R code to calculate and plot national RLIs weighted by the proportion of each species' distribution within a country or region

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Methods for calculating national RLIs weighted by the fraction of each species' distribution occurring within the country or region.

The Red List Index can be downscaled to show national and regional Red List Indices, weighted by the fraction of each species' distribution occurring within the country or region, building on the method published by Rodrigues *et al*. (2014) *PLoS ONE* 9(11): e113934. These show an index of aggregate survival probability (the inverse of extinction risk) for all birds, mammals, amphibians, corals and cycads occurring within the country or region. The index shows how well species are conserved in a country or region to its potential contribution to global species conservation. The index is calculated as:

$$RLI_{(t,u)} = 1 - \frac{\sum_s (W_{(t,s)} \times \frac{r_{su}}{Rs})}{W_{EX} \times \sum_s (\frac{r_{su}}{Rs})}$$

where *t* is the year of comprehensive reassessment, *u* is the spatial unit (i.e. country), $W_{(t,s)}$ is the weight of the global Red List category for species *s* at time *t* (Least Concern =0, Near Threatened =1, Vulnerable =2, Endangered =3, Critically Endangered =4, Critically Endangered (Possibly Extinct) =5, Critically Endangered (Possibly Extinct in the Wild) =5, Extinct in the Wild =5 and Extinct =5), W_{EX} = 5 is the weight for Extinct species, r_{su} is the fraction of the total range of species *s* in unit *u*, and R_s is the total range size of species *s*.

The index varies from 1 if the country has contributed the minimum it can to the global RLI (i.e., if the numerator is 0 because all species in the country are LC) to 0 if the country has contributed the maximum it can to the global RLI (i.e., if the numerator equals the denominator because all species in the country are Extinct or Possibly Extinct).

The taxonomic groups included are those in which all species have been assessed for The IUCN Red List of Threatened Species™ more than once. Red List categories for years in which comprehensive assessments (i.e. those in which all species in the taxonomic group have been assessed) were carried out are determined following the approach of Butchart *et al*. 2007; *PLoS ONE* 2(1): e140, i.e. they match the current categories except for those taxa that have undergone genuine improvement or deterioration in extinction risk of sufficient magnitude to qualify for a higher or lower Red List category.

An aggregate Red List Index across all taxonomic groups for each country or region is calculated following Butchart *et al.* 2010 *Science* 328: 1164-1168. It is calculated as the arithmetic mean of modelled Red List Indices for each taxonomic group. The latter are interpolated linearly for years between data points and extrapolated linearly (with a slope equal to that between the two closest assessed points, except for corals) back to the earliest time point and forwards to the present for years for which estimates are not available. The start year of the aggregated index is set as ten years before the first assessment year for the taxonomic group with the latest starting point. Corals are not extrapolated linearly because declines are known to have been much steeper subsequent to 1996 (owing to extreme bleaching events) than before. Therefore the rate of decline prior to 1996 is set as the average of the rates for the other taxonomic groups.

The Red List Indices for each taxonomic group for each year are modelled to take into account various sources of uncertainty: (i) Data Deficiency: Red List categories (from Least Concern to Extinct) are assigned to all Data Deficient species, with a probability proportional to the number of species in non-Data Deficient categories for that taxonomic group. (ii) Extrapolation uncertainty: although Red List Indices are extrapolated linearly based on the slope of the closest two assessed point, there is uncertainty about how accurate this slope may be. To incorporate this uncertainty, rather than extrapolating deterministically, the slope used for extrapolation is selected from a normal distribution with a probability equal to the slope of the closest two assessed points, and standard deviation equal to 60% of this slope (i.e., the CV is 60%). (iii) Temporal variability: the 'true' RLI likely changes from year to year, but because assessments are repeated only at multi-year intervals, the precise value for any particular year is uncertain. To make this uncertainty explicit, the Red List Index value for a given taxonomic group in a given year is assigned from a moving window of five years, centred on the focal year. Assessment uncertainty cannot yet be incorporated into the index. Practically, these uncertainties are incorporated into the aggregated Red List Index as follows: Data Deficient species are allotted a category as described above, and a Red List Index for each taxonomic group is calculated interpolating and extrapolating as described above. A final Red List Index value is assigned to each taxonomic group for each year from a window of years as described above. Each such 'run' produces a Red List Index for the complete time period for each taxonomic group, incorporating the various sources of uncertainty. One thousand such runs is generated for each taxonomic group, and the mean is calculated.

This code requires the following input files (shapefile or CSV format):

1. Table "list_all_species_wshapes.csv": Metada table to aux the analyses. "mapped"=if map exists; "Shapefile"=name of the shapefile with the range map; "subfolder" =folder where it is stored (assumed that the subfolder is in the folder defined in table "tbfolders.csv" – see above); "size"=size of the shapefile (in Kb; only for non-combined shaped); "combinedshape": if the layers are combined in a single shapefile (1) or in one shapefile per species (0); "mapped": 1 if the species has a range map to be included in the analyses (can be 0 in some cases – e.g. endemic species)

Scientific	**Group**	**TaxonID**	**Cat_latest**	**year_ Cat**	**mapped**	**ende mic**	**ordem**	**shapefile**	**subfolder**	**size**	**combined shape**	**mappedf**
Struthio camelus	*Bird*	*45020636*	*LC*	*2015*	*1*		*1*	*Struthio_camelus_45020636.shp*	*Struthionidae*	*202.072*	*0*	*1*
Zamia wallisii	*Cycad*	*2.14E+09*	*CR*	*2013*	*1*	*Colo mbia*	*24221*	*zamia_wallisii.shp*	*Zamia*	*0.3*	*0*	*1*

2. Table "Iso_countries.csv": list of ISO codes, country names and respective regions/other classifications (note 0 values – not NA – for missing values in “Region”, “Developing”,”LDC” and “LLDC_SIDS” fields)

ordem	country_SIS	countryname	region1	ISO3	ISO_BL	ISO_SDG	uname_BL	uname_SDG	Region	Developing	LDC	LLDC_SIDS
247	*High Seas*	*Areas Beyond National Jurisdiction*	*High Seas*	*ABNJ*	*ABNJ*	*ABNJ*	*High Seas*	*High Seas*	*0*	*0*	*0*	*0*
202	*Aruba*	*Aruba*	*Caribbean Islands*	*ABW*	*ABW*	*ABW*	*Aruba*	*Aruba*	*Latin America & the Caribbean*	*Developing*	*0*	*SIDS*

