Plants and Animals

Trends in the Status of Native Vertebrate Species in B.C.

Methods for adaptating the IUCN Red List Index to use NatureServe-style subnational status ranks

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Background

The Conservation Status Index (CSI) presented here is an adaptation of the "Red List Index" (RLI), first developed in 2004 (Butchart et al. 2004), and subsequently improved in 2007 (Butchart et al. 2004). The RLI provides an aggregated level of global extinction risk for a particular group of species, using IUCN Red List assessments (http://www.iucnredlist.org) of all species within that group. As these assessments are done over time, the trend in the RLI through the years will reflect the trend in the overall global status of the species group.

The idea of adapting the global Red List Index for use at a regional scale, was first explored with birds in British Columbia (Quayle, Ramsay, and Fraser 2007), using species ranks assigned by the BC Conservation Data Centre (BC CDC; http://www.env.gov.bc.ca/cdc/), which uses NatureServe conservation status ranks and assessment methods (Faber-Langendoen et al. 2012). The NatureServe Network (http://www.natureserve.org) is an international network of organizations operating in all 50 U.S. states, most of Canada, Latin America and the Caribbean. Each member program (known as a Conservation Data Centre or Natural Heritage Information Centre) collects biological information about their state, province or territory and periodically assesses the status of the known species in their jurisdiction, and assigns each one a status rank. The entire set of these ranks for a given group of species (e.g., birds) at a particular point in time is the foundation for calculating the CSI for that group at that time. The work by Quayle, Ramsay, and Fraser (2007) showed some important considerations when looking at trends in species status ranks at a regional scale, especially the effects of immigration of species in and out of the province due to range shifts. There has also been more recent work on developing Red List Indices at a national scale, this time looking at birds in Australia (Szabo et al. 2012). Our analysis uses the ranks assigned by the BC CDC to develop CSIs for breeding birds, reptiles and amphibians, mammals, and freshwater fish in BC, and evaluate changes in the index value, from the BC CDCs inception in 1992 to the most recent assessment for each species group.

Retrospective rank correction

It seems intuitive to assume that each time a species status rank changes, it reflects a true change in the probability of extinction of that species. In reality however, species can have changes in their status rank for reasons other than a genuine change in status (Possingham et al. 2002). These reasons include: (1) changes in knowledge, whereby new inventory, new information about a species biology, or new information about threats, etc. shows that a species is more or less imperilled than previously thought; (2) changes in taxonomy, where a lump of a species with other species or a split of a species into two or more newly identified taxa results in a change in status rank; (3) criteria change, where the methods that are used to assess a species status have changed, resulting in a changed status rank without a change in the underlying reasons for the species status.

Following recommendations in Butchart et al. (2007), we examined every change in conservation status rank for each B.C. vertebrate species used in this analysis, and determined the reason for the change. If the rank change was for any reason other than a true change in the conservation status (i.e., probability of extirpation from B.C.), then all of the ranks prior to that change were corrected to reflect the true status of the species at those points in time. These corrections were made using the new information, rank criteria, or taxonomy and applied to that point in time to the best of the assessors ability. In other words, the non-genuine change was nullified and all previous ranks were corrected to what would have been correct at the time.

Rank comparisons and weighting

For the mathematical calculation of the RLI or CSI (henceforth CSI), the value of the status rank is converted to a numerical weight. See Table 1 for a comparison of IUCN and NatureServe conservation status ranks, and their corresponding weights.

Table 1: Comparison of IUCN red list categories with NatureServe S Ranks, and their corresponding numerical weights

IUCN Red List category	NatureServe status rank	Weight
Extinct in the Wild	SX (Extirpated)	5.00
	SH (Historical)*	4.50
Critically Endangered	S1 (Critically Imperiled)	4.00
Endangered	S2 (Imperiled)	3.00
Vulnerable	S3 (Vulnerable)	2.00
Near Threatened	S4 (Apparently Secure)	1.00
Least Concern	S5 (Secure)	0.00

**Not recently located (typically in the last 20 to 40 years), but there is some expectation that it may be rediscovered*

An important note about NatureServe ranks compared to the IUCN Red List categories is that the NatureServe ranks are designed to allow for the inclusion of uncertainty in an assessment. This uncertainty is expressed as a range rank, which is a combination of the two most extreme (most-least imperilled) ranks which the evidence suggests are likely. For example, S1S2 means the species is either S1 or S2 but there is not sufficient evidence to definitively assign the species to one rank or the other. For this analysis, we followed the precautionary principle, assigning the numerical weight according to the most imperilled rank in a range rank (e.g., a species with a rank of S1S2 would receive a weight of 4, corresponding to the S1 portion of the rank).

