Ecography

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Supplementary material

Appendix 1. Data sources

Australian interception and detection data were obtained from the Australian Department of Agriculture and Water Resources; from State, Territory and local biosecurity agencies (requested via email); and from voucher specimens deposited in Australian museums (also requested via email). Additional data were sourced from Henderson et al. (2011) and García-Díaz & Cassey (2014). Records obtained from different sources were cross-checked to avoid including repetitions in the final dataset.

Data on the global occurrence of *D. melanosticus* were taken from the Global Biodiversity Information Facility (gbif.org), Map of Life (mol.org), VertNet (vertnet.org), HerpNET (herpnet.org), iNaturalist (iNaturalist.org), project noah (projectnoah.org), International Union for the Conservation of Nature (iucnredlist.org), and published papers and unpublished reports (Trainor, 2009; Asad, 2011; Asad et al., 2012; Moore et al., 2015; O'Shea et al., 2015).

REFERENCES

Asad S. (2011) An observational study of Nusa Penidas Herpetofauna: A preliminary examination of the islands biodiversity. Report prepared for The Friends of the National Parks Foundation (FNPF). pp 1–29.

Asad S., McKay J.L., & Putra A.P. (2012) The herpetofauna of Nusa Penida, Indonesia. *Herpetological Bulletin*, **122**, 8–15.

García-Díaz P. & Cassey P. (2014) Patterns of transport and introduction of exotic amphibians in Australia. *Diversity and Distributions*, **20**, 455–466.

Henderson W., Bomford M., & Cassey P. (2011) Managing the risk of exotic vertebrate incursions in Australia. *Wildlife Research*, **38**, 501.

Moore M., Fidy J.F.S.N., & Edmonds D. (2015) The new toad in town: Distribution of the Asian toad, Duttaphrynus melanostictus, in the Toamasina area of eastern Madagascar. *Tropical Conservation Science*, **8**, 440–455.

O'Shea M., Sanchez C., Carvalho L., Ribeiro A.V., & Soares Z.A. (2015) Herpetological Diversity of Timor-Leste: Updates and a Review of Species Distributions Herpetological Diversity of Timor-Leste : Updates and a Review of Species Distributions. *Asian Herpetological Research*, **6**, 73–131.

Trainor C.R. (2009) Survey of a population of Black-spined Toad *Bufo melanostictus* in Timor-Leste: confirming identity, distribution, abundance and impacts of an invasive and toxic toad. Report by Charles Darwin University to AusAID, contract agreement no. 52294, 46 pp.

Appendix 2. R code for pathway models and model fitting details.

We ran the models with three chains with 100,000 iterations each, and no thinning. We discarded the first 10,000 iterations (burn-in time) after checking for mixing and convergence of the chains through a visual exploration of trace plots. Using this approach, we obtained 270,000 draws from the marginal posterior distributions for all parameters.