3. Table "genuine_changes.csv": table with the details for species that have qualified for genuine changes in their IUCN Red List since the first comprehensive assessment for the group. All categories in the Genuine changes file must match one of LC, NT, VU, EN, CR, CR(PE), CR(PEW), EW, or EX. (Note DD and NE are not permitted)

Group	Scientific	Taxon ID	Period	cat_start	cat_end	start_year	end_year
Bird	Nothocercus nigrocapillus	22678160	08-12	LC	VU	2008	2012

4. Table "Sp_cnts_pp_FINAL.csv": table with the proportion of each species’ distribution in each country.

Scientific	TaxonID	marine	ISO3	pp	ovl	method	batch
Abditomys latidens	*15337*	*0*	*PHL*	*1*	*terrestrial*	*vector_overlap*	*batch8*

The code outputs several graphs and tables with the results of the analyses (global RLI and per country – XXX = code for each country/region):

1. global_all_taxa.pdf: graph with the global RLI for each taxonomic group and aggregated
2. global_aggregated.pdf: graph with the global aggregated RLI
3. global_birds.pdf: graph with the global RLI for birds
4. XXX.csv: table with national rli values and 95% confidence intervals (qn05 and qn95) for each taxonomic group and year
5. XXX_crli.csv: table with national crli values and 95% confidence intervals (crli05 and crli95) for each taxonomic group and year
6. XXX_aggregated.pdf: graph with the national aggregated RLI
7. XXX_all_taxa.pdf: graph with the national RLI for each taxonomic group and aggregated

8. XXX_birds.pdf: graph with the national RLI for birds
9. XXX_crli.pdf: graph with the national CRLI for each taxonomic group and aggregated
10. allcountries_RLI.csv: table with rli values and 95% confidence intervals (qn05 and qn95) for each country, taxonomic group and year (i.e., several XXX.csv combined in one file)
11. allcountries_CRLI.csv table with crli values and 95% confidence intervals (crli05 and crli95) for each country, taxonomic group and year (i.e., several XXX_crli.csv combined in one file)
12. RLI_all_countries.pdf (graphs XXX_all_taxa.pdf combined in a single file)

Text that is highlighted should be amended to give the appropriate folder names and file paths, number of randomisations (if this is to be adjusted), final year and ISO code/region to use (see grey columns in file Iso_countries.csv below) .

```
# National RLIs calculator v1 26/06/2016

# Maria Dias/BirdLife International; maria.dias@birdlife.org
# Script to calculate and plot the national RLIs
## See formats of input tables above

######################   Parameters that need to be set
wkfolder="ADD FOLDER NAME/LOCATION HERE"      ## copy-paste the working folder, replacing "/" by "/" and ensuring no spaces before & after quotes
setwd(wkfolder)

finfolder="ADD FOLDER NAME/LOCATION HERE"   ##  copy-paste the location of the folder where the country files should be saved, replacing "/" by "/" and ensuring no spaces before & after quotes
finfolder2="ADD FOLDER NAME/LOCATION HERE"    ##  copy-paste the location of the folder where the final plots should be saved, replacing "/" by "/" and ensuring no spaces before & after quotes

isos=read.csv("Iso_countries.csv")          ## file with ISO codes; should be stored in the wkfolder specified above
tabsp1=read.csv("list_all_species_wshapes.csv")   ## file with the name of shapefiles and folders of the species' range maps; should be stored in the wkfolder specified above
gench=read.csv("genuine_changes.csv")        ### file with list of Red List genuine changes; should be stored in the wkfolder specified above
tbf1=read.csv("Sp_cnts_pp.csv")      ## result of spatial analyses to estimate the proportion of the range of each species in each country

slopecv=.6      ### standard devidation of the slope
maxyear=2017     ### max year of the analyses
```

```
repetitions=1000    ## n repetitions
iso2use="M49_Region"    #ISO_SDG   #ISO_BL   #LLDC_SIDS   #LDC   #Region   #Developing    ### iso to use in the analyses; choose from those available in isos table

##############################  custom functions

lu=function (x=x) length(unique(x))   ## function to estimate the number of unique values in a vector
first=function (x=x) x[1]          ## function to output the fisrt value of a vector
q95=function (x=x) quantile(x,.95)    ## function to estimate the quantile 95%
q05=function (x=x) quantile(x,.05)    ## function to estimate the quantile 5%
div0=function (x=x, y=y) trunc((x-1)/y)-((x-1)/y)  ## function that outputs 0 if y-1 is divisible by x (aux open new devices in graphics outputs)
cinz=rgb(217/255,217/255,217/255,.4)   ### grey transparent colour for the plots (in rgb)

#function to calculate global RLI
# nreps=number of repetitions; groups2=list of taxonomic groups to analyse; leftextrapol=if slope should be extrapolated to the left; saveleftslope=if left slope should be
saved; plotit=if each iteraction should be plotted
rlicalc=function (nreps=repetitions, groups2=groups2, years=years, leftextrapol=T, saveleftslope=T, plotit=F){

rliTot=data.frame(group=rep(rep(groups2, each=length(years)),length(nreps)), year=rep(rep(years, length(groups2)), length(nreps)),
nrep=rep(1:nreps,each=length(years)*length(groups2)), rli=NA)
outpts=list()

if (saveleftslope) leftslopes=NULL
for (r in 1:nreps)
{
#r=1
for (g in  1:length(groups2))
{
#g=1
group=as.character(groups2[g])
#group="Bird"
rlig=data.frame()
group
tgroup=tabgrli[tabgrli$group==group,]
yearsa=sort(unique(tgroup$year))
yearsa