In addition, NatureServe ranking methods allow for a rank of SH (Historical), which means that a species has not been located in recent years (typically 20-40 years, varying according to taxonomic group), but there is some likelihood that the species is still extant (for example, sufficient suitable habitat is thought to exist and it has not been searched for extensively). This rank was given a weight of 4.5; the midpoint between Extirpated (SX) and Critically Imperilled (S1).

Index calculation

Once the retrospective rank corrections were completed, and the categorical status ranks were converted to numerical weights, we calculated index values for each of the following four groups of vertebrate species: breeding birds, reptiles and amphibians, mammals, and freshwater fish. Index calculation was performed as per the formulae described in Butchart et al. (2007), which is based on the sum of the rank weights for all species in a group relative to the sum of the maximum possible rank weights for all species within that group. Each of these groups has been assessed four or five times since the BC CDC began ranking species in 1992, and an index value was calculated for each species group at each assessment time period. The CSI values for breeding birds are calculated using 262 of 306 species of birds that breed in BC, because the 2012 ranks are not yet available for all species. See appendix

References

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Appendix: R code for calculating CSI values

First, load the datasets required from our website. Most datasets we host are provided under the BC Government's Open Data License, but please check the indicator's data page to view the license the data are under.

```
## Import data
## First, set the web directory
web.data.dir <- paste("http://www.env.gov.bc.ca/soe/archive/data/"
                      , "plants-and-animals/2012_Vert_Species_Status/"
                      , sep="")

## Import the rank history file
ranks.file <- "Historical_Ranks_Vertebrates_1992-2012.csv"
vert.History <- read.csv(paste(web.data.dir, ranks.file, sep="")
                         , stringsAsFactors=FALSE, na.strings="")

## Import lookup table of rank weights
rank.weights.file <- "CDC_Status_Ranks_Numeric_weights.csv"
rank.weights <- read.csv(paste(web.data.dir, rank.weights.file, sep="")
                         , na.strings=c("NA","N/A",""), stringsAsFactors=FALSE)
```

The following code is used to calculate the Conservation Status Index values for each taxonomic group.

```
## Load required packages
if( !any("plyr" == installed.packages()[,"Package"] ))
  install.packages("plyr")
require(plyr)

## Attach the rank weights to the rank history dataframe
vert.History <- join(vert.History,rank.weights[,c(1,2,4,6,8)]
                     , by="SRank", type="left")

## Build a table of taxonomic groups with short names
## (combine reptiles/amphibians)
Tax.Groups <- data.frame(TaxName_Long =
                           sort(unique(vert.History$Taxonomic_Group))
                         , Tax_Group = c("reptiles_and_amphibians", "birds"
                                         ,"fish","mammals"
                                         ,"reptiles_and_amphibians")
                         , Legend_Labels = c("Reptiles and Amphibians"
                                             , "Breeding Birds"
                                             , "Freshwater Fish", "Mammals"
                                             , "Reptiles and Amphibians")
```

```
                          , stringsAsFactors=FALSE)

## Set the maximum weight (weight of an "extinct" rank)
W <- rank.weights[rank.weights$SRank=="SX",6]

## Loop to build a CSI table for each Taxonomic Group
for (grp in Tax.Groups$Tax_Group) {
  taxGroup <- Tax.Groups$TaxName_Long[Tax.Groups$Tax_Group==grp]
  taxGroup.History <- vert.History[vert.History$Taxonomic_Group %in% taxGroup,]

  ## Calculate the number of assessment periods
  nyears <- length(unique(taxGroup.History$Year))

  ## Mark the species to use which have valid ranks for each assessment
  ## year AND have not been extirpated for the entire rank history
  taxGroup.use <- ddply(.data=taxGroup.History
                        , .variables=.(Scientific_Name, Common_Name)
                        , summarize
                        , Use =
                          length(Wt_Imperilled[!any(is.na(Wt_Imperilled))])==
                          nyears & sum(Wt_Imperilled) < W*nyears)

  ## Join the 'Use' values to the history data frame
  taxGroup.History <- join(taxGroup.History
                           , taxGroup.use[, c(1,3)]
                           , by="Scientific_Name", type="left")

  ## Calculate number of species (N) and the maximium threat score (M)
  N <- nrow(taxGroup.use[taxGroup.use$Use==TRUE,])
  M <- W*N

  ## Make CSI by year table for the tax group, using only species marked above.
  ## Treat range ranks by creating a column for high, median, and low values.
  CSI <- ddply(.data=taxGroup.History[taxGroup.History$Use==TRUE,]
               , .variables=.(Year), summarize
               , Tax_Group = grp, N = N, M = M
               , CSI_Imperilled = (M-sum(Wt_Imperilled))/M
               , CSI_Median = (M-sum(Wt_Median))/M
               , CSI_Secure = (M-sum(Wt_Secure))/M)

  ## Name the table
  assign(paste("CSI.", grp, sep=""), CSI)
}

## Put the results together into one data frame
```

```
CSI.verts <- rbind(CSI.birds, CSI.reptiles_and_amphibians
                   , CSI.mammals, CSI.fish)

## Clean up temporary objects
rm(list=c("CSI", "grp", "M", "N", "taxGroup", "taxGroup.use", "CSI.birds"
          , "CSI.fish", "CSI.reptiles_and_amphibians", "CSI.mammals", "W"
          , "taxGroup.History", "nyears"))

## Join Legend labels from Tax.Groups for nice plotting
CSI.verts <- join(x=CSI.verts, y=unique(Tax.Groups[,c(2:3)]), by="Tax_Group")
```