We used relatively uninformative prior distributions for all the intercepts of the negative binomial models, ~ $N(0, \sigma^2)$, $\sigma^2 = 10$; whereas the overdispersion parameter was drawn from an uninformative uniform distribution, ~ $U(0, 50)$. We used a double exponential, or Laplace, prior distribution for all the slopes of the negative binomial models, ~$Laplace(0, b)$, b~$U(0.1, 3)$. The use of a Laplace prior for the slopes produces a regularized negative binomial model where the slopes of the State-specific route covariates that contribute very little to the variation in $N.tot_{i,j}$ are pulled towards zero, resulting in a marginal posterior distribution centred around zero (Gelman et al., 2013). We used uninformative Beta priors for the probabilities of detection at the border and on-shore, ~$Beta(1, 1)$.

```
#### JAGS code for fitting the Bayesian regularized pathway models described in the main
text.  #### Comments on the code are specified after the # symbols.

#### Air traffic routes

model{

## Uninformative prior distributions for the negative binomial regression for Ntot(i, t)

for (i in 1:n.countries){       ## Prior distribution for the country of origin-
alpha[i]~dnorm(0, 0.1)          ## specific intercepts. n.countries: no. of countries
}                               ## of origin

for (j in 1:n.covs){            ## n.covs: no. of covariates for modeling Ntot(i, t)
beta[j]~ddexp(0, b)             ## Prior distributions for the slopes. Double-
}                               ## exponential distribution for regularization

b~dunif(0.1, 3)                 ## Prior for scale parameter of double exponential
                                ## distribution

r~dunif(0, 50)                  ## Prior distribution for the overdispersion parameter


## Uninformative prior distribution for the probabilities of interception at the border, pb(j)

for (j in 1:n.countries){
pb[j]~dbeta(1, 1)
}
```

```
#### Uninformative prior distributions for the probabilities of detection on-shore, pos(i)

for (i in 1:n.destination){        ## n.destination: number of recipient States in
pos[i]~dbeta(1, 1)                 ## Australia
}

## Likelihood for the complete model

for (i in 1:sample.size) {

## The next three lines of code specify the negative-binomial regression. country: country of
## origin

log(lambda[i])<-alpha[country[i]]+beta[1]*seats[i]+beta[2]*flights[i]
p[i]<-r/(r+lambda[i])
N.tot[i]~dnbinom(p[i], r)

## The next two lines of code specify the number of interceptions and detections

N.intercp[i]~dbinom(pb[country[i]], N.tot[i])
N.detect[i]~dbinom(pos[destination[i]], N.tot[i]-N.intercept[i])     ## destination:
                                                                       ## State/Territory of
                                                                       ## arrival

## Toads introduced in the wild
N.intro[i]<- N.tot[i]- N.intercp[i]- N.detect[i]


}

## Total number of toads introduced in Australia

intro.aus<-sum(N.intro[])

}



#### Shipping traffic routes

model{

## Uninformative prior distributions for the negative binomial regression for Ntot(i, t)

for (i in 1:n.countries){          ## Prior distribution for the country of origin-
alpha[i]~dnorm(0, 0.1)             ## specific intercepts. n.countries: no. of countries
}                                  ## of origin

beta[j]~ddexp(0, b)                ## Prior distributions for the slope. Double-
```

```
}

                              ## exponential distribution for regularization

b~dunif(0.1, 3)               ## Prior for scale parameter of double exponential
                              ## distribution

r~dunif(0, 50)                ## Prior distribution for the overdispersion parameter

## Uninformative prior distribution for the probabilities of interception at the border, pb(j)

for (j in 1:n.countries){
pb[j]~dbeta(1, 1)
}

## Uninformative prior distributions for the probabilities of detection on-shore, pos(i)

for (i in 1:n.destination){   ## n.destination: number of recipient States in
pos[i]~dbeta(1, 1)            ## Australia
}

## Likelihood for the complete model

for (i in 1:sample.size) {

## The next three lines of code specify the negative-binomial regression. country: country of
## origin

log(lambda[i])<- alpha[country[i]]+beta*ships[i]
p[i]<-r/(r+lambda[i])
N.tot[i]~dnbinom(p[i], r)

## The next two lines of code specify the number of interceptions and detections

N.intercp[i]~dbinom(pb[country[i]], N.tot[i])
N.detect[i]~dbinom(pos[destination[i]], N.tot[i]-N.intercept[i])      ## destination:
                                                                       ## State/Territory of
                                                                       ## arrival

## Toads introduced in the wild
N.intro[i]<- N.tot[i]- N.intercp[i]- N.detect[i]


}

## Total number of toads introduced in Australia

intro.aus<-sum(N.intro[])

}
```

REFERENCES

Gelman A., Carlin J.B., Stern H.S., & Rubin D.B. (2013) *Bayesian data analysis.* CRC Press, Boca Raton, USA.

Appendix 3

Table A1. Posterior estimates (median and 95% Credible Intervals) of the intercepts of the country of origin of the total number of *D. melanosticus* transported into seven Australian States via shipping and air routes. Note, not all countries with shipping routes also had air routes into Australia.