```

```
### years of assessment
for (y in 1:length(yearsa))
{
#y=1
year=yearsa[y]
year
tb=tgroup[tgroup$year==year,]
tb=merge(tb,wts)
head(tb)
nrow(tb)
rli1=1-(sum(tb$wg)/(wex*nrow(tb)))
rli1
rlig=rbind(rlig, data.frame(group=group,year=year, rli=rli1))
} ## ends years of assessment
rlig

### intrapolation and extrapolation

dat=rlig
dat
#interpolation
yearsti=min(dat$year): max(dat$year)
irli=approx(dat$year, dat$rli, xout=yearsti, method="linear", rule=2:2)$y
irli

datf=data.frame(year=yearsti, rli=irli)
datf
#with(datf, plot(year, rli, xlim=c(1975,2018), ylim=c(0.6,1.2)))

#extrapolation    # y=a+bx
#left
yearl=c(min(years)-2, min(years)-1, years[which(years<min(yearsti))])
yearl

x1=sort(dat$year)[1:2]
x1   ### years
```

```
y1=c(dat$rli[dat$year==x1[1]],dat$rli[dat$year==x1[2]])
y1    ###rlis
nv=lm(y1~x1)
mnslp <- coef(nv)[2]
useslp <- rnorm(1, mnslp, sd=slopecv*abs(mnslp))
if (leftextrapol==F) useslp <- meanleftslopes
irlel=y1[1] - (useslp*(x1[1] -(yearl)))

if (leftextrapol) leftslopes=c(leftslopes,useslp)
 datf=rbind(datf, data.frame(year=yearl, rli=irlel))

#with(datf, points(year, rli, col=2, pch=19, cex=.6))
datf

#right
yearr=c(years[which(years>max(yearsti))],max(years)+1,max(years)+2)
yearr

x1=sort(dat$year)[(nrow(dat)-1):nrow(dat)]
x1    ## years
y1=c(dat$rli[dat$year==x1[1]],dat$rli[dat$year==x1[2]])
y1    ### rlis
nv=lm(y1~x1)
mnslp <- coef(nv)[2]
useslp <- rnorm(1, mnslp, sd=slopecv*abs(mnslp))
irler=y1[2] - (useslp*(x1[2] -(yearr)))
datf=rbind(datf, data.frame(year=yearr, rli=irler))
#with(datf, points(year, rli, col=2, pch=19, cex=.6))

datf=datf[order(datf$year),]


if (plotit)
{
if (r<30) win.graph()
with(datf, plot(year, rli, pch=19, col=2, main=paste(group,"s", sep="")))
```

```
with(datf[datf$year%in%yearsti,], points(year, rli, pch=19, col=4))
}

restmw=NULL
for (m in 3:(nrow(datf)-2)) restmw=c(restmw, sample(datf$rli[(m-2):(m+2)],1))
finalmw=restmw
rliTot[rliTot$group==group&rliTot$nrep==r,]$rli=finalmw
if (plotit) with(rliTot[rliTot$group==group&rliTot$nrep==r,], lines(year, rli, col=8))

}  #ends loop groups
} #ends loop  nreps

outpts[[1]]=rliTot
if (saveleftslope) outpts[[2]]=mean(leftslopes)

return(outpts)
}

######################

isos$isof=isos[,which(names(isos)==iso2use)]
head(isos)
lu(isos$isof)

nrow(tbf1)
head(tbf1)
tbf1=merge(tbf1, isos[,c("ISO3","isof")])
tbf1=merge(tbf1,tabsp1[,c("Scientific","Group","Cat_latest")], sort=F)
nrow(tbf1)
head(tbf1)
tbf1$iucn=tbf1$Cat_latest
tbf=tbf1[tbf1$iucn!="DD",]
nrow(tbf)
lu(tbf$isof)

unique(tbf$iucn)
```

```
wts=data.frame(iucn=c("LC","NT","VU","EN","CR","CR(PE)","CR(PEW)","EW","EX", "DD"), wg=c(0,1,2,3,4,5,5,5,5,-1))

# verify is all IUCN codes are correct
cds1=unique(tbf$iucn)
length(cds1)
length(cds1[cds1%in%wts$iucn])  ## should be the same as previous

cds1=unique(gench$cat_start)
length(cds1)
length(cds1[cds1%in%wts$iucn])  ## should be the same as previous

cds1=unique(gench$cat_end)
length(cds1)
length(cds1[cds1%in%wts$iucn])   ## should be the same as previous

#verify if all the scientific names in genuine file are correct and are in in sp-cnts table
sp1=unique(gench$Scientific)   #tabf$RLC   #gench$cat_start #gench$cat_end
length(sp1)
length(sp1[sp1%in%tbf$Scientific])
sp1[!sp1%in%tbf$Scientific]      ### species that are missing in the sp-cnts table after excluding the DD (but are in the genuine file)

sprich=with(tbf1, aggregate(Scientific, list(group=Group), lu))
names(sprich)[length(sprich)]="rich"
sprich    ### number of species per taxon

years=min(gench$start_year):maxyear
years

groups=unique(tbf$Group)
groups

################## reconstruct past tables
pastables=data.frame()
for (g in  1:length(groups))
{
#g=1
```

```
group=as.character(groups[g])
#group="Bird"
group
tbgn=gench[gench$Group==group,]
tball=tbf1[tbf1$Group==group,]  ### al sp sp-cnts
nrow(tbgn)
head(tbgn)
yearsa=sort(unique(c(tbgn$start_year,tbgn$end_year)))
yearsa
yearsa2=yearsa[1:length(yearsa)-1]
yearsa2
tabsp=with(tabsp1[tabsp1$Scientific%in%tball$Scientific,], data.frame(Scientific=Scientific, iucn=Cat_latest))
tabsp$year=max(yearsa)
head(tabsp)

sp1=unique(tball$Scientific)
length(sp1)
length(sp1[sp1%in%tabsp$Scientific])

tabsp2=tabsp
tabspnew=tabsp
for (y in length(yearsa2):1)
{
#y=1
tabsp3=tabspnew
tabsp3$year=yearsa2[y]
t2ch=tbgn[tbgn$start_year==yearsa2[y],c("Scientific","cat_start")]
head(t2ch)
nrow(t2ch)

for (z in 1:nrow(t2ch))
{
#z=1
tabsp3$iucn[tabsp3$Scientific==as.character(t2ch$Scientific[z])]=as.character(t2ch$cat_start[z])
}
tabspnew=tabsp3
```

```
tabsp2=rbind(tabsp2,tabsp3)
}

nrow(tabsp2)/lu(tabsp2$Scientific) ## should be the number of years of comprehensive assessments
tabsp2$group=group

pastables=rbind(pastables,tabsp2)