Finally, use R (and the the ggplot2 package) to generate a simple line chart.

```
## Install packages if necessary and load
if( !any("ggplot2" == installed.packages()[,"Package"] ))
  install.packages("ggplot2")
if( !any("grid" == installed.packages()[,"Package"] ))
  install.packages("grid")
require(ggplot2)
require(grid)

## Get a colourblind-friendly palette (from http://wiki.stdout.org/rcookbook/)
cbPalette <- c("#999999", "#E69F00", "#56B4E9", "#009E73", "#F0E442"
               , "#0072B2", "#D55E00", "#CC79A7")

## Create the plot and specify options
plot <- ggplot(data=CSI.verts
               , aes(x=Year, y=CSI_Imperilled, group=Legend_Labels
                     , colour=paste(Legend_Labels," (",N,")", sep="")))

plot.lines <- geom_line(size=1, aes(linetype=paste(Legend_Labels," (",N,")"
                                                   , sep="")))

plot.points <- geom_point(size=3)

plot.linetype <- scale_linetype_manual(values=c("solid", "longdash"
                                                , "dotted", "dotdash"))

plot.colours <- scale_colour_manual(values=cbPalette[c(2,4,6,7)])

plot.guide <- guides(colour=guide_legend("Taxonomic Group", keywidth=3
                                         , override.aes = list(shape = NA))
                     , linetype=guide_legend("Taxonomic Group", keywidth=3))
```

```
plot.labs <- labs(title=paste("Conservation Status Index for four "
                              , "vertebrate\nspecies groups in British "
                              , "Columbia, 1992-2012"
                              , sep="")
                  , x="Assessment Year"
                  , y="Conservation Status Index"
)

plot.scale.x <- scale_x_continuous(breaks=seq(1992, 2012, by=2))
plot.scale.y <- scale_y_continuous(limits=c(min(CSI.verts$CSI_Imperilled)-0.015
                                            ,max(CSI.verts$CSI_Imperilled)+0.015
))

plot.theme <- theme_bw() + theme(plot.title = element_text(vjust=1)
                                 , axis.text.x = element_text(angle = 0)
                                 , axis.title.x = element_text(vjust=-0.5)
                                 , axis.title.y = element_text(vjust=0.2)
                                 , legend.text = element_text(size = 8)
                                 , legend.margin = unit(-0.5, "cm"))

CSIplot <- plot + plot.lines + plot.points + plot.colours + plot.linetype +
  plot.guide + plot.labs + plot.scale.x + plot.scale.y + plot.theme
plot(CSIplot)
```

Conservation Status Index for four vertebrate species groups in British Columbia, 1992−2012