

Baselga, A. and Araújo, M. B. 2009. Individualistic vs community modelling of species distributions under climate change. – *Ecography* 32: 55–65.

Supplementary material

Appendix 1. Species and subspecies modelled with GLM and CQO.

- | | | | |
|----|--|----|--|
| 1 | <i>Abies alba</i> Mill. | 39 | <i>Pinus nigra</i> J.F.Arnold subsp. <i>nigra</i> |
| 2 | <i>Abies borisii-regis</i> Mattf. | 40 | <i>Pinus nigra</i> J.F.Arnold subsp. <i>pallasiana</i> (Lamb.) Holmboe |
| 3 | <i>Alnus cordata</i> (Loisel.) Loisel. | 41 | <i>Pinus nigra</i> J.F.Arnold subsp. <i>salzmannii</i> (Dunal) Franco |
| 4 | <i>Alnus glutinosa</i> (L.) Gaertn. | 42 | <i>Pinus pinaster</i> Aiton |
| 5 | <i>Alnus incana</i> (L.) Moench subsp. <i>incana</i> | 43 | <i>Pinus pinea</i> L. |
| 6 | <i>Alnus incana</i> (L.) Moench subsp. <i>kolaensis</i> (N.I.Orlova) A.Löve & D.Löve | 44 | <i>Pinus rotundata</i> Link |
| 7 | <i>Alnus viridis</i> (Chaix) DC. | 45 | <i>Pinus sylvestris</i> |
| 8 | <i>Betula humilis</i> Schrank | 46 | <i>Pinus uliginosa</i> Neumann |
| 9 | <i>Betula nana</i> L. | 47 | <i>Pinus uncinata</i> Mill. ex Mirb. |
| 10 | <i>Betula pendula</i> Roth | 48 | <i>Populus alba</i> L. |
| 11 | <i>Betula pubescens</i> Ehrh. | 49 | <i>Populus canescens</i> (Aiton) Sm. |
| 12 | <i>Carpinus betulus</i> L. | 50 | <i>Populus nigra</i> L. |
| 13 | <i>Carpinus orientalis</i> Mill. | 51 | <i>Populus tremula</i> L. |
| 14 | <i>Castanea sativa</i> Mill. | 52 | <i>Quercus cerris</i> L. |
| 15 | <i>Celtis australis</i> L. | 53 | <i>Quercus coccifera</i> L. |
| 16 | <i>Corylus avellana</i> L. | 54 | <i>Quercus crenata</i> Lam. |
| 17 | <i>Corylus colurna</i> L. | 55 | <i>Quercus dalechampii</i> Ten. |
| 18 | <i>Fagus sylvatica</i> L. subsp. <i>orientalis</i> (Lipsky) Greuter & Burdet | 56 | <i>Quercus faginea</i> Lam. |
| 19 | <i>Fagus sylvatica</i> L. subsp. <i>sylvatica</i> | 57 | <i>Quercus frainetto</i> Ten. |
| 20 | <i>Ficus carica</i> L. | 58 | <i>Quercus ilex</i> L. |
| 21 | <i>Juglans regia</i> L. | 59 | <i>Quercus macrolepis</i> Kotschy |
| 22 | <i>Juniperus communis</i> L. | 60 | <i>Quercus pedunculiflora</i> K.Koch |
| 23 | <i>Juniperus foetidissima</i> Willd. | 61 | <i>Quercus petraea</i> (Matt.) Liebl. |
| 24 | <i>Juniperus oxycedrus</i> L. subsp. <i>macrocarpa</i> (Sm.) Ball | 62 | <i>Quercus pubescens</i> Willd. subsp. <i>anatolica</i> O.Schwarz |
| 25 | <i>Juniperus oxycedrus</i> L. subsp. <i>oxycedrus</i> | 63 | <i>Quercus pubescens</i> Willd. subsp. <i>pubescens</i> |
| 26 | <i>Juniperus phoenicea</i> L. | 64 | <i>Quercus pyrenaica</i> Willd. |
| 27 | <i>Juniperus sabina</i> L. | 65 | <i>Quercus robur</i> L. |
| 28 | <i>Juniperus thurifera</i> L. | 66 | <i>Quercus rotundifolia</i> Lam. |
| 29 | <i>Larix decidua</i> Mill. | 67 | <i>Quercus suber</i> L. |
| 30 | <i>Myrica gale</i> L. | 68 | <i>Quercus trojana</i> Webb |
| 31 | <i>Ostrya carpinifolia</i> Scop. | 69 | <i>Salix alba</i> L. |
| 32 | <i>Picea abies</i> (L.) H.Karst. subsp. <i>abies</i> | 70 | <i>Salix alpina</i> Scop. |
| 33 | <i>Picea abies</i> (L.) H.Karst. subsp. <i>alpestris</i> (Brügger) Domin | 71 | <i>Salix amplexicaulis</i> Bory |
| 34 | <i>Picea abies</i> (L.) H.Karst. subsp. <i>obovata</i> (Ledeb.) Hultén | 72 | <i>Salix appendiculata</i> Vill. |
| 35 | <i>Pinus cembra</i> L. | 73 | <i>Salix arbuscula</i> L. |
| 36 | <i>Pinus halepensis</i> Mill. | 74 | <i>Salix atrocinerea</i> Brot. |
| 37 | <i>Pinus heldreichii</i> H.Christ | 75 | <i>Salix aurita</i> L. |
| 38 | <i>Pinus mugo</i> Turra | 76 | <i>Salix bicolor</i> Willd. |
| | | 77 | <i>Salix breviserrata</i> Flod. |
| | | 78 | <i>Salix burjatica</i> Nasarov |
| | | 79 | <i>Salix caesia</i> Vill. |
| | | 80 | <i>Salix caprea</i> L. |
| | | 81 | <i>Salix cinerea</i> L. |
| | | 82 | <i>Salix daphnoides</i> Vill. |
| | | 83 | <i>Salix eleagnos</i> Scop. |