}

#write.csv(pastables, "pastables.csv", row.names=F)
#pastables=read.csv("pastables.csv")
wex=wts$wg[wts$iucn=="EX"]
head(pastables)

#### overlall RLI and estimate left slope for corals

ddsp=unique(pastables$Scientific[pastables$iucn=="DD"])
tabgrli=pastables[!pastables$Scientific%in%ddsp,]
head(tabgrli)
unique(tabgrli$iucn)

groupsf=c(as.character(groups[groups!="Coral"]),"Coral")  # to ensure that Corals will be the last (to use the mean slope for left extrapolation)
tt=proc.time()

# non-corals

groups2=as.character(groups[groups!="Coral"])
rliTotGlobal_noncorals_list=rlicalc(nreps=repetitions, groups2=groups2, years=years, leftextrapol=T, saveleftslope=T, plotit=F)

rliTotGlobal_noncorals=rliTotGlobal_noncorals_list[[1]]
head(rliTotGlobal_noncorals)
tail(rliTotGlobal_noncorals)

meanleftslopes=rliTotGlobal_noncorals_list[[2]]
meanleftslopes
```

```
### corals

rliTotGlobal_corals_list=rlicalc(nreps=repetitions, groups2="Coral", years=years, leftextrapol=F, saveleftslope=F, plotit=F)
rliTotGlobal_corals=rliTotGlobal_corals_list[[1]]
head(rliTotGlobal_corals)
tail(rliTotGlobal_corals)

rliTotGlobal=rbind(rliTotGlobal_noncorals,rliTotGlobal_corals)

rlitotagrs=with(rliTotGlobal, aggregate(rli,list(year=year, nrep=nrep), mean))
names(rlitotagrs)[length(rlitotagrs)]="rli"
rlitotagrs$group="aggregated"
head(rlitotagrs)

rliTotF=rbind(rliTotGlobal,rlitotagrs[,c("group","year","nrep","rli")])
head(rliTotF)
tail(rliTotF)
max(rliTotF$nrep)
max(rliTotF$rli)

resg=with(rliTotF, aggregate(rli, list(year=year, group=group), length))
resg$rli=with(rliTotF, aggregate(rli, list(year=year, group=group), median))$x
resg$qn95=with(rliTotF, aggregate(rli, list(year=year, group=group), q95))$x
resg$qn05=with(rliTotF, aggregate(rli, list(year=year, group=group), q05))$x
resg

gs=unique(resg$group)
resgf=data.frame()
for (g in 1:lu(gs))
{
#g=1
gs1=as.character(gs[g])
gs1
if (gs1!="aggregated") yrs=min(gench$start_year[gench$Group==gs1]):max(gench$end_year[gench$Group==gs1]) else yrs=(max(with(gench, aggregate(start_year,
list(Group), min))$x)-10):maxyear
rli3=resg[resg$group==gs1&resg$year%in%yrs,]
```

```
rli3=rli3[order(rli3$year),]
resgf=rbind(resgf,rli3)
}
head(resgf,20)

tab2plot=resgf

par(las=1)
with(tab2plot,plot(year,rli, ylim=c(min(qn05), max(qn95)), xlim=c(min(year), max(year)+4), type="n", xlab="Year", ylab="Red List Index of species survival"))

gs=unique(tab2plot$group[tab2plot$group!="aggregated"])
lu(gs)
for (g in 1:length(gs))
{
#g=1
gs1=as.character(gs[g])
res2=tab2plot[tab2plot$group==gs1,]
with(res2,polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
}
with(tab2plot[tab2plot$group=="aggregated",], polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))

for (g in 1:length(gs))
{
gs1=as.character(gs[g])
res2=tab2plot[tab2plot$group==gs1,]
with(res2,lines(year,rli, col=2, lwd=2))
text(max(res2$year)+0.5, res2$rli[nrow(res2)],paste(gs1,"s", sep=""), cex=.6, adj=c(0,0.5))
}
with(tab2plot[tab2plot$group=="aggregated",], lines(year,rli, col=4, lwd=2))
#abline(v=2015, lty=3, col=8)
#write.csv(resgf, "global_RLIs.csv", row.names=F)
#pastables=read.csv("pastables.csv")
#meanleftslopes=(-0.0009302144)

#####
### pdf with global rlis
```

```
rlinew=resgf
pdfs=T
pdf1name=paste(finfolder2, "/","global","_all_taxa.pdf", sep="")
pdf1name
if (pdfs) pdf(file=pdf1name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,5,4,2), mgp=c(3.5, 1, 0))

#graph all
miny=.15
topy=min(c(1.02, max(rlinew$qn95)*1.1))
topy
basy=min(rlinew$qn05)*.99
difrgy=diff(range(basy, topy))
if (difrgy<miny) {
basy=topy-miny
difrgy=diff(range(basy, topy))}

with(rlinew,plot(year,rli, ylim=c(basy*.99,topy), xlim=c(min(year), max(year)+1), type="n", xlab="Year", yaxt="n", ylab="Red List Index of species survival"))
#with(rlinew,plot(year,rli, ylim=c(0,topy), type="n", xlab="Year", yaxt="n", ylab="Red List Index of species survival", main=namect1))
if (difrgy<0.3) axis(2, seq(0,1, by=.05))
if (difrgy>0.3) axis(2, seq(0,1, by=.1))

gs=unique(rlinew$group[rlinew$group!="aggregated"])
lu(gs)
for (g in 1:length(gs))
{
#g=1
gs1=as.character(gs[g])
res2=rlinew[rlinew$group==gs1,]
with(res2,polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
}
with(rlinew[rlinew$group=="aggregated",], polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))

for (g in 1:length(gs))
{
```

```
gs1=as.character(gs[g])
res2=rlinew[rlinew$group==gs1,]
with(res2,lines(year,rli, col=2, lwd=2))
if (pdfs) text(max(res2$year)+0.5, res2$rli[nrow(res2)],paste(gs1,"s", sep=""), cex=1, adj=c(0,0.5))
}
with(rlinew[rlinew$group=="aggregated",], lines(year,rli, col=4, lwd=2))

if (pdfs) dev.off()

#graph aggregated
pdf2name=paste(finfolder2,"/", "global","_aggregated.pdf", sep="")