	State-specific shipping routes Median ± standard error (95% Credible Intervals)	State-specific air traffic routes Median ± standard error (95% Credible Intervals)
Intercepts (country of origin)		
α (Bangladesh)	-2.54 ± 2.36 (-7.37, 2.14)	NA
α (Brunei)	-0.80 ± 1.74 (-3.99, 3.01)	NA
α (China)	-0.14 ± 1.51 (-2.75, 3.24)	-1.76 ± 1.10 (-4.23, 0.05)
α (Hong Kong)	-0.92 ± 1.68 (-4.04, 2.71)	-3.59 ± 1.83 (-7.80, -0.73)
α (India)	-1.04 ± 1.67 (-4.15, 2.57)	-1.30 ± 1.09 (-3.79, 0.47)
α (Indonesia)	2.19 ± 1.19 (0.13, 4.89)	-0.76 ± 0.80 (-2.51, 0.63)
α (Macao)	-1.27 ± 2.80 (-6.77, 4.36)	NA
α (Malaysia)	0.76 ± 1.33 (-1.48, 3.80)	-1.61 ± 1.06 (-4.03, - 0.11)
α (Myanmar)	-1.73 ± 2.66 (-6.99, 3.66)	NA
α (Pakistan)	-2.54 ± 2.36 (-7.37, 2.10)	NA
α (Papua New Guinea)	-1.43 ± 1.77 (-4.76, 2.39)	-3.03 ± 1.94 (-7.47, 0.05)
α (Singapore)	-3.12 ± 2.33 (-7.85, 1.47)	-3.61 ± 1.84 (-7.85, -0.73)
α (Sri Lanka)	-2.53 ± 2.37 (-7.36, 2.13)	NA
α (Taiwan)	-1.29 ± 1.74 (-4.53, 2.47)	-3.00 ± 1.95 (-7.46, 0.06)
α (Thailand)	-2.75 ± 2.29 (-7.43, 1.75)	1.21 ± 0.42 (0.38, 2.05)
α (Vietnam)	-2.75 ± 2.29 (--7.47, 1.74)	NA

Table A2. Posterior estimates (median and 95% Credible Intervals) of the probability of interception at the border of *D. melanosticus* transported in shipping and air routes from 16 countries of origin. Note, not all countries with shipping routes also had air routes into Australia.

	Shipping routes Median ± standard error (95% Credible Intervals)	Air traffic routes Median ± standard error (95% Credible Intervals)
Probability of interception (country of origin)		
pd (Bangladesh)	0.49 ± 0.29 (0.02, 0.97)	NA
pd (Brunei)	0.61 ± 0.25 (0.11, 0.98)	NA
pd (China)	0.33 ± 0.17 (0.07, 0.70)	0.62 ± 0.25 (0.12, 0.98)
pd (Hong Kong)	0.29 ± 0.23 (0.01, 0.81)	0.48 ± 0.29 (0.02, 0.97)
pd (India)	0.63 ± 0.25 (0.12, 0.99)	0.63 ± 0.25 (0.13, 0.98)
pd (Indonesia)	0.89 ± 0.12 (0.52, 1.00)	0.43 ± 0.22 (0.07, 0.87)
pd (Macao)	0.49 ± 0.29 (0.02, 0.97)	NA
pd (Malaysia)	0.10 ± 0.10 (0.01, 0.36)	0.62 ± 0.25 (0.12, 0.98)
pd (Myanmar)	0.49 ± 0.29 (0.02, 0.97)	NA
pd (Pakistan)	0.48 ± 0.29 (0.02, 0.97)	NA
pd (Papua New Guinea)	0.58 ± 0.26 (0.09, 0.98)	0.48 ± 0.29 (0.02, 0.97)
pd (Singapore)	0.48 ± 0.29 (0.02, 0.97)	0.48 ± 0.29 (0.02, 0.97)
pd (Sri Lanka)	0.48 ± 0.29 (0.02, 0.97)	NA
pd (Taiwan)	0.28 ± 0.22 (0.10, 0.81)	0.48 ± 0.29 (0.02, 0.97)
pd (Thailand)	0.48 ± 0.29 (0.02, 0.97)	0.36 ± 0.13 (0.14, 0.62)
pd (Vietnam)	0.48 ± 0.29 (0.02, 0.97)	NA