- 84 *Salix foetida* Schleich. ex DC. in Lam. & DC.
85 *Salix fragilis* L.
86 *Salix glabra* Scop.
87 *Salix glauca* L.
88 *Salix glaucosericea* Flod.
89 *Salix hastata* L.
90 *Salix hegetschweileri* Heer
91 *Salix helvetica* Vill.
92 *Salix herbacea* L.
93 *Salix lanata* L.
94 *Salix lapponum* L.
95 *Salix myrsinifolia* Salisb.
96 *Salix myrsinites* L.
97 *Salix myrtilloides* L.
98 *Salix pedicellata* Desf.
99 *Salix pentandra* L.
100 *Salix phylicifolia* L.
101 *Salix polaris* Wahlenb.
102 *Salix purpurea* L.
103 *Salix repens* L. subsp. *arenaria* (L.) Hiitonen
104 *Salix repens* L. subsp. *repens*
105 *Salix reticulata* L.
106 *Salix retusa* L.
107 *Salix rosmarinifolia* L.
108 *Salix salviifolia* Brot.
109 *Salix serpillifolia* Scop.
110 *Salix silesiaca* Willd.
111 *Salix starkeana* Willd.
112 *Salix triandra* L.
113 *Salix viminalis* L.
114 *Salix waldsteiniana* Willd.
115 *Salix xerophila* Flod.
116 *Taxus baccata* L.
117 *Ulmus glabra* Huds.
118 *Ulmus laevis* Pall.
119 *Ulmus minor* Mill.

Appendix 2. R scripts used to fit and validate the GLM and CQO models.

a. GLM models

```
## Read the biological and climatic data

data<-read.table("trees-env.txt", header = TRUE)

# data contains presence/absence values for 119 species
# (columns 1:119) and the Gdd and Pann values (columns 120:121)
# in each of the 2130 cells (rows)

clim.pres<-read.table("EnvATEAM.txt", header = TRUE)
clim.2050<-read.table("alfi_Hadcm3_2050.txt", header = TRUE)
clim.2080<-read.table("alfi_Hadcm3_2080.txt", header = TRUE)

# clim.pres, clim.2050 and clim.2080 contain the high resolution
# climatic data (Gdd and Pann) for present, 2050, 2080 conditions

## Run the models for the complete dataset

# Create three matrices to save the model predictions for the present,
# 2050 and 2080, respectively

pred.pres<-matrix(nrow = 29531, ncol=119)
pred.2050<-matrix(nrow=29531, ncol=119)
pred.2080<-matrix(nrow=29531, ncol=119)

# Loop in every column (species) and run a GLM model
# for each of the 119 species

for (i in 1:119){
  spX<-glm(data[,i] ~ I(Gdd^2) + Gdd + I(Pann^2) + Pann, family = binomial, data = data)
  # Compute predictions for species i under present conditions
  predX<-predict(spX, newdata = clim.pres, type="response")
  # save predX in the i column of pred.pres
  pred.pres[,i]<-predX
  # Do the same for 2050 and 2080
  predX.50<-predict(spX, newdata = clim.2050, type="response")
  pred.2050[,i]<-predX.50
  predX.80<-predict(spX, newdata = clim.2080, type="response")
  pred.2080[,i]<-predX.80
}

# Model predictions for the present, 2050 and 2080 are now saved
# in pred.pres, pred.2050 and pred.2080
```