pdf2name
if (pdfs) pdf(file=pdf2name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,5,4,2), mgp=c(3.5, 1, 0))

ttuse=rlinew[rlinew$group=="aggregated",]
topy=min(c(1.02, max(ttuse$qn95)*1.1))
basy=min(ttuse$qn05)*.99
difrgy=diff(range(basy, topy))
if (difrgy<miny) {
basy=topy-miny
difrgy=diff(range(basy, topy))}

with(ttuse,plot(year,rli, yaxt="n", ylim=c(basy,topy), type="n", xlab="Year", ylab="Red List Index of species survival"))
with(ttuse, polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
with(ttuse, lines(year,rli, col=4, lwd=2))
if (difrgy<0.3) axis(2, seq(0,1, by=.05))
if (difrgy>0.3) axis(2, seq(0,1, by=.1))

if (pdfs) dev.off()

# graph birds
pdf3name=paste(finfolder2,"/", "global","_birds.pdf", sep="")
pdf3name
if (pdfs) pdf(file=pdf3name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,7,4,2), mgp=c(5, 1, 0))
```

```
ttuse=rlinew[rlinew$group=="Bird",]

if (nrow(ttuse)==0) plot(1:10, 1:10, type="n", main="no data for birds", xaxt="n", yaxt="n", xlab="", ylab="")
if (nrow(ttuse)>0){
miny=.05
topy=min(c(1.02, max(ttuse$qn95)*1.001))
basy=min(ttuse$qn05)*.999
difrgy=diff(range(basy, topy))
#if (difrgy<miny) {
#basy=topy-miny
#difrgy=diff(range(basy, topy))}

with(ttuse,plot(year,rli, ylim=c(basy,topy), yaxt="n", type="n", xlab="", ylab="Red List Index of species survival"))
with(ttuse, polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
with(ttuse, lines(year,rli, col=2, lwd=2))
if (difrgy<0.3)
{
if (difrgy<0.1) {axis(2, seq(0,1, by=.002))} else axis(2, seq(0,1, by=.05))
}
if (difrgy>0.3) axis(2, seq(0,1, by=.1))
}
par(mgp=c(3.5, 1, 0))
title(xlab="Year")

if (pdfs) dev.off()

##############################################
### rlis per country

tt=proc.time()

nreps=repetitions
plotit=F
plotit2=T
finalrlis=data.frame()
```

```
cts=unique(tbf1$isof)
lu(cts)
cts=cts[cts!="0"]
cts
tt=proc.time()

for (x in 1:length(cts)) #length(cts)
{
#x=1
#x=which(cts=="ABW")
cnt=cts[x]
cnt
print(paste(x, cnt))

tbct=tbf1[tbf1$isof==cnt,]

groupsf=as.character(unique(tbct$Group))
groupsf

rliext=data.frame(country=cnt, group=rep(rep(groupsf, each=length(years)),nreps), year=rep(rep(years, length(groupsf)),nreps),
nrep=rep(1:nreps,each=length(years)*length(groupsf)), rli=NA)
head(rliext)
tail(rliext)

for (r in 1: nreps) #nreps
{
print(paste(x, cnt, r))
#r=1

for (g in 1:length(groupsf))      ### note that loop of groups has to be the first, to save the slopes to apply to corals
{
#g=1
group=as.character(groupsf[g])
group
```

```
spcnt=tbct[tbct$Group==group,]

lu(spcnt$Scientific)
nrow(spcnt)

spcnt2=with(spcnt, aggregate(pp, list(Scientific=Scientific), sum))  ## sum pp for species and country (could be split for marine/terrestrial or disjucnt polygons in country/eez layer with multiple entries)
nrow(spcnt2)
names(spcnt2)[length(spcnt2)]="pp"
head(spcnt2)
max(spcnt2$pp)
spcnt2[spcnt2$pp==1,]   ## endemic species

spcnt3=merge(spcnt2,pastables)
head(spcnt3)
tail(spcnt3)
nrow(spcnt3)/nrow(spcnt2) ## should be the number of years of assessment for this group

yearsa=sort(unique(spcnt3$year))
yearsa
yearsa2=yearsa[1:length(yearsa)-1]
yearsa2

### years of assessment

rlig=data.frame()
for (y in 1:length(yearsa))
{
#y=1
year=yearsa[y]
year

tb=spcnt3[spcnt3$year==year,]
head(tb)
nrow(tb)
```

```
unique(tb$iucn)

tb[tb$iucn=="DD",]
tb[!tb$iucn%in%c("DD", "LC"),]
tb[tb$iucn=="LC",]

tb=merge(tb,wts)
head(tb)
nrow(tb)
dds=tb$Scientific[tb$iucn=="DD"]
dds
tb[tb$iucn=="DD",]
allwgs=tb$wg[tb$wg>(-1)]
if (length(allwgs)==0) allwgs=0
if (length(dds)>0) for (d in 1:length(dds)) tb$wg[tb$Scientific==dds[d]]=sample(allwgs,1)
tb[tb$iucn=="DD",]

tb$wxpp=tb$wg*tb$pp
#tb$wxpp=5*tb$pp
head(tb)

sum(tb$wxpp)
wex*sum(tb$pp)
sum(tb$wxpp)/(wex*sum(tb$pp))
1-round(sum(tb$wxpp)/(wex*sum(tb$pp)),7)
rli1=1-round((sum(tb$wxpp)/(wex*sum(tb$pp))),7)
rli1
crli=round((sum(tb$wxpp)/(wex*sprich$rich[sprich$group==group])),7)
rlig=rbind(rlig, data.frame(group=group,year=year, rli=rli1))

if (y==1) tb1=tb

}  ## ends loop year
rlig
dat=rlig
dat
```

```
#interpolation
yearsti=min(dat$year): max(dat$year)
irli=approx(dat$year, dat$rli, xout=yearsti, method="linear", rule=2:2)$y
irli

datf=data.frame(year=yearsti, rli=irli)
datf
#with(datf, plot(year, rli, xlim=c(1975,2018), ylim=c(0.6,1.2)))

#extrapolation    # y=a+bx
#left
yearl=c(min(years)-2, min(years)-1, years[which(years<min(yearsti))])
yearl

x1=sort(dat$year)[1:2]
x1   ### years
y1=c(dat$rli[dat$year==x1[1]],dat$rli[dat$year==x1[2]])
y1    ###rlis
nv=lm(y1~x1)
mnslp <- coef(nv)[2]
useslp <- rnorm(1, mnslp, sd=slopecv*abs(mnslp))
if (group=="Coral") useslp <- meanleftslopes
irlel=y1[1] - (useslp*(x1[1] -(yearl)))

datf=rbind(datf, data.frame(year=yearl, rli=irlel))
