Non-linear thermal gradients shape broad-scale patterns in geographic range size and can reverse Rapoport's Rule: Appendix B

Authors: Adam Tomašových, David Jablonski, Sarah K. Berke, Andrew Z. Krug, James W. Valentine

Temperature-limited range-expansion model

We use the Western Atlantic transect as an example for predicting the latitudinal gradient in latitudinal range size, in thermal range size, and in the clustering of range limits for three temperature-limited range-expansion scenarios diagrammed in fig. 1A. In the *stringent temperature-limited scenario*, species only occur at latitudes where the temperature is never lower than their minimum temperature at the latitude of their origin and never higher than the maximum temperature at the latitude of their origin. In the *median temperature-limited scenario*, species track mean sea-surface temperature that is bounded by the minimum and maximum temperatures at the latitude of their origin. Therefore, as temperature declines towards higher latitudes, once the range expands up to the latitude where median temperature is equal to the minimum temperature tolerated by a given species, temperature at higher latitudes will be colder for (approximately) more than half the year than the minimum temperature tolerated by that species. In the *relaxed temperature-limited scenario*, species track minimum and maximum sea-surface temperature within the minimum and maximum temperatures at the latitude of their origin, so they can inhabit even those latitudes where either minimum or maximum temperature remains within their bounds for a very short time of a year.

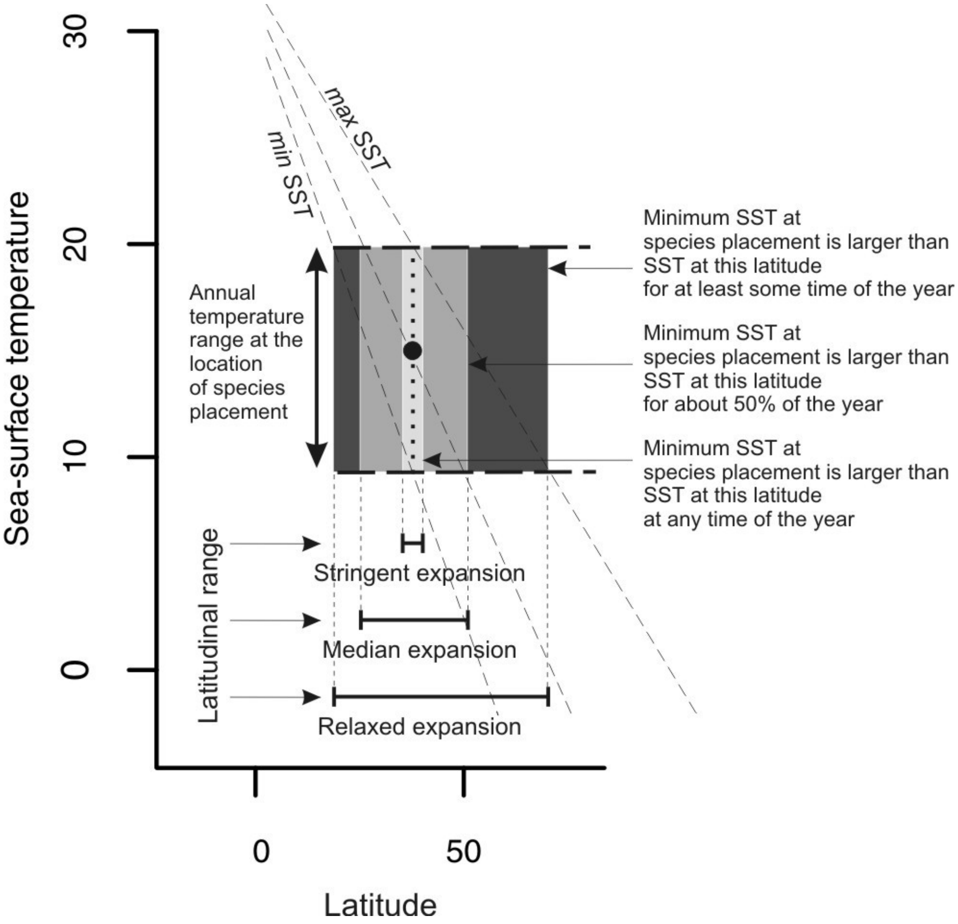

Figure B1 Three scenarios for latitudinal range expansion limited by annual daily SST minima and maxima. In the stringent scenario (light-grey range), species only occupy habitats that lie completely within the minimum and maximum temperature at their initial latitudinal location of placement (latitude of black point); in the median scenario (medium-gray range), species occupy habitats where SST falls between the minimum and maximum temperatures at the latitude of their placement for approximately 50% of the year, and in the relaxed scenario (dark-gray range) they can track habitats if SST remains within those bounds for at least some part of the year.

We upload latitudinal vectors with minimum, median and maximum sea-surface temperature available at 1º resolution. Therefore, we have three vectors with minimum (`minT`), median (`medianT`), and maximum (`maxT`), and one vector with corresponding latitudes for these temperature values (`lats`).

```
load(file="WA gradients in SST.Rdata")
```

We split these gradients into southern and northern hemispheres because the scenarios are first run separately in each hemisphere and species that range up to equator are then allowed to cross the equator if temperatures adjacent to the equator in the other hemisphere are still viable for a given species.

```
#SPLIT SST VECTORS INTO SOUTHERN AND #NORTHERN HEMISPHERES
SEND <- which(lats==0.5)
NBEGIN <- which(lats==-0.5)
NEND <- length(lats)

#SOUTHERN HEMISPHERE GRADIENTS
SmedianT <- medianT[1:SEND]
SminT <- minT[1:SEND]
SmaxT <- maxT[1:SEND]

#NORTHERN HEMISPHERE GRADIENTS
NmedianT <- medianT[NBEGIN:NEND]
NminT <- minT[NBEGIN:NEND]
NmaxT <- maxT[NBEGIN:NEND]
```

Next, we generate two vectors, one for the southern hemisphere (`Sfullgradient`) and one for the northern hemisphere (`Nfullgradient`). They represent latitudinal locations of 1677 species that are placed at equal distances along latitudinal gradients from the northern margin of Antarctica up to Arctic. We use 0.1º distance among species.

```
Sfull=seq(min(lats),0,by=0.1)
Nfull=seq(0,max(lats),by=0.1)
```

Next, we downscale the temperature gradient at 1° resolution to 0.1 ° resolution that matches the resolution of the previous two vectors that give locations of species placement. We use polynomial regression. We generate three vectors for the Northern Hemisphere and three vectors for the Southern Hemisphere (for minimum, median and maximum temperature) that have the same length as the two vectors with initial latitudinal locations of individual species (`Sfull`, `Nfull`). The predicted 0.1 ° temperature gradients should match with 1° gradients as closely as possible.

```
SMOOTH=0.5
predictNTEMP<-predict(loess(NmedianT~ lats[NBEGIN:NEND], span=SMOOTH), newdata=Nfull)
predictNTEMPmax<-predict(loess(NmaxT~ lats[NBEGIN:NEND], span=SMOOTH), newdata=Nfull)
predictNTEMPmin<-predict(loess(NminT~ lats[NBEGIN:NEND], span=SMOOTH), newdata=Nfull)
predictSTEMP<-predict(loess(SmedianT~I(lats[1:SEND]), span=SMOOTH), newdata=Sfull)
predictSTEMPmax<-predict(loess(SmaxT~I(lats[1:SEND]), span=SMOOTH), newdata=Sfull)
predictSTEMPmin<-predict(loess(SminT~I(lats[1:SEND]), span=SMOOTH), newdata=Sfull)
```

We can compare the shapes of original and smoothed temperature gradients:

```
par(cex=1.4)
par(mfrow=c(2,2))
plot(lats, medianT, ylim=c(-2,32), lwd=3,type="l", xlab="Latitude", ylab="Sea-surface
temperature", main="1° gradient")
lines(lats, maxT, lwd=1, lty=2)
lines(lats, minT, lwd=1, lty=2)
plot(c(Sfull, Nfull), c(predictSTEMP, predictNTEMP), ylim=c(-2,32), lwd=3, type="l",
xlab="Latitude", ylab="Sea-surface temperature", main="Smoothed 0.1° gradient")
lines(c(Sfull, Nfull), c(predictSTEMPmin, predictNTEMPmin), lty=2, lwd=1)
lines(c(Sfull, Nfull), c(predictSTEMPmax, predictNTEMPmax), lty=2, lwd=1)
```