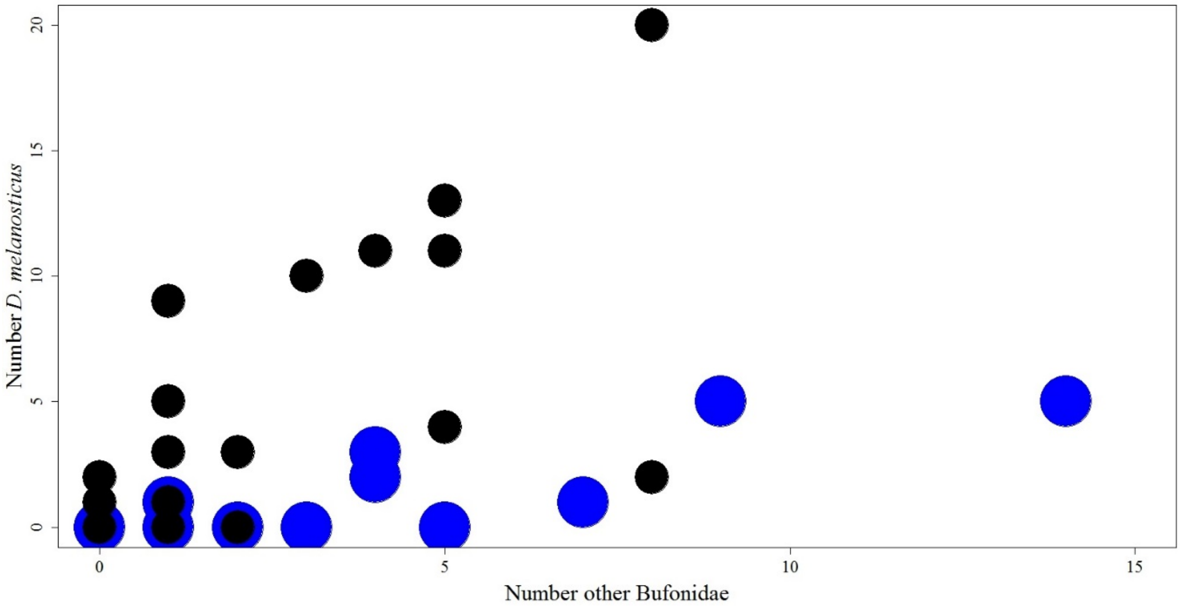
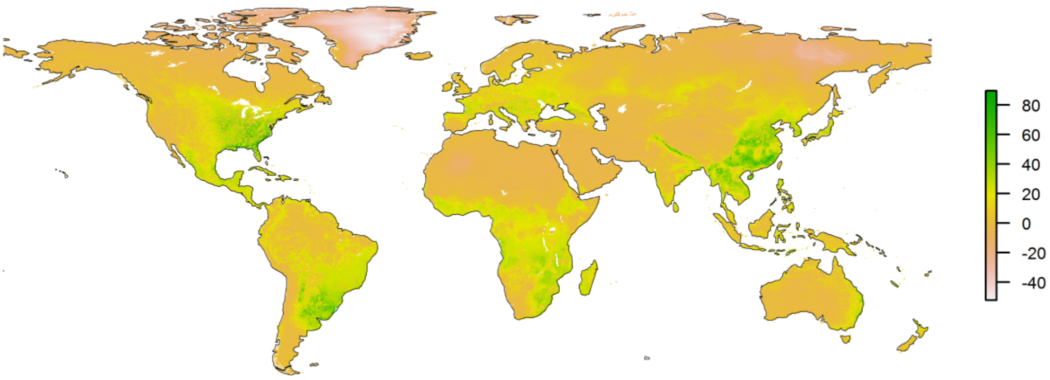


Fig. A1. Relationships between the number of interceptions (blue dots) and detections (black) per year of *D. melanosticus* and other Bufonidae species in Australia (1986–2013). Each dot represents one year.