b. Cross-validation of GLM models

```
library (PresenceAbsence)

# In order to split the data into the training and validation
# sets, create a vector with length equal to the number of cells
# (2130 in this case) and the appropriate proportion of ones and
# zeros (1342 and 788, in this case).
vector.split<-c(rep(1, 1342), rep(0, 788))
# Randomize the positions of zeros and ones
vector.split<-sample(vector.split)
# Split the data into a training and validation set
train1<-subset(data, vector.split==1)
vall<-subset(data, vector.split==0)
# Create a matrix to save the predictions
pred.vall<-matrix(nrow = 788, ncol=119)

# Loop in every column (species) and run a GLM model
# for each of the 119 species, using the training set
for (i in 1:119){
spX<-glm(train1[,i] ~ I(Gdd^2) + Gdd + I(Pann^2) + Pann, family = binomial, data =
train1)
predX<-predict(spX, newdata=vall, type="response")
pred.vall[,i]<-predX
}
# pred.vall contains the probabilities predicted by the model built
# with the training data in each of the 788 cells of the validation
# set, for each of the 119 species

# Create a matrix to save the sensitivity, specificity and kappa
# values (3 rows) for the 119 species (119 columns)

kappal<-matrix(nrow=3, ncol=119)

# Loop in every species and compute the sensitivity, specificity and
# kappa values

for (i in 1:119){
data.kappal<-data.frame(rownames(vall), vall[,i], pred.vall[,i])
cmx1.X<-cmx(data.kappal, threshold = (sum(train1[i])/1342), which.model = 1, na.rm =
FALSE) # threshold is species prevalence
kappal.X<-Kappa(cmx1.X, st.dev = FALSE)
sens1.X<-sensitivity(cmx1.X, st.dev = FALSE)
spec1.X<-specificity(cmx1.X, st.dev = FALSE)
kappal[1,i]<-kappal.X
kappal[2,i]<-sens1.X
kappal[3,i]<-spec1.X
}

# kappal contains sensitivity, specificity and kappa values for each
# species
```

```

# Repeat the same procedure up to 10 times with different randomized
# vectors

c. CQO model
library (VGAM)

# Biological and climatic data are the same as for GLMs
# Run the rank-2 CQO model

cqo.trees<-cqo(cbind(sp1, sp2, sp3, ...sp119)~ Gdd + Pann, family = binomialff(link =
"logit", mv = TRUE), Rank=2, data = data, Bestof = 10)

# Compute model predictions for the present, 2050 and 2080
pred.cqo.pres<-predict(cqo.trees, newdata=clim.pres, type="response")
pred.cqo.2050<-predict(cqo.trees, newdata=clim.2050, type="response")
pred.cqo.2080<-predict(cqo.trees, newdata=clim.2080, type="response")

d. Cross-validation of CQO model
library (PresenceAbsence)

# In order to split the data into the training and validation
# sets, create a vector with length equal to the number of cells
# (2130 in this case) and the appropriate proportion of ones and
# zeros (1342 and 788, in this case)

vector.split<-c(rep(1, 1342), rep(0, 788))

# Randomize the positions of zeros and ones
vector.split<-sample(vector.split)
# Split the data into a training and validation set
train1<-subset(data, vector.split==1)
vall<-subset(data, vector.split==0)

# Run the CQO model with the training data
cqo.val<-cqo(cbind(sp1, sp2, sp3, ...sp119)~ Gdd + Pann, family = binomialff(link =
"logit", mv = TRUE), Rank=2, data = train1, Bestof = 10)
# Compute model predictions for the validation set
pred.cqo.sample1<-predict(cqo.sample1, newdata=vall, type=c("response"))

# Create a matrix to save the sensitivity, specificity and kappa
# values (3 rows) for the 119 species (119 columns)

kappal<-matrix(nrow=3, ncol=119)

# Loop in every species and compute the sensitivity, specificity and
# kappa values

for (i in 1:119){
data.kappal<-data.frame(rownames(vall), vall[,i], pred.cqo.sample1[,i])
cmx1.X<-cmx(data.kappal, threshold = (sum(train1[i])/1342), which.model = 1, na.rm =

```

```
FALSE)
kappa1.X<-Kappa(cmx1.X, st.dev = FALSE)
sens1.X<-sensitivity(cmx1.X, st.dev = FALSE)
spec1.X<-specificity(cmx1.X, st.dev = FALSE)
kappa1[1,i]<-kappa1.X
kappa1[2,i]<-sens1.X
kappa1[3,i]<-spec1.X
}

# kappa1 contains sensitivity, specificity and kappa values for each
# species

# Repeat the same procedure up to 10 times with different randomized
# vectors
```