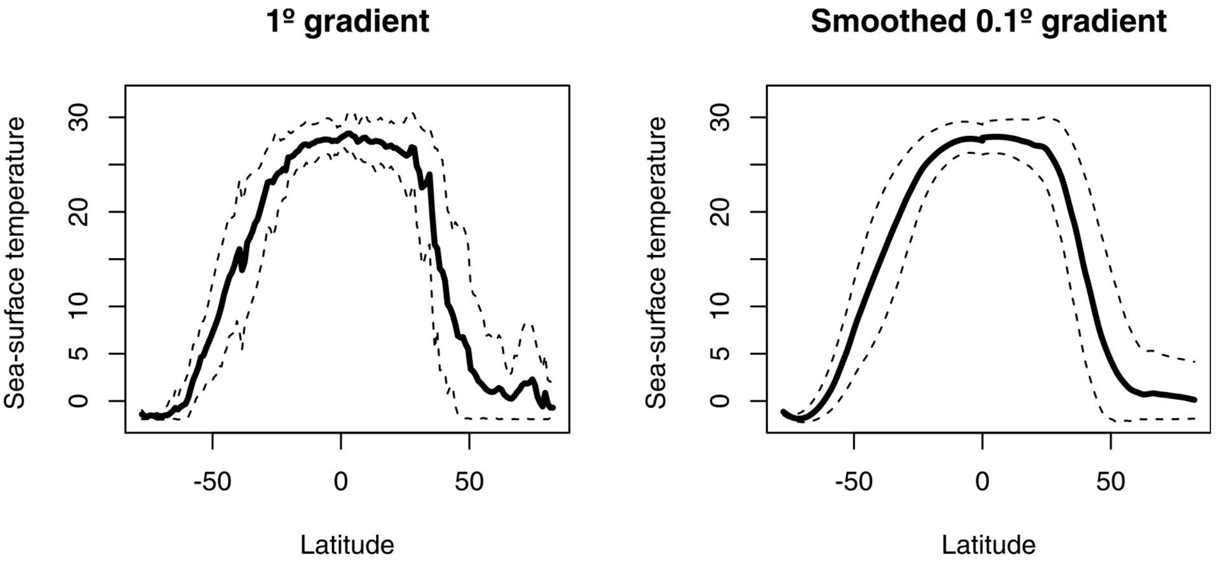

Figure B2 Latitudinal gradient in annual minimum, median and maximum daily sea-surface temperature in the Western Atlantic.

The temperature gradients increase almost monotonically (but not perfectly) towards the equator. First, we change the predicted gradients in minimum, median and maximum temperature into monotonically-increasing gradients, separately for each hemisphere. This transformation has almost no effect on the shape of temperature gradients but allows using the function `findInterval` that finds the temperature value in the vector of all temperature values within each hemisphere. Alternatively, one can use the function `match` to search for temperature values in the vector with non-monotonically-changing values. The six vectors generated below represent minimum, median and maximum temperature at the latitude of initial placement of each species, separately for each hemisphere.

```
NspeciesmedianT  <- lowess(Nfull~predictNTEMP, f=SMOOTH/3)$x
SspeciesmedianT  <- lowess(Sfull~predictSTEMP, f=SMOOTH/3)$x
NspeciesmaxT  <- lowess(Nfull~predictNTEMPmax, f=SMOOTH/3)$x
SspeciesmaxT  <- lowess(Sfull~predictSTEMPmax, f=SMOOTH/3)$x
NspeciesminT  <- lowess(Nfull~predictNTEMPmin, f=SMOOTH/3)$x
SspeciesminT  <- lowess(Sfull~predictSTEMPmin, f=SMOOTH/3)$x
```

The final shape of temperature gradients with monotonic changes in each hemisphere and used in the model:

```
par(cex=1.4)
plot(c(Sfull, Nfull), c(predictSTEMP, predictNTEMP), ylim=c(-2,32), lwd=2, col="gray", type="n", xlab="Latitude", ylab="Sea-surface temperature", main="Downscaled temperature gradient")
lines(Sfull, SspeciesmedianT, lwd=2)
lines(Nfull, rev(NspeciesmedianT), lwd=2)
lines(Sfull, SspeciesminT, lty=2, lwd=1)
lines(Nfull, rev(NspeciesminT), lty=2, lwd=1)
lines(Sfull, SspeciesmaxT, lty=2, lwd=1)
lines(Nfull, rev(NspeciesmaxT), lty=2, lwd=1)

SspeciesmedianT <-  round(SspeciesmedianT, digits=1)
SspeciesminT <-  round(SspeciesminT , digits=1)
SspeciesmaxT <-  round(SspeciesmaxT , digits=1)
NspeciesmedianT <-  round(rev(NspeciesmedianT), digits=1)
NspeciesminT <-  round(rev(NspeciesminT) , digits=1)
NspeciesmaxT <-  round(rev(NspeciesmaxT) , digits=1)
```

Next, we initialize vectors that will represent range limits – each species will initially have two range limits – one poleward range limit and one equatorward range limit - in each hemisphere. We initialize range limits for all three scenarios.

```
Sdecide <- length(Sfull)
Ndecide <- length(Nfull)
Nspecies <- Sdecide+Ndecide

#INITIALIZING RANGE LIMITS FOR SPECIES ORIGINATING IN THE SOUTHERN HEMISPHERE
SOPTTROPICALSspecies <- rep(NA, Sdecide)
SOPTPOLARSspecies <- rep(NA, Sdecide)
NOPTTROPICALSspecies <- rep(NA, Sdecide)
NOPTPOLARSspecies <- rep(NA, Sdecide)
SMAXTROPICALSspecies <- rep(NA, Sdecide)
SMAXPOLARSspecies <- rep(NA, Sdecide)
NMAXTROPICALSspecies <- rep(NA, Sdecide)
NMAXPOLARSspecies <- rep(NA, Sdecide)
SMINTROPICALSspecies <- rep(NA, Sdecide)
SMINPOLARSspecies <- rep(NA, Sdecide)
NMINTROPICALSspecies <- rep(NA, Sdecide)
```

```
NMINPOLARSspecies <- rep(NA, Sdecide)

#INITIALIZING RANGE LIMITS FOR SPECIES ORIGINATING IN THE NORTHERN HEMISPHERE
SOPTTROPICALNspecies <- rep(NA, Ndecide)
SOPTPOLARNspecies <- rep(NA, Ndecide)
NOPTTROPICALNspecies <- rep(NA, Ndecide)
NOPTPOLARNspecies <- rep(NA, Ndecide)
SMAXTROPICALNspecies <- rep(NA, Ndecide)
SMAXPOLARNspecies <- rep(NA, Ndecide)
NMAXTROPICALNspecies <- rep(NA, Ndecide)
NMAXPOLARNspecies <- rep(NA, Ndecide)
SMINTROPICALNspecies <- rep(NA, Ndecide)
SMINPOLARNspecies <- rep(NA, Ndecide)
NMINTROPICALNspecies <- rep(NA, Ndecide)
NMINPOLARNspecies <- rep(NA, Ndecide)
```