(a) Multivariate environmental similarity



(b) SD of environmental suitability

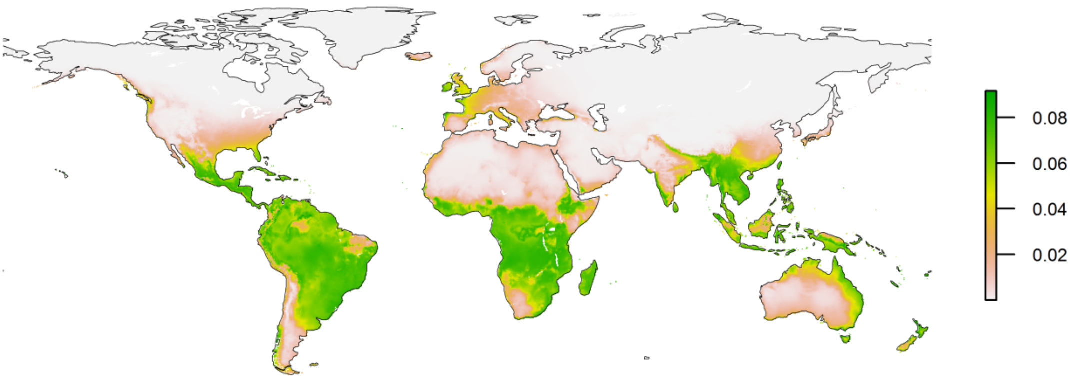


Fig A2. SDM prediction uncertainty due to novel environments, based on a multivariate environmental similarity surface (a); and based on data used to train the SDM (standard deviation across five cross-validation folds; b). Negative values in (a) correspond to grid cells in which at least one climate variable has a value that is outside of the range used to calibrate the native-range SDM; positive values indicate climates that are similar to those within the calibration data. The magnitude of these values indicates how far the least similar predictor is outside of the range of model calibration.

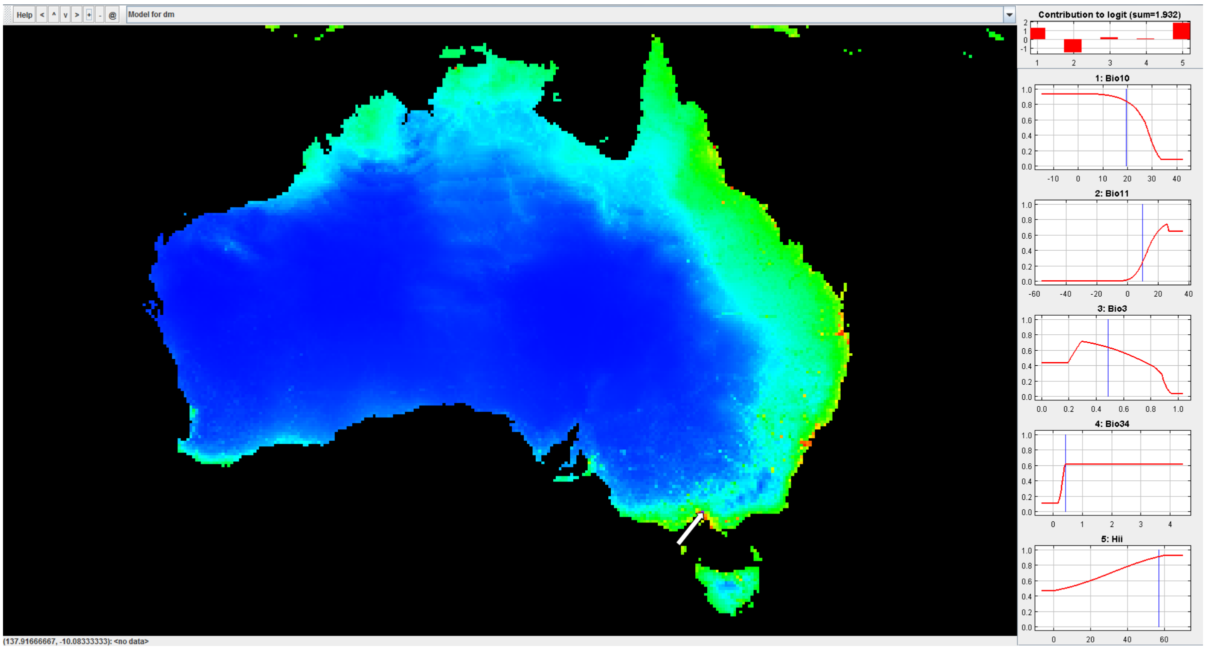


Fig. A3. Exploration of a SDM prediction for a grid cell in Melbourne, Australia (indicated on the map with a white arrow), where *D. melanosticus* has been frequently detected. Also shown is the relative influence of each environmental variable (top right) and fitted response curves. Vertical blue lines represent environmental conditions at the selected cell. Values for several environmental variables are close to their optimum in Melbourne, suggesting that southern predictions are not due to any single environmental variable.

