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Seeing Red: Analyzing IUCN Red List Data of South and Southeast Asian Amphibians

Alexandra Gonzalez
angonzalez@usfca.edu

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THESIS

SEEING RED: ANALYZING IUCN RED LIST DATA OF SOUTH AND SOUTHEAST ASIAN AMPHIBIANS

Submitted by
Alexandra González

Department of Biology, University of San Francisco

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Committee:

Advisor: Dr. Jennifer Dever
Dr. Patricia Francis-Lyon
Dr. Naupaka Zimmerman
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TABLE OF CONTENTS

I. Introduction .......................................................................................................................... 6
Amphibian life history traits .................................................................................................... 7
Southeast Asia ....................................................................................................................... 8
Threatening Processes: Southeast Asian Amphibian Threats ............................................. 9
Threatening Processes: Global Amphibian Threats ............................................................ 10
IUCN Red List of Threatened Species .................................................................................. 13
Purpose .................................................................................................................................. 15

II. Materials and Methods ..................................................................................................... 16
Threat Data Acquisition ........................................................................................................ 16
Threat Data Analyses ........................................................................................................... 17
Threat Data Spatial Mapping ............................................................................................... 19

III. Results ............................................................................................................................. 21
Threat Data Analyses ........................................................................................................... 21
Threat Data Spatial Mapping ............................................................................................... 35

IV. Discussion ........................................................................................................................ 41
Future Directions ................................................................................................................... 44

V. Concluding Remarks ....................................................................................................... 44

References ........................................................................................................................... 46

Appendix I: Increasing the Accessibility to Red List Threat Data ..................................... 50
Appendix II: Reclassifying Red List Categories ................................................................. 60
Appendix III: Hierarchical Clustering of Red List Threats ................................................. 60
Appendix IV: Threat Data .................................................................................................... 61
Appendix V: Scripted Code ................................................................................................. 62
TABLE OF FIGURES

Figure 1: Global amphibians, number of threats by Red List Category ......................................................... 22
Figure 2: Global amphibians, Density Distribution of the number of threats by Red List Category ................ 23
Figure 3: Global amphibians, Total number of threat codes of Threatened (Critically Endangered, .............. 24
Endangered, Vulnerable) and Not Threatened (Least Concern, Near Threatened) amphibians
Figure 4: Threats affecting Least Concern, Global Amphibians ................................................................. 25
Figure 5: Threats affecting Near Threatened, Global amphibians ............................................................ 25
Figure 6: Threats affecting Vulnerable, Global amphibians ........................................................................ 25
Figure 7: Threats affecting Endangered, Global amphibians ..................................................................... 25
Figure 8: Threats affecting Critically Endangered, Global amphibians ..................................................... 25
Figure 9: South and Southeast Asian amphibians, Red List Category by Threat Count ............................ 26
Figure 10: Density Distribution of South and Southeast Asian amphibians, Red List Category by Threat Count .... 27
Figure 11: South and Southeast Asian amphibians, Total number of threat codes of Threatened (Critically .... 28
Endangered, Endangered, Vulnerable) and Not Threatened (Least Concern, Near Threatened) amphibians.
Figure 12: SE Asian amphibian threat totals, Least Concern ....................................................................... 29
Figure 13: SE Asian amphibian threat totals, Near Threatened ................................................................. 29
Figure 14: SE Asian amphibian threat totals, Vulnerable .......................................................................... 29
Figure 15: SE Asian amphibian threat totals, Endangered ....................................................................... 29
Figure 16: SE Asian amphibian threat totals, Critically Endangered .......................................................... 29
Figure 17: Species assessment year by Red List status. (Blue = Least Concern, Purple = Near Threatened, ........30
Pink = Vulnerable, Orange = Critically Endangered, Yellow = Data Deficient, Green = Endangered.
Figure 18: Threat Score count by Threatened vs. Not Threatened category .............................................. 30
Figure 19: Figure 19: Correlation Heatmap of Threat Processes ............................................................... 31
Map 1: Vulnerable amphibian distribution in Southeast Asia ...................................................................... 36
Map 2: Endangered amphibian distribution in Southeast Asia .................................................................... 36
Map 3: Threatened amphibians (Critically Endangered, Endangered, Vulnerable) distribution .................. 36
Map 4: Species with a listed threat of Agriculture 2.1, in the Philippines .................................................... 37
Map 5: Species with a listed threat of Agriculture 2.2 in Borneo ................................................................. 37
Map 6: Distribution of species that are being hunted and collected ............................................................ 37
Map 7: Species threatened by mining ........................................................................................................ 39
Map 8: Species threatened by human disturbances .................................................................................... 39
Map 9: Species threatened by Invasive non-native species/diseases ........................................................... 39
Map 10: Species threatened by Fire and fire suppression (includes threats of all timing) ........................... 40
Map 11: Close up of species threatened by Fire and Figure suppression (includes threats of all timing) ........ 40
Map 12: Species threatened by residential and commercial development in Mindanao Islands, Philippines ...... 41
Map 13: Species threatened by residential and commercial development in Borneo ................................. 41

TABLE OF TABLES

Table 1: Logistic Regression results #1 ........................................................................................................... 32
Table 2: Logistic Regression results #2 .......................................................................................................... 34
Abstract

In the midst of the sixth mass extinction event which is currently underway, it appears that amphibians are one of the most impacted vertebrates. Over 6,500 amphibian species are listed on the IUCN Red List (an assessment tool which provides species’ conservation status, perceived threats, and distribution range). While it is well-known that populations under multiple stressors are more likely to undergo significant declines, there are little to no resources available for visualizing how these threats may work synergistically and interact within a species’ range. This is especially the case for Southeast Asian amphibians, which much less attention has been paid as compared to other parts of the globe. While the IUCN Red List provides a description of threats affecting species and categorizes species into Red List Categories (Least Concern, Near Threatened, Vulnerable, Endangered, Critically Endangered), this data is not easily accessible for wide-scale analyses. The aims of this project were as follows: (1) utilize bioinformatics to increase accessibility to IUCN Red List data, (2) analyze the IUCN data repository to identify trends in South and South East Asian amphibian threat data, and (3) plot IUCN threat data.

I. INTRODUCTION

Plagued by anthropogenic-induced activity, disease, and other threats, amphibian populations have been declining for decades, signaling a modern biodiversity crisis. These biodiversity losses are more than just declines, however. They are indicative of the 6th mass extinction that is currently underway (McCallum 2015). The current extinction rate for endangered amphibians ranges between 25,039-45,474 times the background extinction rate.
González 6

(Alroy 2015). Extinction rates may be greater than these models suggest, however, because single-threat drivers of extinction are often considered instead of synergetic threats (Brook et al. 2008). When the effects of multiple threat processes are considered, the overall risk of extinction is greater than previously speculated (Brook et al. 2008). Approximately 32.4% of amphibian species are threatened with extinction (Stuart 2004), representing 2,030 species (IUCN 2017). While 1/3 of amphibians are threatened with extinction, as many as 22.5% do not have sufficient data for their Red List Category to be characterized. On the IUCN Red List, these species are listed as Data Deficient (DD) and as of the 2017 IUCN update, 191 species (52.5%) of the 366 species added to the database in 2008 were DD. Current mathematical models strongly suggest that DD species are more likely to face extinction than documented amphibians (Howard et al. 2014).