In “median” scenario, we find the median temperature that is equal to the maximum temperature at species origin by searching the vector of median temperatures at 0.1 resolution. `id` then identifies the index of temperature in the vector of latitudes (`Sfull, or Nfull)`. This latitude defines the equatorward range limit. Similarly, we find the median temperature that is equal to the minimum temperature at species origin in the vector of median temperatures, and then the latitude of this match. This latitude defines the poleward range limit. This routine is performed separately for each hemisphere, so each species has initially four limits.

```
############################################################################
# SPECIES ORIGINATING IN SOUTHERN HEMISPHERE – MEDIAN MODEL#
############################################################################

#PREDICTIONS FOR LIMITS FOR SOUTHERN HEMISPHERE
for (i in 1:Sdecide){
	#DETERMINE POLEWARD LIMIT for Southern Hemisphere
	id <- findInterval(SspeciesminT[i], SspeciesmedianT)
		if (id==0) {id=1}
	SOPTPOLARSspecies[i] <-  Sfull[id]

	#DETERMINE EQUATORWARD LIMIT for Southern Hemisphere
```

```
	id <- findInterval(SspeciesmaxT[i],SspeciesmedianT)
	if (id==0) {id=1}
	SOPTTROPICALSspecies[i] <- Sfull[id]

	#DETERMINE POLEWARD LIMIT for N Hemisphere
	id <- findInterval(SspeciesminT[i], rev(NspeciesmedianT))
		if (id==0) {id=1}
	NOPTPOLARSspecies[i] <-  rev(Nfull)[id]

	#DETERMINE EQUATORWARD LIMIT for N Hemisphere
	id <- findInterval(SspeciesmaxT[i], rev(NspeciesmedianT))
		if (id==0) {id=1}
	NOPTTROPICALSspecies[i] <-  rev(Nfull)[id]
}

############################################################################
# SPECIES ORIGINATING IN N HEMISPHERE – MEDIAN MODEL#
############################################################################
for (i in 1:Ndecide){
	#DETERMINE POLEWARD LIMIT for S Hemisphere
	id <- findInterval(NspeciesminT[i], SspeciesmedianT)
	if (id==0) {id=1}
	SOPTPOLARNspecies[i] <-  Sfull[id]

	#DETERMINE EQUATORWARD LIMIT for S Hemisphere
	id <- findInterval(NspeciesmaxT[i], SspeciesmedianT)
	if (id==0) {id=1}
	SOPTTROPICALNspecies[i] <-  Sfull[id]

	#DETERMINE POLEWARD LIMIT for N Hemisphere
	id <- findInterval(NspeciesminT[i], rev(NspeciesmedianT))
	if (id==0) {id=1}
	NOPTPOLARNspecies[i] <-  rev(Nfull)[id]

	#DETERMINE EQUATORWARD LIMIT for N Hemisphere
	id <- findInterval(NspeciesmaxT[i], rev(NspeciesmedianT))
	if (id==0) {id=1}
	NOPTTROPICALNspecies[i] <- rev(Nfull)[id]
}
```

In “relaxed” scenario, we find the minimum temperature that is equal to the maximum temperature at species origin by searching the vector of maximum temperatures. Similarly, we find the maximum temperature that is equal to the minimum temperature at species origin in the vector of minimum temperatures.

```
##############################################################################
# SPECIES ORIGINATING IN S HEMISPHERE - RELAXED SCENARIO#
##############################################################################
for (i in 1:Sdecide){
       #DETERMINE POLEWARD LIMIT for S Hemisphere
       id <- findInterval(SspeciesminT[i], SspeciesmaxT)
       if (id==0) {id=1}
       SMAXPOLARSspecies[i] <-  Sfull[id]

       #DETERMINE EQUATORWARD LIMIT for S Hemisphere
       id <- findInterval(SspeciesmaxT[i], SspeciesminT)
       if (id==0) {id=1}
       SMAXTROPICALSspecies[i] <-  Sfull[id]

       #DETERMINE POLEWARD LIMIT for N Hemisphere
       id <- findInterval(SspeciesminT[i], rev(NspeciesmaxT))
       if (id==0) {id=1}
       NMAXPOLARSspecies[i] <-  rev(Nfull)[id]

       #DETERMINE EQUATORWARD LIMIT for N Hemisphere
       id <- findInterval(SspeciesmaxT[i], rev(NspeciesminT))
       if (id==0) {id=1}
       NMAXTROPICALSspecies[i] <-  rev(Nfull)[id]
}

##############################################################################
# SPECIES ORIGINATING IN N HEMISPHERE - RELAXED SCENARIO#
##############################################################################
for (i in 1:Ndecide){
       #DETERMINE POLEWARD LIMIT for S Hemisphere
       id <- findInterval(NspeciesminT[i], SspeciesmaxT)
       if (id==0) {id=1}
       SMAXPOLARNspecies[i] <-  Sfull[id]
```

```
        #DETERMINE EQUATORWARD LIMIT for S Hemisphere
        id <- findInterval(NspeciesmaxT[i], SspeciesminT)
        if (id==0) {id=1}
        SMAXTROPICALNspecies[i] <-  Sfull[id]

        #DETERMINE POLEWARD LIMIT for N Hemisphere
        id <- findInterval(NspeciesminT[i], rev(NspeciesmaxT))
        if (id==0) {id=1}
        NMAXPOLARNspecies[i] <-  rev(Nfull)[id]

        #DETERMINE EQUATORWARD LIMIT for N Hemisphere
        id <- findInterval(NspeciesmaxT[i], rev(NspeciesminT))
        if (id==0) {id=1}
        NMAXTROPICALNspecies[i] <-  rev(Nfull)[id]
}
```

In “stringent” scenario, we find the minimum temperature that is equal to the minimum temperature at species origin by searching the vector of minimum temperatures. Similarly, we find the maximum temperature that is equal to the maximum temperature at species origin in the vector of maximum temperatures.

```
###############################################################################
# SPECIES ORIGINATING IN S HEMISPHERE - STRINGENT SCENARIO#
###############################################################################
for (i in 1:Sdecide){
        #DETERMINE POLEWARD LIMIT for S Hemisphere
        id <- findInterval(SspeciesminT[i], SspeciesminT)
        if (id==0) {id=1}
        SMINPOLARSspecies[i] <-  Sfull[id]

        #DETERMINE EQUATORWARD LIMIT for S Hemisphere
        id <- findInterval(SspeciesmaxT[i], SspeciesmaxT)
        if (id==0) {id=1}
        SMINTROPICALSspecies[i] <-  Sfull[id]

        #DETERMINE POLEWARD LIMIT for N Hemisphere
        id <- findInterval(SspeciesminT[i], rev(NspeciesminT))
        if (id==0) {id=1}
```

```
        NMINPOLARSspecies[i] <-  rev(Nfull)[id]

        #DETERMINE EQUATORWARD LIMIT for N Hemisphere
        id <- findInterval(SspeciesmaxT[i], rev(NspeciesmaxT))
        if (id==0) {id=1}
        NMINTROPICALSspecies[i] <-  rev(Nfull)[id]
}

##############################################################################
#SPECIES ORIGINATING IN THE N HEMISPHERE – STRINGENT SCENARIO
##############################################################################
for (i in 1:Ndecide){
        #DETERMINE POLEWARD LIMIT for S Hemisphere
        id <- findInterval(NspeciesminT[i], SspeciesminT)
        if (id==0) {id=1}
        SMINPOLARNspecies[i] <-  Sfull[id]

        #DETERMINE EQUATORWARD LIMIT for S Hemisphere
        id <- findInterval(NspeciesmaxT[i], SspeciesmaxT)
        if (id==0) {id=1}
        SMINTROPICALNspecies[i] <-  Sfull[id]

        #DETERMINE POLEWARD LIMIT for N Hemisphere
        id <- findInterval(NspeciesminT[i], rev(NspeciesminT))
        if (id==0) {id=1}
        NMINPOLARNspecies[i] <- rev(Nfull)[id]

        #DETERMINE EQUATORWARD LIMIT for N Hemisphere
        id <- findInterval(NspeciesmaxT[i], rev(NspeciesmaxT))
        if (id==0) {id=1}
        NMINTROPICALNspecies[i] <-  rev(Nfull)[id]
}
```

