory1 -0.342 0.186 -0.182 -0.078

Cavity\_nest1 -0.004 0.023 -0.054 0.079 0.069

Structures1 0.092 -0.296 0.227 0.225 -0.110 -0.062

DB -0.614 -0.322 0.256 0.160 0.111 -0.206 0.013

HB -0.452 -0.178 0.131 0.012 0.006 0.020 -0.144 0.198

Standardized residuals:

Min Q1 Med Q3 Max

-2.09068163 -0.72252668 -0.07094201 0.63730554 2.30383240

Residual standard error: 0.2309163

Degrees of freedom: 52 total; 43 residual

**GLS (Non-phylogenetic)**

gls\_EBd <- gls(EBUrban~log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB, data = EBdata20\_df, na.action=na.exclude)

Generalized least squares fit by REML

Model: EBUrban ~ log(adult\_body\_mass\_g) + NestHt\_low + Forage\_ground\_only + Migratory + Cavity\_nest + Structures + DB + HB

Data: EBdata20\_df

AIC BIC logLik

49.69454 67.30654 -14.84727

Coefficients:

Value Std.Error t-value p-value

(Intercept) -0.03812067 0.13131611 -0.2902970 0.7730

log(adult\_body\_mass\_g) -0.03053409 0.03386661 -0.9015987 0.3723

NestHt\_low 0.01040714 0.00606129 1.7169848 0.0932

Forage\_ground\_only1 -0.07134329 0.09804761 -0.7276393 0.4708

Migratory1 -0.13364434 0.08063088 -1.6574833 0.1047

Cavity\_nest1 -0.20608938 0.08017750 -2.5704139 0.0137

Structures1 0.19168921 0.07515657 2.5505316 0.0144

DB 0.03263487 0.03117602 1.0467937 0.3010

HB -0.05140388 0.04293839 -1.1971544 0.2378

Correlation:

(Intr) l(\_\_\_) NstHt\_ Frg\_\_1 Mgrtr1 Cvty\_1 Strct1 DB

log(adult\_body\_mass\_g) -0.358

NestHt\_low 0.028 -0.612

Forage\_ground\_only1 -0.042 -0.402 0.396

Migratory1 -0.316 0.169 -0.175 -0.061

Cavity\_nest1 -0.046 0.052 -0.069 0.066 0.065

Structures1 0.065 -0.285 0.227 0.210 -0.087 -0.094

DB -0.543 -0.330 0.216 0.185 0.113 -0.179 0.012

HB -0.441 -0.177 0.143 0.015 0.006 -0.003 -0.133 0.166

Standardized residuals:

Min Q1 Med Q3 Max

-2.03069137 -0.70659589 -0.06128047 0.65200608 2.27033384

Residual standard error: 0.2353772

Degrees of freedom: 52 total; 43 residual