While the 6th mass extinction threatens all life, it seems as though amphibian species are faring worse than when compared to other vertebrates. Approximately 427 species (7.4%) of amphibians are categorized as Critically Endangered (CE) (IUCN), compared with 179 birds (1.8%) and 184 mammals (3.8%) (Stuart 2004). Moreover, when considering Data Deficient (DD) species, the gap between amphibians, birds, and mammals widens. Only 256 mammals (5.3%) and 78 birds (0.8%) are DD compared to 1,294 amphibians (22.5%) (IUCN 2017).

**Amphibian Life History Traits**

The large discrepancy between amphibians and other vertebrates are due to differences in geographic range, ecological guilds, body composition and reliance on multiple environments (Payne et al. 2007). For example, one explanation for the severity of potential extinction
amphibians face may be attributed to their limited geographic range. When species geographic range was compared to survivorship in the fossil record, a positive correlation between large geographic range and survivorship was found (Payne et al. 2007). Moreover, researchers found that in the marine fossil record, the most significant predictor of extinction risk was a species geographic range (Payne et al. 2007).

Additionally, life history traits of amphibians also contribute to their susceptibility to the current mass extinction. In Australian wet tropics rainforest frogs, researchers found three similar ecological factors of declining species: low fecundity, a high degree of habitat specialization, and reproduction in flowing streams (Williams et al. 1998). Species with low fecundity and a high degree of habitat specialization may not be able to respond to environmental fluctuations (Williams et al. 1998) in time to recover. Amphibians often have a small geographic range and many exhibit a high degree of habitat specialization. They also occupy both aquatic and terrestrial environments during their lifetime. Because their juvenile and adult life stages are spent in different environments, they are susceptible to the threats present in both habitats (Quaranta et al. 2009). Additionally, the body composition of amphibians undergoes gas, water and electrolyte exchanges with its environments. This incredible skin permeability makes amphibians more sensitive to xenobiotics (Quaranta et al. 2009) than mammals and birds. The limited geographic range, life history traits, body composition and life stages in multiple environments have created the perfect storm for amphibians, making them extremely vulnerable to the myriad of threats they are currently facing.
Southeast Asia

While the risk of amphibian extinctions worldwide is increasing, this risk is heightened in Southeast Asia. Southeast Asia is a global biodiversity hotspot (Woodruff 2010) and is home to one of the highest concentrations of endemic species in the world (Myers et al. 2000). Despite this, Southeast Asia is understudied, and flora and fauna are poorly understood. Specifically, diversity, distribution, and biology of amphibians in the region are lacking (Rowley et al. 2009; Dever 2017). There are also high levels of cryptic species (Stuart et al. 2006) and data deficient species. Both cryptic species and data deficient species are more likely to be vulnerable to extinction because of their small geographic ranges (Rowley et al. 2009), and many data deficient species may be silently going extinct (Howard et al. 2014). Although Southeast Asia has high levels of endemism and species richness, Southeast Asia has been largely ignored from wide-scale conservation initiatives. From 732 scientific articles that included “amphibian” and “conservation” in 2009, only eight articles referenced Southeast Asian countries (Rowley et al. 2009). This lack of research attention coupled with Southeast Asia’s high levels of cryptic species diversity and the highest deforestation rate on the planet have created the epitome of a biodiversity crisis.

Understanding why Southeast Asia is a biodiversity hotspot full of rich levels of species endemism and species richness can be attributed to its unique geological history (Sodhi 2004). During the Pleistocene glacial episodes, Northeastern Asian species expanded to the Indo-Burma region. Additionally, sea-level changes periodically connected the islands of Sundaland to the Asian mainland and converted mountains into geographically isolated islands (Sodhi 2008). These periodic changes in sea-levels facilitated speciation. Because Wallacea originated
from Gondwanaland land fragments, its biogeography is unique. In addition to Wallacea, the Philippines also hosts multiple centers of endemism because its many islands (~ 7000) have contributed to genetic differentiation (Mittermeier 1999). These geological historical changes and Southeast Asia’s tropical ecosystem are responsible for Southeast Asia’s high degree of endemism and species richness.

**Threatening Processes: Southeast Asian Amphibian Threats**

Several anthropogenic-induced events threaten amphibian biodiversity. Habitat destruction (Sodhi et al. 2010), overexploitation, and human population growth are the foremost threats plaguing Southeast Asian amphibians. Given the minimal research that has been conducted in Southeast Asia, this list of threat processes is likely the tip of the iceberg (Sodi et al. 2004). While amphibians around the world are threatened by habitat destruction, habitat destruction is particularly aggressive in Southeast Asia (Rodrigues et al. 2014). If the current rate of deforestation continues in the region, 42% of its biodiversity and three-quarters of its original forest will be depleted by the year 2100 (Sodi et al. 2004). Compared to other tropical ecosystems in the world, habitat destruction is occurring at higher rates in Southeast Asia than in other tropical regions (Archard 2002). This habitat destruction is largely driven by growing human populations and the need to convert forests for agriculture.

Amphibians in Southeast Asia are also threatened by over-harvesting from the wild for consumption, traditional medicine, and pet trades (Rowley et al. 2009). Illegal wildlife trafficking is a large conservation problem, and the number of illegal or undeclared international trades is significantly larger than the levels of official exports (Nijman 2009). Often, amphibians such as Southeast Asian salamandridae are harvested from the wild to feed
into the international pet trade, with rare species having a higher price tag. While exotic amphibians are in danger of being caught in the illegal pet trade, large amphibians are in danger of being over-harvested for consumption. In particular, species in the family Dicroglossidae may be targeted for human consumption, although baseline data is lacking (Rowley et al. 2009).

In addition to habitat destruction, overexploitation, and human population growth, forest fires and climate change also threaten amphibians. Southeast Asian amphibians have a high concentration of species that are climate change vulnerable and threatened (Foden et al. 2013). Specifically, climate change can affect amphibians by increasing their risk of desiccation. Moreover, researchers point to the need for future work to focus on how climate change will interact with ongoing threats to biodiversity (Brook et al. 2008). In regard to the forest fires, while fires have occurred throughout Southeast Asia’s history, increasing deforestation has made these fires more intense. Additionally, because much of Southeast Asia’s amphibians have yet to be identified (Rowley et al., 2010; Dever 2017), the risk of losing undiscovered species is significantly high.

**Threatening Processes: Global Amphibian Threats**

Overall, the threats driving the amphibian extinction are largely anthropogenic-induced, geographically based and synergetic processes. The greatest threat to endangered amphibians is habitat loss and degradation (Ficetola et al. 2014), affecting about 1,800 threatened species or 36% of amphibians since 2008 (IUCN). A comprehensive list of amphibian threats includes habitat destruction, pollution, disease, UVB radiation, climate change, introduced invasive
species, human intrusions, over-harvesting, geological events and natural system modifications (IUCN 2017).

Given the high degree of skin permeability of amphibians and their ability to conduct gas, water and electrolyte exchange with their environment, amphibians are extremely susceptible to the effects of pollution. Even in protected areas, long-term exposure to acidic environments past a species threshold is believed to cause tadpole declines, developmental abnormalities and delayed metamorphosis (Farquharson et. al 2016). The effects of agricultural runoff polluting nearby streams, ponds, lakes, and rivers have also had detrimental effects on local amphibians (Mccoy et al. 2008), increasing intersex gonads as agriculture exposure increases (Abdel-Moneim et al. 2015). Specifically, the herbicide atrazine causes males to become chemically castrated and feminized (Hayes et. al. 2010). Other studies have shown that the synergetic effects between parasites and pesticides increase limb deformities (Hays et al. 1996). Furthermore, increasing nitrogen pollution in water has the ability to cause death and developmental abnormalities (Rouse et al. 1999).