Next, we allow only those species to cross the equator that expand their ranges completely up to the equator, otherwise species originating in the southern hemisphere do not expand to northern hemisphere and vice versa. Temporarily, we assign zero values to species that do not cross the equator (zero latitude).

```
NOPTPOLARSspecies[SOPTTROPICALSspecies<0 | NOPTTROPICALSspecies>0] <- 0
NOPTTROPICALSspecies[SOPTTROPICALSspecies<0 | NOPTTROPICALSspecies>0] <- 0
```

```
SOPTPOLARNspecies[NOPTTROPICALNspecies>0 | SOPTTROPICALNspecies<0] <- 0
SOPTTROPICALNspecies[NOPTTROPICALNspecies>0 | SOPTTROPICALNspecies<0] <- 0
NMAXPOLARSspecies[SMAXTROPICALSspecies<0 | NMAXTROPICALSspecies>0] <- 0
NMAXTROPICALSspecies[SMAXTROPICALSspecies<0 | NMAXTROPICALSspecies>0] <- 0
SMAXPOLARNspecies[NMAXTROPICALNspecies>0 | SMAXTROPICALNspecies<0] <- 0
SMAXTROPICALNspecies[NMAXTROPICALNspecies>0 | SMAXTROPICALNspecies<0] <- 0
NMINPOLARSspecies[SMINTROPICALSspecies<0 | NMINTROPICALSspecies>0] <- 0
NMINTROPICALSspecies[SMINTROPICALSspecies<0 | NMINTROPICALSspecies>0] <- 0
SMINPOLARNspecies[NMINTROPICALNspecies>0 | SMINTROPICALNspecies<0] <- 0
SMINTROPICALNspecies[NMINTROPICALNspecies>0 | SMINTROPICALNspecies<0] <- 0
SENDinShemisphere <- length(Sfull)
```

Next, we compute latitudinal range sizes for each species for all three scenarios.

```
############################################################################
#PER-SPECIES RANGE SIZES AND LIMITS - MEDIAN MODEL
############################################################################

#INITIALIZE VECTORS
Slatrange <- numeric(); Nlatrange <- numeric()
SOUTHERNSlimit <- numeric(); SOUTHERNNlimit <- numeric()
NORTHERNSlimit <- numeric(); NORTHERNNlimit <- numeric()

#SPECIES THAT ORIGINATED IN S HEMISPHERE
for (i in 1:Sdecide) {
      if (NOPTTROPICALSspecies[i]==0 &
                  NOPTPOLARSspecies[i]>0) {
            Nlimit <- NOPTPOLARSspecies[i]
      }

      if (NOPTTROPICALSspecies[i]==0 &
                  NOPTPOLARSspecies[i]==0) {
            Nlimit <- SOPTTROPICALSspecies[i]
      }

      Slatrange[i] <- abs(diff(c(Nlimit,SOPTPOLARSspecies[i])))
      SOUTHERNSlimit[i] <- SOPTPOLARSspecies[i]
      SOUTHERNNlimit[i] <- Nlimit

      if(Nlimit<SOPTPOLARSspecies[i]) {
            Slatrange[i] <- 0.1; SOUTHERNSlimit[i] <-  Sfull[i]
```

```
            SOUTHERNNlimit[i] <- Sfull[i]
        }
}

#SPECIES THAT ORIGINATED IN N HEMISPHERE
for (i in 1:Ndecide) {
        if (SOPTTROPICALNspecies[i]==0 &
                    SOPTPOLARNspecies[i]<0) {
            Slimit <- SOPTPOLARNspecies[i]}

        if (SOPTTROPICALNspecies[i]==0 &
                    SOPTPOLARNspecies[i]==0) {
            Slimit <- NOPTTROPICALNspecies[i]
        }

        Nlatrange[i] <- abs(diff(c(Slimit,NOPTPOLARNspecies[i])))
        NORTHERNSlimit[i] <- Slimit
        NORTHERNNlimit[i] <- NOPTPOLARNspecies[i]

        if(Slimit>NOPTPOLARNspecies[i]) {
            Nlatrange[i] <- 0.1;NORTHERNSlimit[i] <-  rev(Nfull)[i];
            NORTHERNNlimit[i] <- rev(Nfull)[i]
        }
}

#OUTPUT
meanlatrange <- c(Slatrange,Nlatrange)
meanSlimit <- c(SOUTHERNSlimit,NORTHERNSlimit)
meanNlimit <- c(SOUTHERNNlimit,NORTHERNNlimit)

##############################################################################
#PER-SPECIES RANGE SIZES AND LIMITS     FOR RELAXED MODEL#
##############################################################################
#
#SPECIES THAT ORIGINATED IN S HEMISPHERE
for (i in 1:Sdecide) {
        if (NMAXTROPICALSspecies[i]==0 &
                    NMAXPOLARSspecies[i]>0) {
            Nlimit <- NMAXPOLARSspecies[i]
        }
```

```
	if (NMAXTROPICALSspecies[i]==0 &
			NMAXPOLARSspecies[i]==0) {
		Nlimit <- SMAXTROPICALSspecies[i]
	}

	Slatrange[i] <- abs(diff(c(Nlimit,SMAXPOLARSspecies[i])))
	SOUTHERNSlimit[i] <- SMAXPOLARSspecies[i]
	SOUTHERNNlimit[i] <- Nlimit

	if(Nlimit<SMAXPOLARSspecies[i]) {
		Slatrange[i] <- 0.1; SOUTHERNSlimit[i] <-  Sfull[i];
		 SOUTHERNNlimit[i] <- Sfull[i]
	}
}
#SPECIES THAT ORIGINATED IN N HEMISPHERE
for (i in 1:Ndecide) {
	if (SMAXTROPICALNspecies[i]==0 &
			SMAXPOLARNspecies[i]<0) {
		Slimit <- SMAXPOLARNspecies[i]
	}

	if (SMAXTROPICALNspecies[i]==0 &
			 SMAXPOLARNspecies[i]==0) {
		Slimit <- NMAXTROPICALNspecies[i]
	}

	Nlatrange[i] <- abs(diff(c(Slimit,NMAXPOLARNspecies[i])))
	NORTHERNSlimit[i] <- Slimit
	NORTHERNNlimit[i] <- NMAXPOLARNspecies[i]

	if(Slimit>NMAXPOLARNspecies[i]) {
		Nlatrange[i] <- 0.1;NORTHERNSlimit[i] <-  rev(Nfull)[i];
		NORTHERNNlimit[i] <-  rev(Nfull)[i]
	}
}

#OUTPUT
maxlatrange <- c(Slatrange,Nlatrange)
maxSlimit <- c(SOUTHERNSlimit,NORTHERNSlimit)
maxNlimit <- c(SOUTHERNNlimit,NORTHERNNlimit)

#############################################################################
```

```
# PER-SPECIES RANGE SIZES AND LIMITS-STRINGENT MODEL#
##############################################################################

#SPECIES THAT ORIGINATED IN S HEMISPHERE
for (i in 1:Sdecide) {
       if (NMINTROPICALSspecies[i]==0 &
                     NMINPOLARSspecies[i]>0) {
              Nlimit <- NMINPOLARSspecies[i]
       }

       if (NMINTROPICALSspecies[i]==0 &
                    NMINPOLARSspecies[i]==0) {
              Nlimit <- SMINTROPICALSspecies[i]
       }

       Slatrange[i] <- abs(diff(c(Nlimit,SMINPOLARSspecies[i])))
       SOUTHERNSlimit[i] <- SMINPOLARSspecies[i]
       SOUTHERNNlimit[i] <- Nlimit

       if(Nlimit<SMINPOLARSspecies[i]) {
              Slatrange[i] <- 0.1; SOUTHERNSlimit[i] <-  Sfull[i];
              SOUTHERNNlimit[i] <- Sfull[i]
       }
}

#SPECIES THAT ORIGINATED IN N HEMISPHERE
for (i in 1:Ndecide) {
       if (SMINTROPICALNspecies[i]==0 &
                    SMINPOLARNspecies[i]<0) {
              Slimit <- SMINPOLARNspecies[i]
       }

       if (SMINTROPICALNspecies[i]==0 &
                    SMINPOLARNspecies[i]==0) {
              Slimit <- NMINTROPICALNspecies[i]
       }

       Nlatrange[i] <- abs(diff(c(Slimit,NMINPOLARNspecies[i])))
       NORTHERNSlimit[i] <- Slimit
       NORTHERNNlimit[i] <- NMINPOLARNspecies[i]

       if(Slimit>NMINPOLARNspecies[i]) {
```

```
                Nlatrange[i] <- 0.1;NORTHERNSlimit[i] <-  rev(Nfull) [i];
                NORTHERNNlimit[i] <-  rev(Nfull)[i]
        }
}

#OUTPUT
minlatrange <- c(Slatrange,Nlatrange)
minSlimit <- c(SOUTHERNSlimit,NORTHERNSlimit)
minNlimit <- c(SOUTHERNNlimit,NORTHERNNlimit)
```