datf

#right
yearr=c(years[which(years>max(yearsti))],max(years)+1,max(years)+2)
yearr

x1=sort(dat$year)[(nrow(dat)-1):nrow(dat)]
x1    ## years
y1=c(dat$rli[dat$year==x1[1]],dat$rli[dat$year==x1[2]])
y1    ### rlis
```

```
nv=lm(y1~x1)
mnslp <- coef(nv)[2]
useslp <- rnorm(1, mnslp, sd=slopecv*abs(mnslp))
irler=y1[2] - (useslp*(x1[2] -(yearr)))
datf=rbind(datf, data.frame(year=yearr, rli=irler))
datf=datf[order(datf$year),]

if (plotit)
{
win.graph()
with(datf, plot(year, rli, pch=19, col=2, main=paste(group,"s", sep="")))
with(datf[datf$year%in%yearsti,], points(year, rli, pch=19, col=4))
}

restmw=NULL
for (m in 3:(nrow(datf)-2)) restmw=c(restmw, sample(datf$rli[(m-2):(m+2)],1))
finalmw=restmw
rliext[rliext$group==group&rliext$nrep==r,]$rli=finalmw
if (plotit) with(rliext[rliext$group==group&rliext$nrep==r,], lines(year, rli, col=8))
} # ends loop group
} # ends loop rep

head(rliext)
tail(rliext)
max(rliext$nrep)
max(rliext$rli)

rlitotagrs=with(rliext, aggregate(rli,list(year=year, nrep=nrep), mean))
names(rlitotagrs)[length(rlitotagrs)]="rli"
rlitotagrs$group="aggregated"
rlitotagrs$country=cnt
head(rlitotagrs)

rliextF=rbind(rliext,rlitotagrs[,c("country","group","year","nrep","rli")])
head(rliextF)
tail(rliextF)
```

```
max(rliextF$nrep)
max(rliextF$rli)

resg=with(rliextF, aggregate(rli, list(year=year, group=group), length))
resg$rli=with(rliextF, aggregate(rli, list(year=year, group=group), median))$x
resg$qn95=with(rliextF, aggregate(rli, list(year=year, group=group), q95))$x
resg$qn05=with(rliextF, aggregate(rli, list(year=year, group=group), q05))$x
head(resg)

resg$rli[resg$rli>1]=1
resg$rli[resg$rli<0]=0
resg$qn95[resg$qn95>1]=1
resg$qn95[resg$qn95<0]=0
resg$qn05[resg$qn05>1]=1
resg$qn05[resg$qn05<0]=0

gs=unique(resg$group)
resgf=data.frame()
for (g in 1:lu(gs))
{
#g=1
gs1=as.character(gs[g])
gs1
if (gs1!="aggregated") yrs=min(gench$start_year[gench$Group==gs1]):max(gench$end_year[gench$Group==gs1]) else yrs=(max(with(gench, aggregate(start_year, 
list(Group), min))$x)-10):maxyear
rli3=resg[resg$group==gs1&resg$year%in%yrs,]
rli3=rli3[order(rli3$year),]
resgf=rbind(resgf,rli3)
}
head(resgf,30)

final=resg
final$country=cnt
head(final)
finalrlis=rbind(finalrlis,final)
```

```
final2save=final[, c("country","group","year","rli","qn05","qn95")]
finalname=paste(finfolder, "/", cnt,".csv", sep="")
finalname
write.csv(final2save,finalname, row.names=F)

if (plotit2){
if (div0(x,6)==0)
{
win.graph(50,30)
par(mfrow=c(2,3), mar=c(2,2,2,1))
}

tab2plot=resgf
with(tab2plot,plot(year,rli, ylim=c(min(qn05), max(qn95)), xlim=c(min(year), max(year)+4), type="n", xlab="Year", ylab="Red List Index of species survival", main=cnt))

gs=unique(tab2plot$group[tab2plot$group!="aggregated"])
lu(gs)
for (g in 1:length(gs))
{
#g=1
gs1=as.character(gs[g])
res2=tab2plot[tab2plot$group==gs1,]
with(res2,polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
}
with(tab2plot[tab2plot$group=="aggregated",], polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))

for (g in 1:length(gs))
{
gs1=as.character(gs[g])
res2=tab2plot[tab2plot$group==gs1,]
with(res2,lines(year,rli, col=2, lwd=2))
text(max(res2$year)+0.5, res2$rli[nrow(res2)],paste(gs1,"s", sep=""), cex=.6, adj=c(0,0.5))
}
with(tab2plot[tab2plot$group=="aggregated",], lines(year,rli, col=4, lwd=2))
}
} # ends loop country
```

```
print((proc.time()-tt)[1]/60) ## time in minutes

str(finalrlis)
head(finalrlis)
lu(finalrlis$country)
max(finalrlis$x)
max(finalrlis$rli)
min(finalrlis$rli)

#####################################################################################################

### combine all files in 1 (in case the country files are calculated in different machines, to save time
cmbfiles=F

if(cmbfiles){
allfics=data.frame()
fics=dir("//AZ-FILESERVER2/gis_data/Tracking Ocean Wanderers/IUCN_R_scripts/RLI/country_files/ISO_BL_test/", pattern = ".csv", full.names =T)   ### copy paste here the folder with the countries' files
for (u in 1:length(fics))  allfics=rbind(allfics, read.csv(fics[u]))
lu(allfics$country)
finalrlis=allfics
}

str(finalrlis)
head(finalrlis)
lu(finalrlis$country)
max(finalrlis$rli)


##################################################
 ## country final files and graphs
iso2use
sumspp=with(tbf1, aggregate(pp, list(country=isof, group=Group), sum))
names(sumspp)[length(sumspp)]="sumpp"
head(sumspp)
```

```
sum(sumspp$sumpp)

rliextf=finalrlis
min(rliextf$rli)
max(rliextf$rli)
head(rliextf)
tail(rliextf)

pdfs=T
plotit=T
writefiles=T
if (pdfs) plotit=F

allcountries_RLI=data.frame()
allcountries_CRLI=data.frame()

cts=unique(rliextf$country)
length(cts)

#graphics.off()
for (i in 1:length(cts))    #length(cts)
{
#i=1
#i=which(cts=="ABW")