Often referred to as atmospheric or light pollution, UVB radiation can have dangerous effects on both humans and amphibians worldwide. While there is a varying degree of susceptibility to UV radiation, exposure to UVA and UVB in some species causes high mortality and developmental abnormalities (Hayes et al. 2010). Other studies suggest the effects of herbicides is influenced by the level of UV-B radiation. As human activity continues to deplete the ozone, the threat of UV radiation will only increase. Anthropogenic-induced events like habit modification will decrease canopy cover and increase amphibian exposure to UV light (Levis et al. 2015). While areas may be protected, amphibians will still be subjected to harsh UV
light. Furthermore, if protected areas are located toward the bottom of a watershed, the amphibians in protected areas will still be susceptible to contaminated water as well.

Another threat that can sweep through protected and unprotected areas with ease is Chytrid Fungus (*Batrochochytrium dendrobatidis*). Chytrid fungus is an aggressive external pathogen that spreads rapidly and effectively. Although *bd* has been found in museum species as early as the 1930s, in the past three decades Chytrid Fungus has contributed to severe population declines and extinction (Olson et al. 2013). While *bd* has been found worldwide, Australia, North America, and Central America have the most aggressive cases of *bd*. In the United States alone, *bd*-Maps shows that there have been at least 2,259 positive samples (Olsen et al. 2013). Lipps (1999) predicted that once *bd* entered into an area, within four to six months half of the species were eliminated completely. An example of the emergence of *bd* and the subsequent decline of amphibian biodiversity can be found in Panama, where *bd* caused a rapid decline in local amphibians (Lips et al. 2006). Most concerning is the fact that *bd* is particularly unforgiving to endemic species. Over the last thirty years, Chytrid Fungus has caused the decline or extinction of approximately 200 frogs species (Skerratt et al. 2007).

Currently, captive breeding and reintroduction of these impacted species is the only answer to combat the problem. When *bd* works hand in hand with climate change, the effects are disheartening. Research suggests that temperatures are nearing the “growth optimum” of *bd*, encouraging outbreaks (Pounds et al. 2006). While climate change brings us closer to the growth optimum of *bd*, invasive species have also been reported to spread the fungus (Miaud et al. 2016). Invasive species have the potential to bring disease and competition and can often
disrupt delicate ecosystems. This is especially dangerous when exotic amphibians are introduced to new environments through the pet trade (Kopecký et al. 2016).

When these threats are considered, the global amphibian population decline problem becomes clearer. While measures have been made to curb amphibian extinction (e.g. the Amphibian Action Plan), the reality of mass amphibian extinction is almost inevitable especially when threats work synergistically. For example, research has shown how pathogenic outbreaks in amphibian populations can be linked to climate-induced changes in UV-B exposure (Kiesecker et al. 2001). From climate change inducing a Chytrid Fungus outbreak to environmental pollution enabling Chytrid Fungus’s lethal impacts, amphibian threats are working together aggressively. The causes of amphibian declines and extinctions, therefore, are complex and multifaceted. Because of this, tackling these issues is one of the greatest conservation challenges of our times (Bishop et al. 2012; Blaustein 2011).

**IUCN Red List of Threatened Species**

An organization that is key to addressing species declines is the International Union for Conservation of Nature (IUCN) which has created the IUCN Red List of Threatened Species (Red List). The Red List is the most comprehensive tool available for evaluating the extinction risk of plants and animals (Rodrigues et al. 2006). To spearhead conservation efforts, the Red List was established in 1964. The Red List maintains the largest data repository detailing species threats, habitats, extinction risk, taxonomy, and range. By evaluating the extinction risk of species and providing assessment data, the Red List has become a powerful tool for conservation planning, management, monitoring, and decision making utilized by a wide range of audiences (Rodrigues
et al. 2006; Hayward 2011). While the Red List is an excellent resource that is used worldwide to facilitate conservation initiatives, there are several limitations to the database.

As outlined by the Red List, limitations to the data as a whole include missing species, missing ranges, and data deficient species. While the goal of the Red List is to be as up to date with current information and recognition of as many recently discovered species as possible, this is not always feasible. The current rate of amphibian discovery is high and the Red List funding and support is low, thus it is often not up to date with the latest species’ descriptions. However, these newly described species often come from countries with the highest amphibian species diversity under the highest rates of deforestation (Tapley et al. 2018). Recently, the rate of new species descriptions from Sri Lanka is twice as large as Panama, the country with the highest number of species described per square kilometer (Catenazzi 2015). In regard to missing species’ ranges, the Red List took a conservative approach when mapping species. Therefore, the species’ ranges presented are minimum estimates and the species are likely to occur more widely than what has been presented (IUCN 2017). While missing species and missing ranges are limitations to the database, many species are also listed as Data Deficient given the incomplete information in the record.

Threats listed on the Red List are further limited by the fact that the relative importance of different threatening processes to each species is not included. For example, a species may be subject to habitat loss but is being driven to extinction by over-harvesting. Furthermore, while extinction risk is robust and objectively calculated, threatening processes are subjective and lack the rigorous review of extinction risk (Hayward 2009). In addition to the limitations described by the Red List, the threat data listed on the site for wide-scale analyses is also hard
to access (Appendix I: Accessing IUCN Red List Data and Increasing Data Accessibility).

Therefore, providing a comprehensive assessment of Red List threat data from a taxonomic class is extremely difficult. This lack of accessibility to Red List threat data for wide-scale analyses prevents thorough assessments of the data to identify threat process trends and areas for improvement. This may be why a wide-scale analysis of all co-occurring threats by species on the Red List has not been completed.

**Purpose**

In order to increase the odds of minimizing amphibian species loss, particularly in Southeast Asia, one must understand the threat processes driving amphibians to extinction. This information will allow managers to formulate more successful adaptive wildlife conservation plans (Hayward 2011). As described above, there are often certain life history traits that are highlighted as making a species more or less susceptible to extinction. While it is well known that species with narrow ranges and small clutch sizes require further protection, the types of threats endangering some species and not others and how threats work synergistically must be understood for effective conservation outcomes to be made (Murray 2010). Given the relative importance of the Red List Data to wildlife assessments coupled with the fact that Red List information is often used to create conservation strategies, thoroughly evaluating threat processes within the Red List is crucial to preventing mass amphibian extinctions.

Using Southeast Asia as a case study, threatening processes within the IUCN Red List were evaluated to answer the following questions:
1. How do multiple threat processes affect an amphibian’s extinction risk?
2. What are the primary threats to Southeast Asian amphibians?
3. Which threats are driving Southeast Asian amphibians to extinction?

II. Materials and Methods

To address the questions listed above, three separate processes were carried out. First, functions were developed to increase the accessibility to the Red List Threat Data (Appendix I: Accessing IUCN Red List Data and Increasing Accessibility). Utilizing the data collected from the scripted functions, data analyses on global amphibian data and South and Southeast Asian amphibian data were then possible. As threat processes are often location-based, Southeast Asian amphibian threats were mapped using species ranges to provide further insight.