Next, we compute latitudinal range size and thermal range size per 5-degree latitudinal bands for all three scenarios. We use medians.

```
#################################################################
#      COMPUTING PER-REGION RANGE AND PER-REGION SST RANGE   #
#################################################################

#Remove those 5-degree bands not available in empirical dataset
remove <- c(1,2,4,5,6,7,34,35,36)
remove<-c(1,2,36)

#DEFINE THE WIDTH OF LATITUDINAL BANDS IN DEGREES
INT=5
latgradient <- seq(-90,85,by=INT)
Nspecies<-Sdecide+Ndecide


#INITIALIZE SPECIES PRESENCE-ABSENCE TABLES: ROWS ARE SPECIES AND COLUMNS ARE
#LATITUDINAL BANDS
MAXcomp <- array(0,dim=c(Nspecies, length(latgradient)))
MEDIANcomp <- array(0,dim=c(Nspecies, length(latgradient)))
MINcomp <- array(0,dim=c(Nspecies, length(latgradient)))

#INITIALIZE OUTPUT TABLES FOR MEDIAN LATITUDINAL RANGES: ROWS ARE SPECIES AND #COLUMNS
#ARE LATITUDINAL BANDS
MEDIANrangecomp <- array(NA,dim=c(Nspecies, length(latgradient)))
MAXrangecomp <- array(NA,dim=c(Nspecies, length(latgradient)))
MINrangecomp <- array(NA,dim=c(Nspecies, length(latgradient)))

#INITIALIZE OUTPUT TABLES FOR MEDIAN THERMAL RANGES: ROWS ARE SPECIES AND #COLUMNS
#ARE LATITUDINAL BANDS
```

```
MEDIANspSSTrangecomp <- array(NA,dim=c(Nspecies, length(latgradient)))
MEDIANspSSTranges <- array(NA,dim=c(Nspecies, length(latgradient)))
MAXspSSTrangecomp <- array(NA,dim=c(Nspecies, length(latgradient)))
MAXspSSTranges <- array(NA,dim=c(Nspecies, length(latgradient)))
MINspSSTrangecomp <- array(NA,dim=c(Nspecies, length(latgradient)))
MINspSSTranges <- array(NA,dim=c(Nspecies, length(latgradient)))

#INITIALIZE VECTORS WITH SPECIES THERMAL RANGES
MEDIANspeciesspSSTrange <- numeric()
MAXspeciesspSSTrange <- numeric()
MINspeciesspSSTrange <- numeric()



########################################
#MEDIAN MODEL#
#########################################
latsequence=seq(-90,90,by=INT)
temp=cut(lats, latsequence)
newmeanT=tapply(medianT, temp, mean)
newminT=tapply(minT, temp, mean)
newmaxT=tapply(maxT, temp, mean)

#PER-BAND LATITUDINAL RANGE AT 0 m
for (i in 1:Nspecies) {
       #for each species, find its limits in latitudinal bands
       sequence <- seq(meanSlimit[i],meanNlimit[i],by=1)

       # comment about this loop?
       for (j in 1:length(sequence)) {
              id <- findInterval(sequence[j], latgradient)
              MEDIANrangecomp [i,id] <- meanlatrange[i]
              MEDIANcomp[i,id] <- 1
              MEDIANspSSTranges[i,id] <- newmeanT[id]
       }

       MEDIANspeciesspSSTrange[i] <- IQR(MEDIANspSSTranges[i,], na.rm=T)
}

#PER-BAND SPATIAL THERMAL AND SEASONAL THERMAL RANGE
for (i in 1: Nspecies) {
       sequence <- seq(meanSlimit[i],meanNlimit[i],by=1)
```

```
		for (j in 1:length(sequence)) {
			id <- findInterval(sequence[j], latgradient)
			MEDIANspSSTrangecomp [i,id] <- MEDIANspeciesspSSTrange[i]
		}
}

##########################################
#RELAXED MODEL#
##########################################
#PER-BAND LATITUDINAL RANGE AT 0 m
for (i in 1:(Sdecide+Ndecide)) {
		#for each species, find its limits in latitudinal bands
		sequence <- seq(maxSlimit[i],maxNlimit[i],by=1)

		# comment?
		for (j in 1:length(sequence)) {
			id <- findInterval(sequence[j], latgradient)
			MAXrangecomp [i,id] <- maxlatrange[i]
			MAXcomp [i,id] <- 1
			MAXspSSTranges[i,id] <- newmeanT[id]
		}

		MAXspeciesspSSTrange[i] <- IQR(MAXspSSTranges[i,], na.rm=T)
}

#PER-BAND SPATIAL THERMAL AND SEASONAL THERMAL RANGE
for (i in 1:(Sdecide+Ndecide)) {
		sequence <- seq(maxSlimit[i],maxNlimit[i],by=1)

		for (j in 1:length(sequence)) {
			id <- findInterval(sequence[j], latgradient)
			MAXspSSTrangecomp [i,id] <- MAXspeciesspSSTrange[i]
		}
}

##########################################
#STRINGENT MODEL#
##########################################
#PER-BAND LATITUDINAL RANGE AT 0 m
for (i in 1:(Sdecide+Ndecide)) {
		sequence <- seq(minSlimit[i],minNlimit[i],by=1)
```

```
	for (j in 1:length(sequence)) {
		id <- findInterval(sequence[j], latgradient)
		if (id == 0) {id=1}
		MINrangecomp [i,id] <- minlatrange[i]
		MINcomp [i,id] <- 1
		MINspSSTranges[i,id] <- newmeanT[id]
	}

	MINspeciesspSSTrange[i] <- IQR(MINspSSTranges[i,], na.rm=T)
}

#PER-BAND SPATIAL THERMAL AND SEASONAL THERMAL RANGE
for (i in 1:(Sdecide+Ndecide)) {
	sequence <- seq(minSlimit[i],minNlimit[i],by=1)

	for (j in 1:length(sequence)) {
		id <- findInterval(sequence[j], latgradient)
		MINspSSTrangecomp [i,id] <- MINspeciesspSSTrange[i]
	}
}

##################################################################################
#VISUALIZE THE EXPECTED RELATION BETWEEN MODELED LATITUDINAL RANGE AND THERMAL RANGE
#PER SPECIES IN BOXPLOTS – GROUP LATITUDINAL RANGES INTO RANGE-SIZE CLASSES
##################################################################################
latbins<-seq(0,12750, by=750)
latrangebins<-cut(meanlatrange*111.5, breaks=latbins)
thermalFORboxplots<-split(MEDIANspeciesspSSTrange, latrangebins)
thermalFORboxplots<-thermalFORboxplots[-c(26:31)]

par(cex=1.2)
namesforbins=latbins[-1]
namesforbins<-namesforbins[namesforbins<13000]
par(mfcol=c(2,2))
boxplot(thermalFORboxplots, breaks=latbins[latbins<12500], names=namesforbins, las=2,
ylab="Thermal range", col="gray",
cex.axis=0.8, ylim=c(0,20), range=1.5, pars = list( medlwd= 0.8), outline=FALSE)
medians<-boxplot(thermalFORboxplots, plot=F)$stats[3,]
LCI<-boxplot(thermalFORboxplots, plot=F)$conf[1,]
UCI<-boxplot(thermalFORboxplots, plot=F)$conf[2,]
points(c(1:length(medians)), medians, pch=16, cex=1)
for (i in 1:length(medians)) {
```

```
        lines(c(i,i), c(LCI[i], UCI[i]), lwd=2)
        }
```