i

ct1=as.character(cts[i])
ct1
rli2=rliextf[rliextf$country==ct1,]

namect1=as.character(ct1)
if (iso2use=="ISO_BL") namect1=paste(isos$uname_BL[isos$isof==as.character(ct1)][1] ," (", ct1, ")", sep="")
if (iso2use=="ISO_SDG") namect1=paste(isos$uname_SDG[isos$isof==as.character(ct1)][1] ," (", ct1, ")", sep="")
namect1
```

```
gs=unique(rli2$group)
lu(gs)
rlinew=data.frame()
crlis=data.frame()
for (g in 1:lu(gs))
{
#g=1
gs1=as.character(gs[g])
gs1
if (gs1!="aggregated") yrs=min(gench$start_year[gench$Group==gs1]):max(gench$end_year[gench$Group==gs1]) else yrs=(max(with(gench, aggregate(start_year,
list(Group), min))$x)-10):maxyear
rli3=rli2[rli2$group==gs1&rli2$year%in%yrs,]
rli3=rli3[order(rli3$year),]
if (gs1!="aggregated")
{
crli1=rli2[rli2$group==gs1,]
crli1$crli=crli1$rli*sumspp$sumpp[sumspp$group==gs1&sumspp$country==ct1][1]/sprich$rich[sprich$group==gs1]
crli1$crli05=crli1$qn05*sumspp$sumpp[sumspp$group==gs1&sumspp$country==ct1][1]/sprich$rich[sprich$group==gs1]
crli1$crli95=crli1$qn95*sumspp$sumpp[sumspp$group==gs1&sumspp$country==ct1][1]/sprich$rich[sprich$group==gs1]
crlis=rbind(crlis,crli1[,c("country","group","year","crli","crli05","crli95")])
}
rlinew=rbind(rlinew,rli3)
}
rlinew
tail(crlis)
crlisag=with(crlis, aggregate(crli, list(country=country,  year=year), mean))
names(crlisag)[length(crlisag)]="crli"
crlisag$group="aggregated"
crlisag$crli05=with(crlis, aggregate(crli05, list(country=country,  year=year), mean))$x
crlisag$crli95=with(crlis, aggregate(crli95, list(country=country,  year=year), mean))$x
yrs=(max(with(gench, aggregate(start_year, list(Group), min))$x)-10):maxyear
```

```
crlisag=crlisag[crlisag$year%in%yrs,]
crlisag
crlisag[,c("country","group","year","crli","crli05","crli95")]

crlisf=data.frame()
gs2=unique(crlis$group)
for (g in 1:length(gs2))
{
gs1=as.character(gs2[g])
yrs=min(gench$start_year[gench$Group==gs1]):max(gench$end_year[gench$Group==gs1])
crlisf=rbind(crlisf, crlis[crlis$group==gs1&crlis$year%in%yrs,])
}
crlisf=rbind(crlisf,crlisag)

rlinew2save=rlinew[, c("country","group","year","rli","qn05","qn95")]
fnamect=paste(finfolder2, "/", ct1,".csv", sep="")
fnamect
if (writefiles) write.csv(rlinew2save,fnamect, row.names=F)

fnamect2=paste(finfolder2,"/", ct1,"_crli.csv", sep="")
fnamect2
if (writefiles) write.csv(crlisf,fnamect2, row.names=F)

allcountries_RLI=rbind(allcountries_RLI,rlinew2save)
allcountries_CRLI=rbind(allcountries_CRLI,crlisf)

if (plotit) {
if (div0(i,4)==0)
{
win.graph(30,20)
par(las=1, mfrow=c(4,4))
}
}

pdf1name=paste(finfolder2, "/", ct1,"_all_taxa.pdf", sep="")
pdf1name
```

```
if (pdfs) pdf(file=pdf1name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,5,4,2), mgp=c(3.5, 1, 0))

#graph all
miny=.15
topy=min(c(1.02, max(rlinew$qn95)*1.1))
topy
basy=min(rlinew$qn05)*.99
difrgy=diff(range(basy, topy))
if (difrgy<miny) {
basy=topy-miny
difrgy=diff(range(basy, topy))}

with(rlinew,plot(year,rli, ylim=c(basy*.99,topy), xlim=c(min(year), max(year)+1), type="n", xlab="Year", yaxt="n", ylab="Red List Index of species survival"))
if (plotit) title(main=namect1)
#with(rlinew,plot(year,rli, ylim=c(0,topy), type="n", xlab="Year", yaxt="n", ylab="Red List Index of species survival", main=namect1))
if (difrgy<0.3) axis(2, seq(0,1, by=.05))
if (difrgy>0.3) axis(2, seq(0,1, by=.1))

gs=unique(rlinew$group[rlinew$group!="aggregated"])
lu(gs)
for (g in 1:length(gs))
{
#g=1
gs1=as.character(gs[g])
res2=rlinew[rlinew$group==gs1,]
with(res2,polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
}
with(rlinew[rlinew$group=="aggregated",], polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))

for (g in 1:length(gs))
{
gs1=as.character(gs[g])
res2=rlinew[rlinew$group==gs1,]
with(res2,lines(year,rli, col=2, lwd=2))
#res22=rli2[rli2$group==gs1,]
```

```
#with(res22,lines(year,rli, col=2, lwd=1))
if (plotit) text(max(res2$year)+0.5, res2$rli[nrow(res2)],paste(gs1,"s", sep=""), cex=.6, adj=c(0,0.5))
if (pdfs) text(max(res2$year)+0.5, res2$rli[nrow(res2)],paste(gs1,"s", sep=""), cex=1, adj=c(0,0.5))
}
with(rlinew[rlinew$group=="aggregated",], lines(year,rli, col=4, lwd=2))

if (pdfs) dev.off()

#graph aggregated
pdf2name=paste(finfolder2, "/", ct1,"_aggregated.pdf", sep="")
pdf2name
if (pdfs) pdf(file=pdf2name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,5,4,2), mgp=c(3.5, 1, 0))

ttuse=rlinew[rlinew$group=="aggregated",]
topy=min(c(1.02, max(ttuse$qn95)*1.1))
basy=min(ttuse$qn05)*.99
difrgy=diff(range(basy, topy))
if (difrgy<miny) {
basy=topy-miny
difrgy=diff(range(basy, topy))}

with(ttuse,plot(year,rli, yaxt="n", ylim=c(basy,topy), type="n", xlab="Year", ylab="Red List Index of species survival"))
with(ttuse, polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