Threat Data Acquisition

Global amphibian data were exported from the IUCN Red List in March 2017. South and Southeastern Asian amphibian data were exported from the IUCN Red List Website in February 2018. The exported comma separated value files for global amphibian data and South and Southeastern Asian amphibian data were imported into R version 3.3.2 (2016-10-31). These CSV files contained general information for each species assessment, including Red List Status, taxonomy, year assessed, infraspecific rank, infraspecific name, infraspecific authority, common names, Red List Status, Red List criteria, population trend and petitioned status. Utilizing the developed code described in Appendix I: Increasing the Accessibility to IUCN Red List Threat Data, threat data was collected using functions threat_details, sp_threat_count, threat_codes, and threat_tables. Third tier threats were removed (Schulze et al. 2018). Threat tables were
then joined to the original IUCN Data to create a large table with all IUCN Red List Data. In addition to collecting data from the IUCN Red List, external data was also utilized. AmphiBIO is a global database of amphibian ecological traits. For the analyses focused on South and Southeast Asian amphibian species, the AmphiBIO database was utilized for ecological data (Oliveria et al. 2017).

**Threat Data Analyses**

To calculate the number of threats for both global amphibian data and South and Southeastern Asian amphibian data, the developed function `sp_threat_count` was utilized (Appendix I). Because the Levene test is less sensitive to departures in normality as opposed to the Barlett test, the Levene test from the car package was selected to test the homogeneity of variances in both datasets. For both global amphibian data and Southeast Asian amphibian data, the type of ANOVA carried out depended on the results of the Levene test. If the data did not display homogeneity of variances, a Welch’s ANOVA was utilized. If the data did display a homogeneity of variances, a classic one-way ANOVA was carried out. For data where the Welch’s ANOVA had been selected, a Games-Howell post hoc test was executed from the userfriendlyscience package a standard one-way ANOVA, the post hoc test was completed using Tukey’s HSD (McDonald 2014).

Exploratory data analyses for both global amphibian data and South and Southeast Asian amphibian data utilized ggplot2 (Wickham, 2009). A category, “Threatened or Not Threatened” was developed by splitting the Red List Statuses (Appendix II). Species listed as Least Concern or Near Threatened were coded as ‘Not Threatened’ because of their lower risk designation from the Red List. ‘Threatened’ species included those that are listed as Vulnerable,
Endangered, or Critically Endangered. Data deficient, Extinct, or Extinct in the Wild species were removed from the list to perform the density distributions, bar plots, and boxplots. In addition to exploratory data analysis by threats, the year of assessment and threat score were visualized as well for Southeast Asian amphibians.

Before a logistic regression model could be created, correlated variables were removed from the dataset. The type of correlation test that was selected depended on the variables within the data. For a species with a given threat, this is captured in the developed tables as 0 or 1, where 0 represents no threat and 1 represents the threat. These variables are not true binary variables because threatening processes are measured on a continuous scale. Therefore, instead of using a Pearson correlation, a tetrachoric correlation was utilized and variables that had greater than 0.7 correlation were removed. After removing correlated variables, threats were hierarchically clustered and a dendrogram was created from the remaining variables.

Logistic regression models were created using the step function from the MASS package. The purpose of the logistic regression models was to estimate the effects of threatening processes on Red List Status. Red List Statuses were represented by the Threatened or Not Threatened category, described above. Species present in the AmphiBIO dataset were matched with those listed in the corresponding IUCN Data, unmatched species were removed from the list. The first logistic regression model utilizes only threat processes as predictor variables, with the Threatened (Critically Endangered, Endangered, Vulnerable) or Not Threatened (Least Concern, Near Threatened) category as the response variable. The second logistic regression model tests the effects of both threat processes and AmphiBIO data on threat category. Because a large percent of AmphiBIO data is missing, only variables with higher
than 50% completeness were tested. These variables include body size, reproductive output, and breeding strategy. Although Red List Threat Processes have been reclassified to smaller subcategories in the previous studies (Ducatez 2017), reclassifying the South and Southeast Asian amphibian data in this manner would have eliminated variation in Southeast Asia threat processes. To compare logistic regression models, the pseudo R-squared values were evaluating using the package pR2.

**Threat Data Spatial Mapping**

Threat tables generated from the functions developed in Appendix I were utilized to import co-occurring threat data into ArcMap. Available amphibian spatial data were downloaded from the IUCN site directly and extracted in January 2018. IUCN spatial and non-spatial data containing the threat tables were then joined by species name. Within ArcMap, threats were filtered by column using the “Select by Attribute” tool, and a separate layer of this selected data was created and added to the map layer. Because columns are saved as respective threat codes, an example of filtering the data for species threatened by Residential and Commercial Development, Housing and Urban areas would be R1.1 == 1. After the desired threat processes had been selected from the main data table and a new layer was created, this layer was exported, saved as shapefile, and added to the map layer. Because there were overlapping species ranges, without additional processing, many species ranges would be hidden. To avoid this, overlapping polygons were created to visualize the species range data. The Feature to Polygons Tool in the Data Management Toolbox within ArcMap was utilized to create a feature class containing polygons. From here, the output of the Feature to Polygons tool was input into the Feature to Point tool to create a point within each polygon. Then, a
spatial join was completed between the original data and the point data, generating a count for each polygon (join_count). In other words, if there were three overlapping polygons, the count would be three. This represents three species with overlapping ranges. The count data was then joined to the original Feature to Polygons Tool output, and polygons with a count of zero were removed from the attribute table. The count data was then visualized through the Symbology panel and the layer exported and saved as a shapefile. Maps were created using ArcGIS base map Terrain with Labels.

Maps were created for Residential and commercial development, Housing and urban areas (1.1), Agriculture and aquaculture, annual and perennial non-timber crops (2.1), Biological Resource Use, Hunting and collecting terrestrial animals (5.1), Energy Production and Mining, mining and quarrying (3.2), Human intrusions and disturbance, Recreational activities (6.1), Natural system modifications, Fire and fire suppression (7.1), Invasive and other problematic species, genes and diseases, and Invasive non-native/alien species/diseases (8.1). In addition to mapping threat processes, Red List Category maps for threatened amphibians in Southeast Asia were also created. In addition to individual maps by threatened Red List Category, an aggregate map of Critically Endangered, Endangered and Vulnerable amphibians was also created to mimic the threatened variable created for data analysis purposes. Furthermore, creating this aggregated map allowed for Critically Endangered amphibians to be included as there were not sufficient spatial records in Southeast Asia for these species to be mapped on their own.
III. Results

Threat Data Analyses

*Global Amphibians*

All amphibian assessments excluding Data Deficient, Extinct and Extinct in the Wild (n = 4013) averaged 3.35 ± 2.34 threats per species. A boxplot illustrating these values can be found below (Figure 1). The Levene test on global amphibian data revealed the variances were not homogenous (Levene’s Test for Homogeneity of Variance, df = 4, F value = 5.93, p-value = 9.13e-05). Because the variances of global amphibians displayed heteroscedasticity, a Welch’s ANOVA was selected for further analyses. The results of the Welch’s ANOVA provide evidence that there is a significant difference between Red List Categories and threat means (p<.001). The post hoc Games-Howell test resulted in true differences between NT-LC (p<.001), VU-LC (p<.001), EN-LC (p<.001), CR-LC (<.001), EN-NT (p<.001), EN-VU (p<.001), CR-VU (p = .011). In addition to the Welch’s ANOVA, a Kruskal-Wallis rank sum test and a multiple comparison test after Kruskal-Wallis were also carried out. When analyzing significant differences between the groups, the results of a Kruskal-Wallis rank sum test revealed that there is a significant difference between the number of threat means between Red List Categories (Kruskal-Wallis chi-squared = 347.69, df = 4, p-value = 2.2e-16). The Multiple comparison test after Kruskal-Wallis resulted in true differences between LC-NT (observed difference(od) = 505.463, critical difference(cd) = 176.67), LC-VU (od = 413, cd = 142), LC-EN (od = 777, cd = 131), LC-CR (od = 643, cd = 156), NT-EN (od = 271, cd = 199), VU-EN (od = 363, cd = 160) and VU-CR (od = 230, cd = 181). Both tests illustrate that there is a significant difference between Red List Threat Categories and threat means. In addition, true differences between groups were the same in
the post hoc games-Howell test and in the multiple comparison test after Kruskal-Wallis. These significant differences can also be seen on a density distribution plot (Figure 2) of the number of threats by Red List Category.