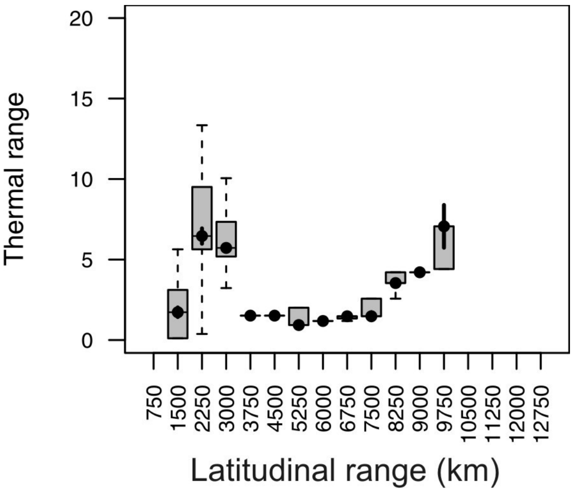

Figure B3 The expected relationship between latitudinal ranges (grouped into classes along the x-axis) and thermal ranges, using the median scenario. Black points represent medians with 95% confidence intervals.

```
#########################################
#RAPOPORT PATTERNS IN DEGREES
#########################################
latgradient <- seq(-90,85,by=INT)
latgradient=latgradient[-remove]


meanPERBANDrange<-apply(MEDIANrangecomp[,-remove], MARGIN=2, median, na.rm=T)
meanPERBANDspSSTrange<-apply(MEDIANspSSTrangecomp[,-remove], MARGIN=2, median,
na.rm=T)

maxPERBANDrange<-apply(MAXrangecomp [,-remove], MARGIN=2, median, na.rm=T)
maxPERBANDspSSTrange<-apply(MAXspSSTrangecomp [,-remove], MARGIN=2, median, na.rm=T)

minPERBANDrange<-apply(MINrangecomp[,-remove], MARGIN=2, median, na.rm=T)
minPERBANDspSSTrange<-apply(MINspSSTrangecomp [,-remove], MARGIN=2, median, na.rm=T)
```

For plotting, we can choose one of the scenarios (i.e., `"Minimum", "Median", or "Maximum"`):

```
model="Median"
```

```
#########################################
#      RANGE DISTRIBUTIONS
#########################################

plot(c(Sfull,Nfull),c(1:length(c(predictSTEMP, predictNTEMP))), type="n",
xlab="Latitude", cex.lab=1.2, cex.axis=1.2,
ylab="Latitude of of species origin",  cex.main=1, xlim=c(-90,90), yaxt="n")
full <- length(c(predictSTEMP, predictNTEMP))
axis(2, at=c(0.25*full, 0.5*full, 0.75*full), labels=c(-40, 0, 40), cex.lab=1.2,
cex.axis=1.2)


if (model=="Maximum") {
for (i in 1:length(predictSTEMP)){
       lines(c(SMAXTROPICALSspecies[i],SMAXPOLARSspecies[i]),c(i,i),col="gray51")
       }
for (i in 1:length(predictSTEMP)) {
       lines(c(NMAXTROPICALSspecies[i],NMAXPOLARSspecies[i]),c(i,i),col="gray51")
       }
for (i in 1:length(predictNTEMP)){
       lines(c(SMAXTROPICALNspecies[i],SMAXPOLARNspecies[i]),
       c(i+length(Sfull),i+length(Sfull)),col="gray51")
}
for (i in 1:length(predictNTEMP)) {
       lines(c(NMAXTROPICALNspecies[i],NMAXPOLARNspecies[i]),
       c(i+length(Sfull),i+length(Sfull)),col="gray51")
       }
}

if (model=="Median") {
for (i in 1:length(predictSTEMP)){
       lines(c(SOPTTROPICALSspecies[i],SOPTPOLARSspecies[i]),c(i,i), col="gray51")
       }
for (i in 1:length(predictSTEMP)){
       lines(c(NOPTTROPICALSspecies[i],NOPTPOLARSspecies[i]),c(i,i),col="gray51")
       }
for (i in 1:length(predictNTEMP)){
       lines(c(SOPTTROPICALNspecies[i],SOPTPOLARNspecies[i]),
       c(i+length(Sfull),i+length(Sfull)), col="gray51")
       }
```

```
for (i in 1:length(predictNTEMP)){
       lines(c(NOPTTROPICALNspecies[i],NOPTPOLARNspecies[i]),
       c(i+length(Sfull),i+length(Sfull)), col="gray51")
       }

}

if (model=="Minimum") {
for (i in 1:length(predictSTEMP)) {
       lines(c(SMINTROPICALSspecies[i],SMINPOLARSspecies[i]),c(i,i),col="gray51")
       }
for (i in 1:length(predictSTEMP)) {
       lines(c(NMINTROPICALSspecies[i],NMINPOLARSspecies[i]),c(i,i),col="gray51")
       }

for (i in 1:length(predictNTEMP)) {
       lines(c(SMINTROPICALNspecies[i],SMINPOLARNspecies[i]),
       c(i+length(Sfull),i+length(Sfull)),col="gray51")
       }

for (i in 1:length(predictNTEMP)) {
       lines(c(NMINTROPICALNspecies[i],NMINPOLARNspecies[i]),
       c(i+length(Sfull),i+length(Sfull)),col="gray51")
       }
}

for (i in 1:length(predictSTEMP)) {
       points(c(Sfull[i],Sfull[i]), c(i,i), pch=16, cex=0.4)
}

for (i in 1:length(predictNTEMP)) {
       points(c(Nfull[i],Nfull[i]),c(i+length(Sfull),i+length(Sfull)),pch=16, cex=0.4)
}
abline(v=-30, lty=3);abline(v=0, lty=3);abline(v=30, lty=3);
```