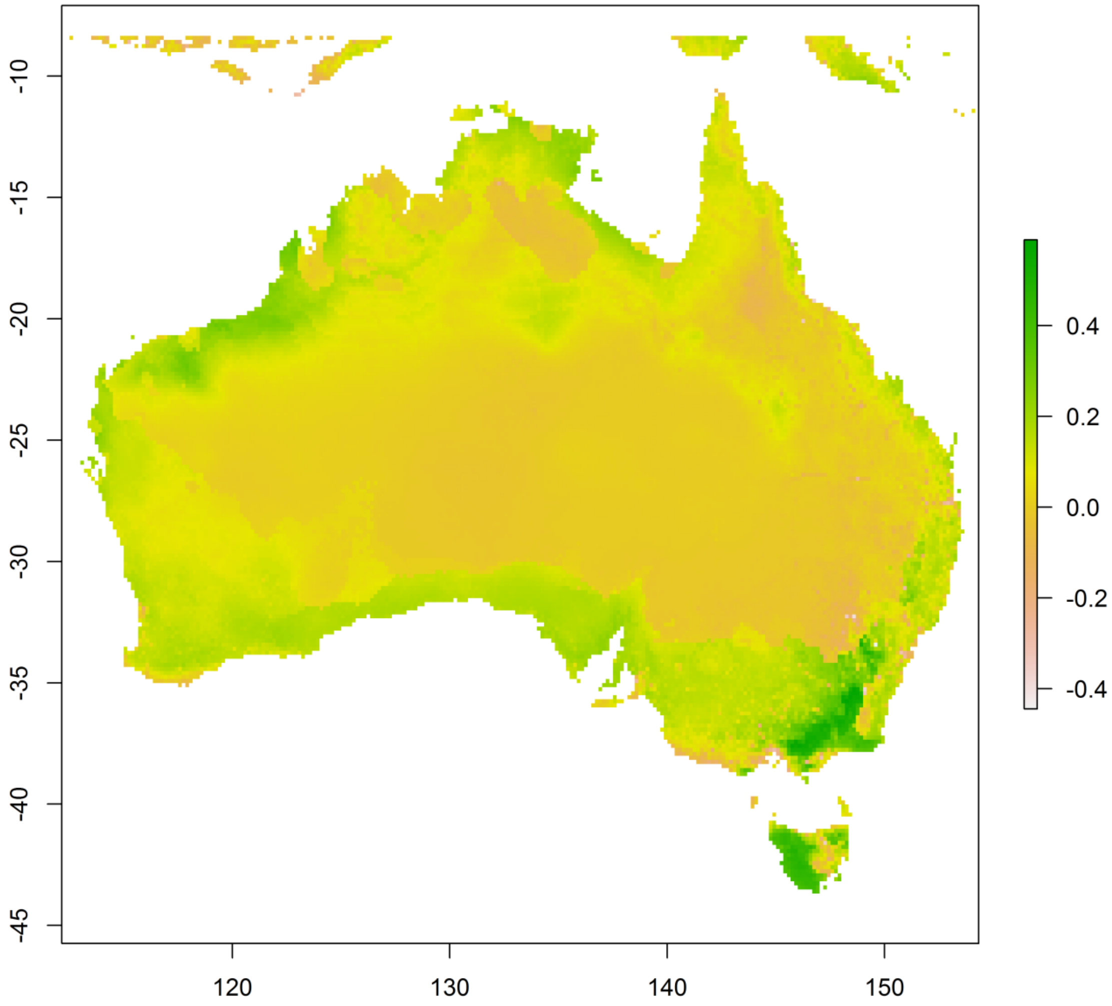


Fig. A3. Difference between SDM predictions from a model based on the 16 climate variables used in the Australian Department of Agriculture risk assessment (Page et al., 2008) and a model based on the five environmental variables used in the current study. Note that the climate database used here (Climond) reports the mean temperature of the coldest and warmest weeks, whereas the data in Climatch used by Page et al. (2008) reports the mean temperature of the coldest and warmest months. All other climate variables were similarly defined in the two datasets. Refitting the model with 16 climate variables resulted in predictions that are generally higher, not lower in southern regions. The disparity between earlier predictions and ours potentially reflect the fact that we used finer-grained occurrence data (instead of a coarse-resolution range map) and a presence-background SDM that accounts for environmental availability (instead of a presence-only approach).