with(ttuse, lines(year,rli, col=4, lwd=2))
if (difrgy<0.3) axis(2, seq(0,1, by=.05))
if (difrgy>0.3) axis(2, seq(0,1, by=.1))

if (pdfs) dev.off()

# graph birds
pdf3name=paste(finfolder2,"/", ct1,"_birds.pdf", sep="")
pdf3name
if (pdfs) pdf(file=pdf3name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,5,4,2), mgp=c(3.5, 1, 0))
```

```
ttuse=rlinew[rlinew$group=="Bird",]

if (nrow(ttuse)==0) plot(1:10, 1:10, type="n", main="no data for birds", xaxt="n", yaxt="n", xlab="", ylab="")
if (nrow(ttuse)>0){
topy=min(c(1.02, max(ttuse$qn95)*1.1))
basy=min(ttuse$qn05)*.99
difrgy=diff(range(basy, topy))
if (difrgy<miny) {
basy=topy-miny
difrgy=diff(range(basy, topy))}

with(ttuse,plot(year,rli, yaxt="n", ylim=c(basy,topy), type="n", xlab="Year", ylab="Red List Index of species survival"))
with(ttuse, polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
with(ttuse, lines(year,rli, col=2, lwd=2))
if (difrgy<0.3) axis(2, seq(0,1, by=.05))
if (difrgy>0.3) axis(2, seq(0,1, by=.1))
}
if (pdfs) dev.off()


### crli

pdf3name=paste(finfolder2, "/", ct1,"_crli.pdf", sep="")
pdf3name
if (pdfs) pdf(file=pdf3name, width = 12, height = 10)
if (pdfs) par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,6,4,2), mgp=c(4.5, 1, 0))

with(crlisf,plot(year,crli, ylim=c(min(crli05),max(crli05)), xlim=c(min(year), max(year)+1), type="n", xlab="", ylab="National contribution to the global RLI"))
par(mgp=c(3.5, 1, 0))
title(xlab="Year")

gs=unique(crlisf$group[crlisf$group!="aggregated"])
lu(gs)
for (g in 1:length(gs))
{
#g=1
```

```
gs1=as.character(gs[g])
res2=crlisf[crlisf$group==gs1,]
with(res2,polygon(c(year,rev(year)),c(crli05,rev(crli95)), col=cinz, border=cinz))
}
with(crlisf[crlisf$group=="aggregated",], polygon(c(year,rev(year)),c(crli05,rev(crli95)), col=cinz, border=cinz))

for (g in 1:length(gs))
{
gs1=as.character(gs[g])
res2=crlisf[crlisf$group==gs1,]
with(res2,lines(year,crli, col=2, lwd=2))
#res22=rli2[rli2$group==gs1,]
#with(res22,lines(year,rli, col=2, lwd=1))
if (plotit) text(max(res2$year)+0.5, res2$crli[nrow(res2)],paste(gs1,"s", sep=""), cex=.6, adj=c(0,0.5))
if (pdfs) text(max(res2$year)+0.5, res2$crli[nrow(res2)],paste(gs1,"s", sep=""), cex=1, adj=c(0,0.5))
}
with(crlisf[crlisf$group=="aggregated",], lines(year,crli, col=4, lwd=2))

if (pdfs) dev.off()

}
 # ends loop countries

lu(allcountries_RLI$country)
lu(allcountries_CRLI$country)

rliallcntsfile=paste(finfolder2,"/",  "allcountries_RLI.csv", sep="")
if (writefiles) write.csv(allcountries_RLI,rliallcntsfile, row.names=F)

crliallcntsfile=paste(finfolder2,"/",  "allcountries_CRLI.csv", sep="")
if (writefiles) write.csv(allcountries_CRLI,crliallcntsfile, row.names=F)

###### single pdf with all plots

pdfallname=paste(finfolder2,"/",  "RLI_all_countries.pdf", sep="")
pdfallname
```

```
pdf(file=pdfallname, width = 12, height = 10)
par(las=1,cex.axis=1.2, cex.lab=1.3, cex.main=1.5, mar=c(5,5,4,2), mgp=c(3.5, 1, 0))

cts=unique(allcountries_RLI$country)
for (i in 1:length(cts))    #length(cts)
{
#i=1
#i=which(cts=="ABW")
i

ct1=as.character(cts[i])
ct1
rli2=rliextf[rliextf$country==ct1,]

namect1=as.character(ct1)
if (iso2use=="ISO_BL") namect1=paste(isos$uname_BL[isos$isof==as.character(ct1)][1] ," (", ct1, ")", sep="")
if (iso2use=="ISO_SDG") namect1=paste(isos$uname_SDG[isos$isof==as.character(ct1)][1] ," (", ct1, ")", sep="")
namect1

fspct=pastables[pastables$Scientific%in%unique(tbf1$Scientific[tbf1$isof==ct1]),]
head(fspct)
respc=with(fspct, aggregate(year, list(iucn=iucn, year=year,  group=group), length))

rlinew=allcountries_RLI[allcountries_RLI$country==ct1,]


#graph all
miny=.15
topy=min(c(1.02, max(rlinew$qn95)*1.1))
topy
basy=min(rlinew$qn05)*.99
difrgy=diff(range(basy, topy))
if (difrgy<miny) {
basy=topy-miny
difrgy=diff(range(basy, topy))}
with(rlinew,plot(year,rli, ylim=c(basy*.99,topy), xlim=c(min(year), max(year)+1), type="n", xlab="Year", yaxt="n", ylab="Red List Index of species survival", main=namect1))
```

```
if (difrgy<0.3) axis(2, seq(0,1, by=.05))
if (difrgy>0.3) axis(2, seq(0,1, by=.1))
gs=unique(rlinew$group[rlinew$group!="aggregated"])
lu(gs)
for (g in 1:length(gs))
{
#g=1
gs1=as.character(gs[g])
res2=rlinew[rlinew$group==gs1,]
with(res2,polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
}
with(rlinew[rlinew$group=="aggregated",], polygon(c(year,rev(year)),c(qn05,rev(qn95)), col=cinz, border=cinz))
for (g in 1:length(gs))
{
gs1=as.character(gs[g])
res2=rlinew[rlinew$group==gs1,]
with(res2,lines(year,rli, col=2, lwd=2))
text(max(res2$year)+0.5, res2$rli[nrow(res2)],paste(gs1,"s", sep=""), cex=1, adj=c(0,0.5))
}
with(rlinew[rlinew$group=="aggregated",], lines(year,rli, col=4, lwd=2))

}
dev.off()
```