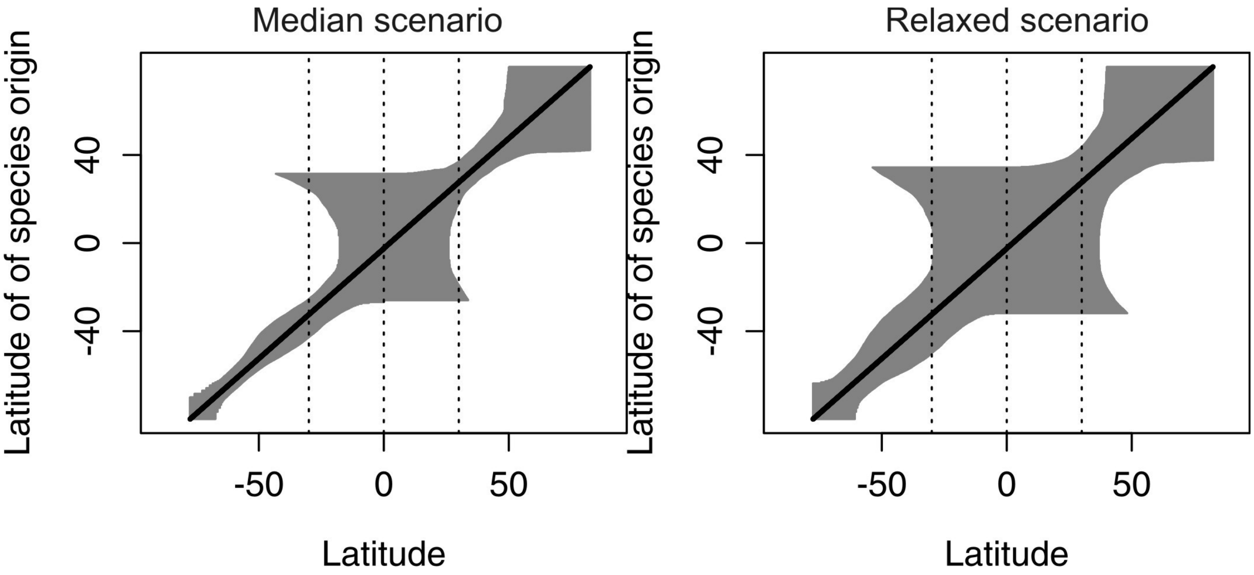

Figure B4 Distribution of latitudinal range sizes, ordered according to the initial latitudinal location of origin of individual species, predicted by the median scenario (left) and by the relaxed scenario (right). 1677 individual species are placed along latitude at 0.1° steps (represented by the y-axis), from the northern margins of the Antarctica to the Arctic shelf. The locations of species origin along the y-axis are represented by the black points (that merge into one line for all species), with initial range size equal to 0.1°. Species then expand their latitudinal ranges along the x-axis by tracking temperatures within their thermal bounds (set by temperature minima and maxima at the point of their location).

```
##########################################
#      RANGE SIZE VERSUS LATITUDE #
##########################################

plot(latgradient+2.5,meanPERBANDrange, ylim=c(0,120), type="n", cex.lab=1.2,
cex.axis=1.2, lwd=3, ylab="Latitudinal range (km)", xlab="Latitude", yaxt="n")
abline(v=-30, lty=3);abline(v=0, lty=3);abline(v=30, lty=3);
if (model=="Median") {
       lines(latgradient+2.5,meanPERBANDrange, lwd=3)
```

```
}
if (model=="Maximum") {
       lines(latgradient+2.5,maxPERBANDrange, col="black", lwd=3)
}
if (model=="Minimum") {
       lines(latgradient+2.5,minPERBANDrange, col="black", lwd=3)
}
axis(2, at=c(0,17.97,53.93, 89.88), labels=c(0,2000,6000,10000), cex.lab=1.2,
cex.axis=1.2)

factor <- 70/15
if (model=="Median") {
       lines(latgradient, meanPERBANDspSSTrange*factor, lwd=3, col="gray")
}
if (model=="Maximum") {
       lines(latgradient, maxPERBANDspSSTrange*factor, lwd=3, col="gray")
}
if (model=="Minimum") {
       lines(latgradient, minPERBANDspSSTrange*factor, lwd=3, col="gray")
}
axis(4, at=c(5*factor,10*factor,15*factor,20*factor), labels=c(5,10,15,20),  las=2,
cex.lab=1.2, cex.axis=1.2)
legend(-85,130, c("Latitudinal", "Thermal"), col=c("black","gray51","gray71"),
lwd=c(3,3), cex=1, lty=c(1,1), bg="white", bty="n")
```

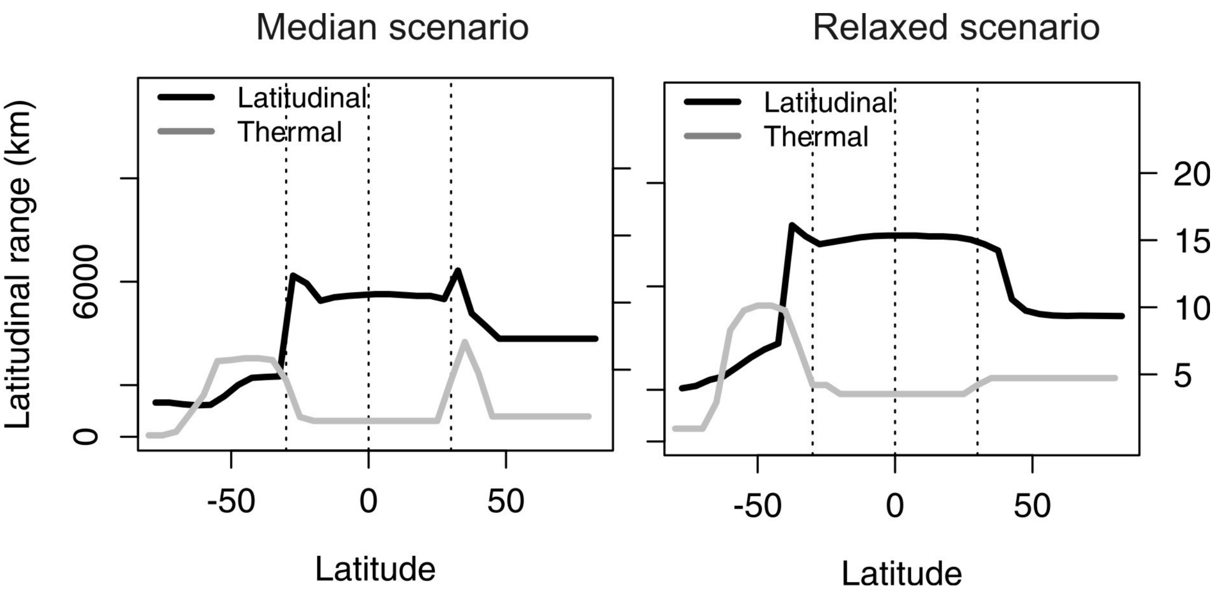

Figure B5 Latitudinal gradient in median latitudinal range and in median thermal range per 5º latitudinal bands predicted by the median scenario.

