**Appendix S2.** Goodness-of-fit test for multi-season multi-species occupancy models.

We assessed model fit using a the Bayesian *p*-value ([Gelman, Meng & Stern 1996](#_ENREF_1)) based on the Pearson’s *χ2* discrepancy for binomial data.

To avoid division by zero we added 0.001 to *pij* in the denominator. For the RN model *pij* is replaced by .We calculated the χ2 discrepancy for our observed dataset and a simulated ideal dataset based on the estimated parameters at each iteration of the MCMC algorithm. We calculated the Bayesian *p*-value as Pr() with values larger than 0.95 or smaller than 0.05 indicating a lack of fit. We also calculated a “lack-of –fit” statistics which is expected to be equal to 1 if the model fits the data perfectly ([Kéry & Schaub 2012](#_ENREF_2)).

Binary model:



DIC=16919

p-value=1

lack-of-fit=1.908

Binary model pooled data (6 days as one primary interval):



DIC=15873

p-value=0.999

lack-of-fit=1.433

Royle-Nichols model:



DIC=14778

p-value=0.954

lack-of-fit: 1.077

Royle-Nichols pooled (6 days as one primary interval):



DIC=14947

p-value=0.855

lack-of-fit: 1.052

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Records 1-d (N) | Records 6-d (N) | p-value  Binary 1-d | p-value  Binary 6-d | p-value  RN 1-d | p-value  RN 6-d |
| *Atelocynus microtis* | 74 | 67 | 0.77 | 0.64 | 0.54 | 0.50 |
| *Cuniculus paca* | 355 | 280 | 1.00 | 1.00 | 0.82 | 0.76 |
| *Dasyprocta punctata* | 724 | 501 | 1.00 | 1.00 | 0.95 | 0.95 |
| *Dasypus spp.* | 144 | 136 | 0.07 | 0.99 | 0.20 | 0.75 |
| *Didelphis marsupialis* | 114 | 93 | 0.98 | 0.86 | 0.65 | 0.62 |
| *Eira barbara* | 59 | 57 | 0.65 | 0.70 | 0.44 | 0.44 |
| *Galicitis vittata* | 1 | 1 | 0.26 | 0.24 | 0.25 | 0.23 |
| *Leopardus pardalis* | 357 | 287 | 1.00 | 0.99 | 0.65 | 0.61 |
| *Leopardus wiedii* | 80 | 77 | 0.63 | 0.52 | 0.47 | 0.45 |
| *Mazama americana* | 385 | 325 | 1.00 | 1.00 | 0.70 | 0.73 |
| *Mazama nemorivaga* | 305 | 230 | 1.00 | 1.00 | 0.98 | 0.95 |
| *Mitu tuberosum* | 375 | 294 | 1.00 | 0.88 | 0.53 | 0.43 |
| *Myoprocta pratti* | 152 | 101 | 1.00 | 1.00 | 0.98 | 0.88 |
| *Myrmecophaga tridactyla* | 57 | 52 | 0.67 | 0.57 | 0.46 | 0.43 |
| *Nasua nasua* | 24 | 24 | 0.78 | 0.82 | 0.71 | 0.73 |
| *Panthera onca* | 233 | 209 | 0.82 | 0.83 | 0.49 | 0.45 |
| *Pecari tajacu* | 324 | 275 | 1.00 | 1.00 | 0.60 | 0.59 |
| *Penelope jacquacu* | 121 | 110 | 0.84 | 0.79 | 0.50 | 0.52 |
| *Priodontes maximus* | 47 | 43 | 0.67 | 0.69 | 0.55 | 0.56 |
| *Procyon cancrivorus* | 13 | 12 | 0.50 | 0.39 | 0.50 | 0.40 |
| *Psophia leucoptera* | 573 | 394 | 1.00 | 1.00 | 0.93 | 0.76 |
| *Puma concolor* | 110 | 105 | 0.65 | 0.55 | 0.39 | 0.39 |
| *Puma yagouaroundi* | 15 | 14 | 0.36 | 0.32 | 0.32 | 0.28 |
| *Speothos venaticus* | 2 | 2 | 0.29 | 0.27 | 0.27 | 0.27 |
| *Sylvilagus brasiliensis* | 80 | 49 | 0.95 | 0.77 | 0.66 | 0.58 |
| *Tapirus terrestris* | 723 | 536 | 1.00 | 1.00 | 0.70 | 0.69 |
| *Tayassu pecari* | 567 | 428 | 1.00 | 1.00 | 0.66 | 0.57 |

Bayesian *p*-value based on the Pearson’s *χ2* discrepancy for each species for two different multi-session multi-species occupancy models with the full data (1-d) and 6-day pooled data (6-d). Values >0.95 or <0.05 indicate a lack of fit.

### Literature cited

Gelman, A., Meng, X.-L. & Stern, H. (1996) Posterior predictive assessment of model fitness via realized discrepancies. *Statistica Sinica,* **6,** 733-760.

Kéry, M. & Schaub, M. (2012) *Bayesian population analysis using WinBUGS a hierarchical perspective*. Elsevier, Amsterdam.