Figure 1: Global amphibians, number of threats by Red List Category (LC = 1546, NT = 399, VU = 670, EN = 852, CR = 546)
After the difference between mean threat count by different Red List Categories was determined to be significant, threat processes were evaluated further. Figure 3 illustrates the top threat processes that are affecting amphibians, separated by whether the species is classified as threatened or not threatened. The five most prevalent threat processes are: Residential & commercial development, housing and urban areas (1.1) (n = 1469), Agriculture & aquaculture, annual & perennial non-timber crops (2.1) (2354), Agriculture & aquaculture, livestock farming & ranching (2.3) (1206), Biological resource use, logging & wood harvesting (5.3) (2149), and Invasive and other problematic species, genes & diseases, invasive non-native/alien species/diseases (8.1) (1163). In all five of these threat processes, there are more threatened species than non-threatened species. These findings coincide with the IUCN Red List.
Data on the trends of threat processes within the database because habitat destruction is a prominent threat (IUCN 2017).

Figure 3: Global amphibians, Total number of threat codes of Threatened (Critically Endangered, Endangered, Vulnerable) and Not Threatened (Least Concern, Near Threatened) amphibians.

In addition to dividing the data by threatened and not threatened, threats were evaluated by each Red List Category (Figures 4-8).
Figure 4: Threats affecting Least Concern, Global Amphibians

Figure 5: Threats affecting Near Threatened, Global amphibians

Figure 6: Threats affecting Vulnerable, Global amphibians

Figure 7: Threats affecting Endangered, Global amphibians

Figure 8: Threats affecting Critically Endangered, Global amphibians
South and Southeast Asia Amphibians

Similarly to the global amphibian analyses, box plots and density distributions were created to analyze the relationship between threat processes and extinction risk (Figure 9,10). The Levene test for Southeast Asian amphibians illustrates the variance is homogeneous (Levene’s Test for Homogeneity of Variance, df = 4, F value = 0.918, p-value = 0.4628). Because the variance is homogeneous, a One-way ANOVA was selected. The ANOVA provides evidence that the effect of extinction risk (Red List Category) on species threat count is significant (p = 1.89e-06). A Tukey multiple comparisons of the means determined that EN-LC (p = 1.2e-06), CR-LC (p = 0.034), EN-NT (p = 0.04), EN-VU (p = 0.03) all had significant differences in threat count means.

Figure 9: South and Southeast Asian amphibians, Red List Category by Threat Count (LC = 377, NT = 89, VU = 136, EN = 131, CR = 44)
South and Southeast Asia Amphibian threat processes were plotted by threatened and non-threatened species (Figure 11). In this case, the top four most prevalent threats were Residential and commercial development (1.1), Agriculture and aquaculture, non-timber crops (2.1), Biological resource use, logging and wood harvesting (5.3), and Pollution, agricultural and forestry effluents (9.3). One noticeable difference between the global amphibian data and the South and Southeast Asian amphibian data is the lack of Invasive and other problematic species in the data (8.1).
Threats were also evaluated by Red List Category (Figures 12-16), with differences between the presence and absence of specific threats categories. For example, Least Concern species have no records of the following Climate change threats: Habitat alteration (11.1), temperature extremes (11.3) and storms and flooding (11.4). However, these threats are present (although in low numbers) in critically endangered species. In addition, while least concern species have Residential and Commercial development, Commercial and Industrial areas (1.2) as a listed threat, critically endangered species do not. Critically endangered species have Biological resource use, gathering terrestrial plants (5.2) and Other impact (12.1) listed as a threat, whereas Least concern does not. Therefore, when considering species on opposite ends of the extinction spectrum, there are differences in the presence or absence of threats, and between South and Southeast Asia and global amphibian threat trends.

Figure 11: South and Southeast Asian amphibians, Total number of threat codes of Threatened (Critically Endangered, Endangered, Vulnerable) and Not Threatened (Least Concern, Near Threatened) amphibians.
Figure 12: SE Asian amphibian threat totals, Least Concern

Figure 13: SE Asian amphibian threat totals, Near Threatened

Figure 14: SE Asian amphibian threat totals, Vulnerable

Figure 15: SE Asian amphibian threat totals, Endangered

Figure 16: SE Asian amphibian threat totals, Critically Endangered
**Figure 17**: Species assessment year by Red List status. (Blue = Least Concern, Purple = Near Threatened, Pink = Vulnerable, Orange = Critically Endangered, Yellow = Data Deficient, Green = Endangered.

**Figure 18**: Threat Score Count by Threatened vs. Not Threatened category.
The recent Red List assessment years of Southeast Asian amphibians is illustrated in Figure 17. The majority of listings are from 2004, and additional assessments have been few to none. Figure 18 illustrates the threat scores present in South and Southeast Asian amphibian data. Most of the threat processes are listed as low impact or N/A. Both of these visualization processes reveal the paucity of data available for amphibian assessment in this region.

Figure 19: Correlation Heatmap of Threat Processes

Figure 19 illustrates the correlation matrix after the highly correlated variables were removed before creating the logistic regressions. Two different logistic regression models were
built to evaluate the impact of threat processes on threatened or not threatened status. The first model, relies only on threat processes as predictor values, while the second model incorporates information from the AmphiBIO database.

<table>
<thead>
<tr>
<th>Threat Processes</th>
<th>Logistic Regression Coefficient</th>
<th>OR (Odds Ratio)</th>
<th>P-Value</th>
<th>95% Confidence Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Annual &amp; perennial non-timber crops (A2.1)</td>
<td>1.1492</td>
<td>3.15</td>
<td>5.46e-10***</td>
<td>2.20, 4.55</td>
</tr>
<tr>
<td>Energy production &amp; mining (E3.2)</td>
<td>1.3201</td>
<td>3.74</td>
<td>0.004**</td>
<td>1.56, 10.03</td>
</tr>
<tr>
<td>Hunting &amp; collecting terrestrial animals (B5.1)</td>
<td>-1.357</td>
<td>0.25</td>
<td>2.35e-05***</td>
<td>0.13, 0.47</td>
</tr>
<tr>
<td>Human intrusions, recreational activities (H6.1)</td>
<td>5.183</td>
<td>178.35</td>
<td>2.81e-05***</td>
<td>23.47, 4130.01</td>
</tr>
<tr>
<td>Invasive species, genes and disease (I8.1)</td>
<td>-2.227</td>
<td>0.10</td>
<td>0.032*</td>
<td>0.009, 0.625</td>
</tr>
<tr>
<td>Pollution, domestic &amp; urban waste water (P9.1)</td>
<td>-2.345</td>
<td>0.095</td>
<td>0.001***</td>
<td>0.020, 0.345</td>
</tr>
</tbody>
</table>
As illustrated in Table 1, the presence of the agricultural threat A2.1 multiplies the odds of a species being threatened by a factor of 3.15 (95% CI [2.2, 4.55]). Other threats that increase the odds of a species being threatened are energy production and mining (E3.2), human intrusions, recreational activities (H6.1), pollution from industrial and military effluents (P9.2) and climate change induced droughts (C11.2). Threats that did not increase the odds of a species being threatened on the Red List were hunting and collecting terrestrial animals (B5.1), invasive species, genes and disease (I8.1), and pollution from domestic and urban waste water (P9.1). The McFadden pseudo R-squared value of this regression was 0.15.