Finally, we compute the clustering of range limits per 5º latitudinal bands as the number of range limits in a given band relative to all ranges present in that band.

```
#########################################
#      PROPORTIONS OF RANGE LIMITS      #
#########################################
MEDIANcomposition2.5 <- array(0,dim=c(Nspecies, length(latgradient)))
MAXcomposition2.5 <- array(0,dim=c(Nspecies, length(latgradient)))
MINcomposition2.5 <- array(0,dim=c(Nspecies, length(latgradient)))

MEDIANforbandSlimit <- array(0,dim=c(Nspecies, length(latgradient)))
MEDIANforbandNlimit <- array(0,dim=c(Nspecies, length(latgradient)))
MAXforbandSlimit <- array(0,dim=c(Nspecies, length(latgradient)))
MAXforbandNlimit <- array(0,dim=c(Nspecies, length(latgradient)))
MINforbandSlimit <- array(0,dim=c(Nspecies, length(latgradient)))
MINforbandNlimit <- array(0,dim=c(Nspecies, length(latgradient)))

#MEDIAN SCENARIO
for (i in 1: Nspecies) {
       sequence <- seq(meanSlimit[i],meanNlimit[i],by=1)

       for (j in 1:length(sequence)) {
              id <- findInterval((sequence[j]), latgradient)
              MEDIANcomposition2.5[i,id] <- 1

              if (sequence[j] == sequence[1]) {
                     MEDIANforbandSlimit[i,id] <- 1
              }
              if (sequence[j] == sequence[length(sequence)]) {
                     MEDIANforbandNlimit[i,id] <- 1
              }
       }
}

MEDIANbandrichness <- apply(MEDIANcomposition2.5, MARGIN=2,sum)
```

```
names(MEDIANbandrichness) <- latgradient+2.5

#MAXIMUM SCENARIO
for (i in 1: Nspecies) {
	sequence <- seq(maxSlimit[i],maxNlimit[i],by=1)

	for (j in 1:length(sequence)) {
		id <- findInterval((sequence[j]), latgradient)
		MAXcomposition2.5[i,id] <- 1

		if (sequence[j] == sequence[1]) {
			MAXforbandSlimit[i,id] <- 1
		}
		if (sequence[j] == sequence[length(sequence)]) {
			MAXforbandNlimit[i,id] <- 1
		}
	}
}
MAXbandrichness <- apply(MAXcomposition2.5, MARGIN=2,sum)
names(MAXbandrichness) <- latgradient+2.5

#MINIMUM SCENARIO
for (i in 1: Nspecies) {
	sequence <- seq(minSlimit[i],minNlimit[i],by=1)

	for (j in 1:length(sequence)) {
		id <- findInterval((sequence[j]), latgradient)
		MINcomposition2.5[i,id] <- 1

		if (sequence[j] == sequence[1]) {
			MINforbandSlimit[i,id] <- 1
		}

		if (sequence[j] == sequence[length(sequence)]) {
			MINforbandNlimit[i,id] <- 1}
		}
}

MINbandrichness <- apply(MINcomposition2.5, MARGIN=2,sum)
names(MINbandrichness) <- latgradient+2.5

MEDIANbandSlimit <- apply(MEDIANforbandSlimit, MARGIN=2,sum)
```

```
MEDIANbandNlimit <- apply(MEDIANforbandNlimit, MARGIN=2,sum)
MAXbandSlimit <- apply(MAXforbandSlimit, MARGIN=2,sum)
MAXbandNlimit <- apply(MAXforbandNlimit, MARGIN=2,sum)
MINbandSlimit <- apply(MINforbandSlimit, MARGIN=2,sum)
MINbandNlimit <- apply(MINforbandNlimit, MARGIN=2,sum)

coordinates=as.numeric(names(MEDIANbandrichness))
start=2.5
S <- which(coordinates==-2.5)
NB <- which(coordinates==2.5)
NE <- length(coordinates)

#MEDIAN MODEL#
#Removing edges for POLEWARD range limits, removing the last polar band
meanSrangelimitsTROPtoPOLES=MEDIANbandSlimit[S:2]/MEDIANbandrichness[S:2]
meanSrangelimitsPOLEStoTROP=MEDIANbandNlimit[S:2]/MEDIANbandrichness[S:2]
meanNrangelimitsTROPtoPOLES=MEDIANbandNlimit[NB:(NE-1)]/MEDIANbandrichness[NB:(NE-1)]
meanNrangelimitsPOLEStoTROP=MEDIANbandSlimit[NB:(NE-1)]/MEDIANbandrichness[NB:(NE-1)]
meanPOLEWARD <- c(rev(meanSrangelimitsTROPtoPOLES),meanNrangelimitsTROPtoPOLES)
meanEQUATORWARD <- c(rev(meanSrangelimitsPOLEStoTROP),meanNrangelimitsPOLEStoTROP)

#MAXIMUM MODEL#
maxSrangelimitsTROPtoPOLES=MAXbandSlimit[S:2]/MAXbandrichness[S:2]
maxSrangelimitsPOLEStoTROP=MAXbandNlimit[S:2]/MAXbandrichness[S:2]
maxNrangelimitsTROPtoPOLES=MAXbandNlimit[NB:(NE-1)]/MAXbandrichness[NB:(NE-1)]
maxNrangelimitsPOLEStoTROP=MAXbandSlimit[NB:(NE-1)]/MAXbandrichness[NB:(NE-1)]
maxPOLEWARD=c(rev(maxSrangelimitsTROPtoPOLES),maxNrangelimitsTROPtoPOLES)
maxEQUATORWARD=c(rev(maxSrangelimitsPOLEStoTROP),maxNrangelimitsPOLEStoTROP)

#MINIMUM MODEL#
minSrangelimitsTROPtoPOLES=MINbandSlimit[S:2]/MINbandrichness[S:2]
minSrangelimitsPOLEStoTROP=MINbandNlimit[S:2]/MINbandrichness[S:2]
minNrangelimitsTROPtoPOLES=MINbandNlimit[NB:(NE-1)]/MINbandrichness[NB:(NE-1)]
minNrangelimitsPOLEStoTROP=MINbandSlimit[NB:(NE-1)]/MINbandrichness[NB:(NE-1)]
minPOLEWARD=c(rev(minSrangelimitsTROPtoPOLES),minNrangelimitsTROPtoPOLES)
minEQUATORWARD=c(rev(minSrangelimitsPOLEStoTROP),minNrangelimitsPOLEStoTROP)



#MEDIAN MODEL#
       if (model=="Median") {
       gradient=names(meanEQUATORWARD)
       #par(mfcol=c(2,2))
```

```
        plot(gradient, meanPOLEWARD, xlab="Latitude", type="l", ylab="Proportion of
        limits", lwd=3, ylim=c(0,1), cex.main=0.9, cex.lab=1.2,cex.axis=1.2, xaxt="n")
        axis(1, at=c(-50,0,50), labels=c(-50,0,50))
        lines(gradient, meanEQUATORWARD, lwd=3, col="gray51", lty=2)
        legend(-80,1.05, c("Poleward limits", "Equatorward limits"), lwd=c(3,3),
        col=c("black", "gray51"), bty="n", cex=1)
}

#RELAXED MODEL#
if (model=="Maximum") {
        gradient=names(meanEQUATORWARD)
        #par(mfcol=c(2,2))
        plot(gradient, maxPOLEWARD, xlab="Latitude", type="l", ylab="Proportion of
        limits", lwd=3, ylim=c(0,1),cex.main=0.9,cex.lab=1.2,cex.axis=1.2, xaxt="n")
        axis(1, at=c(-50,0,50), labels=c(-50,0,50))
        lines(gradient, maxPOLEWARD, col="black", lwd=3, lty=2)
        lines(gradient, maxEQUATORWARD, col="gray51", lwd=3, lty=2)
        legend(-80,1.05, c("Poleward limits", "Equatorward limits"), lwd=c(3,3),
        col=c("black", "gray51"), bty="n", cex=1)
}

#STRINGENT MODEL#
if (model=="Minimum") {
        gradient=names(meanEQUATORWARD)
        plot(gradient, minPOLEWARD, pch=16, xlab="Latitude", type="l", ylab="Proportion
        of limits", lwd=3, ylim=c(0,1), cex.main=0.9, main=coast, xaxt="n")
        lines(gradient, minEQUATORWARD, lwd=3, col="gray51", lty=2)
        axis(1, at=c(-50,0,50), labels=c(-50,0,50))
        #legend(-80,1.05, c("Poleward limits", "Equatorward limits"), lwd=c(3,3),
        col=c("black", "gray51"), bty="n", cex=0.9)
}
```

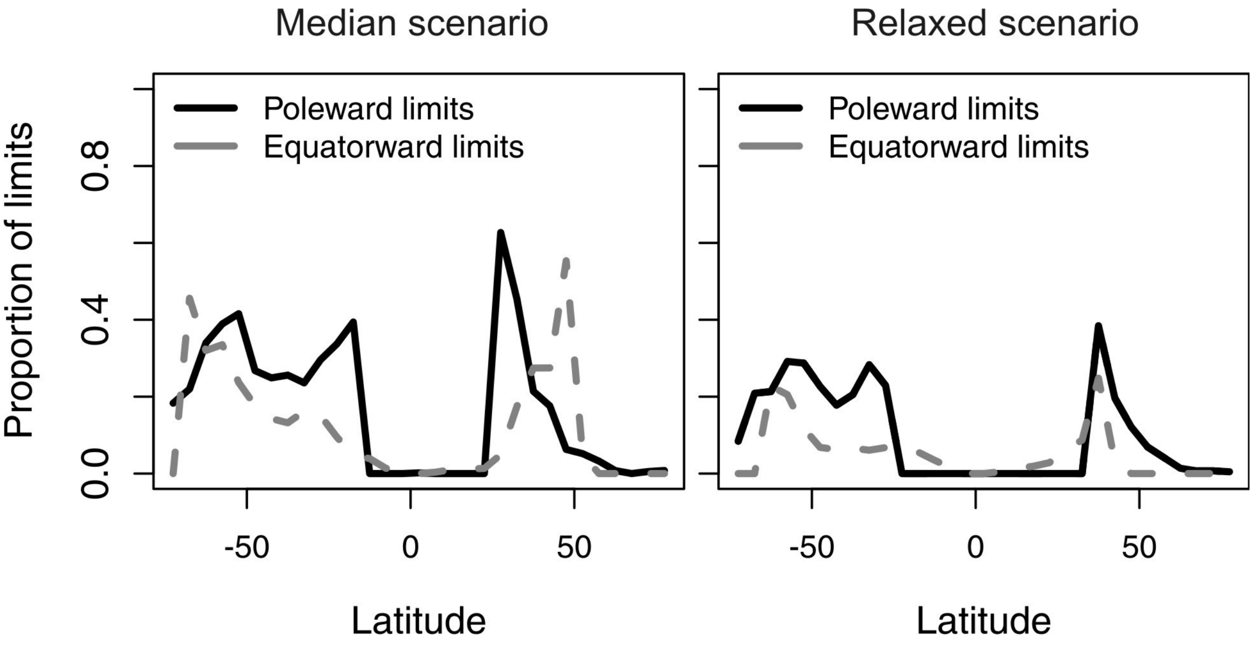

Figure B6 Latitudinal gradient in the proportion of poleward and equatorward range limits per 5º latitudinal bands predicted by the median scenario and relaxed scenario.