Because intrinsic and extrinsic factors are important when considering species extinction data (Gonzalez-Suarez, 2013), a second model was created. In the second logistic regression, threatened or not threatened is the dependent variable and the predictors are threat processes and ecological data. In addition, interactions between threat processes were evaluated. As described in the methods section above, only certain categories of ecological data could be considered in the analysis due to missing data. The results from the second model are illustrated in Table 2.
<table>
<thead>
<tr>
<th>Threat Processes</th>
<th>Logistic Regression Coefficient</th>
<th>OR (Odds Ratio)</th>
<th>P-Value</th>
<th>95% Confidence Interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Annual &amp; perennial non-timber crops (A2.1)</td>
<td>0.84</td>
<td>2.32</td>
<td>6.59e-05***</td>
<td>1.54, 3.53</td>
</tr>
<tr>
<td>Hunting &amp; collecting terrestrial animals (B5.1)</td>
<td>-0.01</td>
<td>0.99</td>
<td>0.018*</td>
<td>0.98, 0.99</td>
</tr>
<tr>
<td>and Body size</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Human intrusions, recreational activities (H6.1)</td>
<td>4.75</td>
<td>116.18</td>
<td>9.69e-05***</td>
<td>16.23, 2662</td>
</tr>
<tr>
<td>Pollution, domestic &amp; urban waste water (P9.1)</td>
<td>-1.92</td>
<td>0.145</td>
<td>0.012*</td>
<td>0.02, 0.56</td>
</tr>
<tr>
<td>Pollution, Industrial &amp; military effluents (P9.2)</td>
<td>1.43</td>
<td>4.18</td>
<td>0.019*</td>
<td>1.28, 14.97</td>
</tr>
</tbody>
</table>

Table 2: Logistic Regression for threatened or not threatened status using threat processes, threat interactions, and ecological data as predictor variables

From the second logistic regression, the presence of agricultural threat A2.1 multiplied the odds of a species being threatened by 2.32. When hunting and collecting terrestrial animals (B5.1) interacts with species Body Size in the regression model, the odds of a species being threatened are multiplied by a factor of 0.99. Compared to the first regression model, the interaction between body size and hunting animals increased the odds ratio bringing the number from 0.25 to 0.99. The presence of human intrusions multiplies the odds of a species...
being threatened or not threatened by 116 (95% CI [16.23, 2662]). The presence of pollution from domestic and urban waste water multiplied the odds of a species being threatened or not threatened by 0.145; this is a decrease. The presence of pollution from industrial and military effluents multiplied the odds by 4.18; this is an increase. The McFadden pseudo R-squared value for the second logistic regression model is 0.364. Including interactions and ecological data in the logistic regression increased the pseudo R-squared to 0.364 from 0.15, indicating the importance of ecological data when considering threatening processes. Appendix III illustrates the hierarchical clustering of Red List threat processes in a dendrogram. Threatening processes on the Red List generally group as expected, with similar threat processes more closely related than non-closely related threat processes.

**Threat Data Spatial Mapping**

Endangered and Vulnerable amphibians are located in the same proximity, as illustrated in Maps 1, 2, and 3. Malaysia, Brunei, Indonesia and the Philippines all hold concentrated pockets of threatened amphibians. In particular, the Philippine islands of Mindanao and Pulo ng Bohol, in addition to the Northeast region of Borneo have 11-15 threatened species. There are a limited number of threatened species in Myanmar (Burma), Laos, Thailand, Cambodia, Vietnam, and Singapore.
Map 1 (left): Vulnerable amphibian distribution in Southeast Asia.
Map 2 (right): Endangered amphibian distribution in Southeast Asia.

Map 3: Threatened amphibians (Critically Endangered, Endangered, Vulnerable) distribution
Map 4 (left): Species with a listed threat of Agriculture, 2.1 in the Philippines
Map 5 (right): Species with a listed threat of Agriculture 2.2 in Borneo.

Map 6: Distribution of species that are being hunted and collected
When species under Agriculture threats were plotted (2.1), the focus was placed on areas occupied by threatened amphibians. Maps 4 and 5 show the high intensity of species listed with this threat in Borneo and the Philippines. In Malaysia, the distribution of species with agricultural threats falls in line with the distribution of threatened species described above. There are more than 13 species with agricultural threats in Malaysia, and neighboring Indonesia contains a pocket in the Southwest region with 7-9 species. Borneo and the Philippines both have high concentrations of species threatened by Agriculture.

Species that are threatened by hunting and collecting of terrestrial animals (5.1) (Map 6) have a different distribution. While there are some species (3-5) that are listed as being threatened by hunting and collection in Maritime Southeast Asia (Brunei, East Malaysia, Indonesia, Philippines, Singapore and Timor-Leste), the highest concentration of species that are being hunted and collected can be seen in Indochinese peninsula (Cambodia, Laos, Myanmar (Burma), Thailand, Vietnam and West Malaysia) with 16-20 species specifically in Thailand and Vietnam.

For species threatened by energy production and mining (3.2) (Map 7), these threats are distributed mostly in the Philippines and Indonesia. There are no recorded species in Borneo and a limited number on the Indochinese peninsula. Similar to species threatened by energy production and mining, there are a limited number of species that are recorded as threatened by Human Intrusions and disturbance (6.1) (Map 8). A small pocket of species threatened by Human intrusions and disturbance, however, can be found near Hanoi, Vietnam.
Map 7 (left): Species threatened by mining.
Map 8 (right): Species threatened by human disturbances.

Map 9: Species threatened by Invasive non-native species/diseases (8.1)

Species threatened by invasive non-native/alien species/diseases(8.1)(Map 9) are similar to energy production and mining in that there are a limited number of species affected.
However, of the recorded threats, no threats are listed on Borneo. 1-2 species threatened by invasive non-native/alien species/disease can be found in the found in the Philippines and 3-4 species affected by this threat process are located in Indonesia and Myanmar.

Natural system modifications paint a different picture. These threats are almost exclusively in Indochina with concentrated pockets of up to 16-20 species located throughout (Map 10, map 11).

Map 10 (left): Species threatened by Fire and fire suppression (includes threats of all timing).
Map 11 (right): Close up of species threatened by Fire and Figure suppression (includes threats of all timing).

Finally, Residential and commercial threats were mapped. Unlike Agricultural threats where many species overlapped areas containing high numbers of threatened species, Residential and Commercial threat presence in Borneo is not as intense, with only 2-5 species threatened by this threat process. In the Philippines, however, concentrated pockets of residential and commercial development threats align with threatened areas (Figure 12, 13).
IV. Discussion

In both global amphibian analyses and South and Southeast Asian amphibian analyses, the number of threats affecting a species is correlated with its extinction risk, with greater threat numbers seen in Vulnerable, Endangered and Critically Endangered species. Given the variation in distribution as seen in the density distribution plots, threat count alone does not predict extinction risk. The types of threats and life history traits of a species are important to consider as well. In global amphibian analyses, the top five threats are two different types of Agriculture, (annual & perennial non-timber crops and livestock farming & ranching), logging & wood harvesting, Invasive non-native/alien species/diseases and Residential and commercial development. In Southeast Asian amphibian analyses, the top threats are Residential and commercial development, Agriculture (non-timber crops), logging and wood harvesting and Pollution (agricultural and forestry effluents). Across all amphibians, habitat destruction is a
prevalent and deadly threat. While the dramatic presence of habitat destruction in Southeast Asia is reflected in this data, the presence of overharvesting threatened amphibians in Southeast Asia is not. Overharvesting for the pet trade, medicinal uses and consumption is cited frequently in the literature. However, the presence of this threat appears to be underrepresented in the Red List data. Additionally, the difference between global amphibian data threats and South and Southeast Asian threats illustrates the importance of finer scale conservation strategies. Chytrid fungus, which would be represented under the threat 8.1 (Invasive non-native diseases) for example, has a strong presence in global amphibian data but is in low numbers in the South and Southeast Asian amphibian data. While \textit{bd} has recently been detected in Southeast Asia, it appears as though the fungus is not driving significant declines in the region (Le DTT et al. 2017). This is also represented in the first logistic regression where invasive species as a threatening process did not increase the odds of being threatened or not threatened.

Furthermore, although Southeast Asian amphibians have a high concentration of species that are climate change vulnerable and threatened (Foden et al. 2013), there are relatively low numbers of species that have climate change as a listed threat. However, climate change numbers that are low or missing in Least Concern species are present in Critically Endangered species. This is supported in the first logistic regression model, where climate change was a significant variable in predicting whether or not a species is threatened or not threatened. While this trend supports previous findings that vulnerable amphibians are threatened by climate change, the number of species listed with climate change as a threat appears to be underestimated. Another discrepancy in the Red List data can be seen when examining the
threatening process Human intrusions and disturbance, H6.1. Despite the limited number of species that have this recorded threat, from the logistic regressions it is considered a highly significant predictor of whether a species is threatened or not threatened. When examining the data closer, only species that had this threat listed were either Critically Endangered, Vulnerable or Endangered. While human intrusions and disturbance clearly affect threatened species, it is unlikely that other species in the area are not affected by this threatening process. Therefore, Red List Assessors may be over assigning this threat process to threatened amphibians even though this threat also affects other species in the area. This illustrates the importance of a more objective assessment process of threats that will illuminate subjective reporting.

In addition to potential biases, discrepancies in the data may be addressed by the lack of recent assessments. Because the majority of the data was collected and assessed in 2004, the threatening processes for some amphibian may be outdated or underestimated, given the high presence of habitat destruction in the area and aggressive onset of climate change. In addition, while the Red List now includes a threat score, a large number of threats are listed as either Low Impact or NA. To increase the utility of Red List threat data, threat processes and impact scores should be included regardless of Red List Status.

While the map of threatened species illustrates a high number of threatened amphibians in Borneo and the Philippines, given the unique geological history of Maritime Southeast Asia that encouraged speciation along with the high intensity of threats in the area, the number of threatened species may be underrepresented by the Red List. In addition, the
Indochinese peninsula has few threatened species, despite the fact that part of the region contains tropical rainforest and is heavily affected by hunting of terrestrial animals.

Although the Red List is the most comprehensive tool for assessing plant and animal extinction risk, it is evident from both these maps and from the results derived in the analyses, that threat processes need to be given more attention for wide-scale analyses. Furthermore, because Southeast Asian amphibians have data that is collected more than ten years ago, several hundred species must be reassessed. Because Southeast Asia is a biodiversity hotspot with a unique history and sound promise of containing high levels of species richness, researchers should make Southeast Asia a conservation priority. By mapping threats and analyzing how they interact with multiple species ranges, further assessments of the Red List can be carried out.

**Future Directions**

Although extinction risk is a continuous scale, the current regression model divides species as threatened or not threatened. Future analyses could build a model where the dependent variable, extinction risk, is represented as a continuous scale. In addition, as the AmphiBIO database improves and more ecological data becomes available, variables should be selected and incorporated into the models. Future analyses including different tiers of threat data (i.e. tier 1, tier 2 and tier 3), may also provide more insight into Red List Threat Data.

**Concluding Remarks**

Species extinction is a complicated, multi-faceted problem. Accurately identifying threats that are driving amphibian declines is an important step to saving them from the 6th mass extinction. Here, I have increased the accessibility to Red List threat data through code.
Moreover, in using Southeast Asia as a case study, I have illustrated the impact of threat processes on threatened and not threatened amphibians and the importance of ecological data when shaping these models. By mapping amphibian threats that have been designated by the Red List, I have shown areas that need further attention and species assessments. While these analyses are not a comprehensive assessment of all threat data, they are an important step towards improving the IUCN Red List database.
References


Cardoso P. 2017. red - an R package to facilitate species red list assessments according to the IUCN criteria. Biodiversity Data Journal 5.


Sodhi NS, Posa MRC, Lee TM, Bickford D, Koh LP, Brook BW. 2010. The state and conservation of Southeast Asia biodiversity. Biodivers Conserv 19:317-328


Appendix I: Increasing the Accessibility to Red List Threat Data

Introduction

Because of the importance of the IUCN Red List as described above in wildlife conservation, it is imperative to have access to expert-curated threats for each species. The ability to analyze all Red List threats by species and see co-occurring threats can facilitate wide-scale analyses and provide deeper access to needed synergistic threat data. Therefore, the goals of this effort were to increase accessibility to Red List threat data and to capture the multifaceted threat details that come with each listing.

Threat Data Description

There are currently 11 major threats classified on the Red List: Residential & Commercial Development, Agriculture & Aquaculture, Energy Production & Mining, Transportation & Service Corridors, Biological Resource Use, Human Intrusions & Disturbance, Natural System Modifications, Invasive & Other Problematic Species, Genes & Diseases, Pollution, Geological Events, and Climate Change & Severe Weather. Each threat is assigned a threat code by the Red List (Appendix I: Threat Data). The Red List provides working documentation to distinguish species threats from stressors and to provide in-depth descriptions of the types of threats listed on the Red List (IUCN). When assessing a species, the Red List separates required supporting information under all conditions and required supporting information under specific conditions. Species threat data falls under the latter classification. According to this classification scheme, major threats to the taxon are required for taxa listed as Extinct, Extinct in the Wild, Critically Endangered, Endangered, Vulnerable and Near Threatened. Within this threat data, coding of
threat timing and threat scope are not required. Upon successful completion of a Red List Assessor training course, anyone can assess a species to be then verified by an expert.

**IUCN Red List Limitations**

While the Red List of Threatened Species is the most comprehensive animal and plant conservation resource (Rodrigues et.al), there are several limitations to the site in regard to missing data (IUCN 2017) and data accessibility. As described above (Section I: IUCN Red List of Threatened Species), the limitations that the Red List indicates are missing species data, missing range data, threat processes ranking and data deficient species (IUCN 2017). Furthermore, a case study in taxa with high rates of species discovery recently found that while there has been a 25% increase in known amphibian species since 2004, 61% of amphibian species assessments are either missing or out of date (Tapley et al. 2018). When considering rapid increases in amphibian species specifically, the majority of these species are more likely to have a small range size and thus be threatened with extinction (Tapley et al. 2018; Pimm et al. 2014). In addition to limitations in the data itself, threat data from the Red List is hard to access.

**Accessing IUCN Red List Threat Data**

In order to access data from the Red List, it is important to distinguish what types of information will be accessed. For both taxonomic and spatial range data, a passcode from the IUCN is necessary. After the passcode is obtained, the Red List offers a myriad of options to access species-specific data. For taxonomic data, these options include either querying the Red List directly or utilizing the Red List API – v3. In regard to the Red List API – v3, the IUCN provides extensive documentation on the variety of different querying options for using the Red List API –v3.
Options to query the data include the following: Species count, citation by species name, citation by species ID, individual species category, individual species by name, individual species by ID, narrative text by species name, narrative text by species ID, synonyms by name, country occurrence by species name, country occurrence by species ID, historical assessments by species names, historical assessments by species ID, threats by species name, threats by species id, habitats by species name, habitats by species ID, conservation measures by species name, conservation measures by species ID, plant growth forms by species names, plant growth forms by species ID, list comprehensive groups, species by comprehensive group, website link, and website redirect (IUCN 2017). Across all of these options, the way the IUCN Red List API- v3 allows for querying the data is on a species by species basis. The large majority of the queries generated, therefore, provides detailed information from the desired species. From the provided list, however, there is no simple way to access threat data across multiple species. For the threat data, in particular, there are only two options when utilizing the IUCN Red List API: querying threats by species name or querying threats by species id. In order to conduct a wide-scale assessment of all the threats affecting amphibians of SE Asia, the Red List API is not a practical option.

The API, however, is not the only option for querying data from the IUCN Red List. The Red List also offers users the ability to query the database directly. On the IUCN homepage, under “OTHER SEARCH OPTIONS” there are several different filters available to search through the IUCN Red List database. These filters include “Keywords”, “Taxonomy”, “Location”, “Systems”, “Habitat”, “Threats”, “Assessment”, and “Life History.” In addition, the IUCN Red List allows users to select the taxa to show with “Species”, “Subspecies and varieties”, “Stocks and
subpopulations”, and “Regional assessments” as options. After users have selected the information to query and run the search, the Red List displays the species assessments in a list formatted by individual species. From this page, the IUCN offers a Save/Export Search feature that allows users to export all of the data to a Comma-Separated Values (CSV) file or an Extensible Markup Language (XML) file where further analyses can be executed. When the data is exported, however, limited information is available. The information that is available includes the Species ID, Kingdom, Phylum, Class, Order, Family, Genus, Species, Authority, Infraspecific rank, Infraspecific name, Stock/subpopulation, Synonyms, Common name (Eng), Common name (Fre), Common name (Spa), Red List status, Red List criteria, Red List criteria version, Year assessed, Population trend, and Petitioned. This data does not include threat, habitat, or conservation data for each species. Even if the search filters include threat data, the threat process is not available in the file export. Therefore, from the list of data that is available from the export, it is not possible to do a wide-scale analysis of the types of threats affecting each species because the data is not included.

Instead of accessing the data through the IUCN directly, an alternative path utilizes the package rredlist created by S. Chamberlain. The package is intended to cover all of the Red List ‘API’ routes in R (Chamberlain 2017). Similar to the IUCN Red List API feature, rredlist queries information species by species. For example, the function rl_threats returns a detailed record of the threats affecting a species. The information in this output is identical to the information used when querying through IUCN Red List API – v3. Below, is an example of the information displayed when querying threats for the species Theloderma asperum.
Appendix 1, Table 1: rredlist, rl_threats output. rl_threats returns detailed threat information on a species by species basis.

In addition to the rredlist, there are other packages that have been developed to analyze IUCN Red List Data (Cardoso 2017). These include rCAT (Moat et al. 2017), redlistr (Lee et al. 2017), and ConR (Dauby 2017). rCAT, redlistr, and ConR packages primarily focus on calculating Extent of Occurrence (EOO) or Area of Occurrence (AOO). To date, the only package that has been developed to query non-spatial data is the rredlist, described above. While the rredlist package is suitable for querying species on a species by species basis, it does not produce an output where threats of multiple species can be analyzed simultaneously. To address this problem, a series of functions were developed to increase the accessibility to the Red List Threat data.

Materials and Methods

Access to the IUCN Red List was granted in February 2017. The Red List distributed a private key that enabled access to the data. Targeted amphibian species assessments were collected from the IUCN in February 2017 and February 2018. Utilizing the first method described above, querying directly from the IUCN Red List, the following search parameters

<table>
<thead>
<tr>
<th>code</th>
<th>title</th>
<th>timing</th>
<th>scope</th>
<th>severity</th>
<th>score</th>
<th>invasive</th>
</tr>
</thead>
<tbody>
<tr>
<td>5.3</td>
<td>Logging &amp; wood harvesting</td>
<td>Ongoing</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>5.3.5</td>
<td>Motivation</td>
<td>Ongoing</td>
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<td>NA</td>
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<tr>
<td></td>
<td>Unknown/Unrecorded</td>
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</table>
were chosen: Taxonomy = Amphibia, Location = South & Southeast Asia. The search was then saved, exported as a CSV file, and imported to R. Before the species names could be used by the developed code, genus and species must be combined into a new column. From here, the list of species was utilized by developed functions to produce an output of threats affecting amphibians in Southeast Asia. The taxon name was utilized to traverse the functions as opposed to the IDs because the IUCN suggests utilizing the taxon name when making API calls because the IDs are not immovable (Chamberlain 2017). The functions were created in R version 3.3.2 (R Core Team 2016) utilizing the output from the rredlist package (Chamberlain 2017). Data reshaping and configuring relied on plyr (Wickham et al. 2011), dyplr (Wickham et al. 2017) and sqldf (Grothendieck 2017).

Because the Red List API advises against too frequent or too many calls (IUCN), the sys.sleep function, or suspend execution for a time interval, is included in the Additional Functions at 2 seconds. For threat data and habitat data functions, however, this suspended execution is not included. Instead, species lists were divided into segments of one-hundred species or less and run through the developed functions. The outputs were then joined together to create a master data frame by using dyplr. If more than one-hundred species are run through each function, an error occurs.

Results

All scripted functions are located in the Appendix V: Scripted Code.

Threat Functions

1) Threat details (threat_details): Provides the threat code, title, timing, scope, severity, score, and invasive status of each species. This function employs the package rredlist (Chamberlain
to query the IUCN Red List through the `rredlist`'s function `rl_threats`. The function’s parameter is a vector of species names that are characters. `threat_details` traverses through the vector of species and accumulates the resulting data frame within a list. Once a data frame containing threat information for each species has been saved into a list, `dplyr` is used to reformat the list to a data frame. Lastly, within `threat_details`, third level threats were removed (Schulze et al. 2018). By selecting the species name column from the IUCN Red List output of Southeast Asian amphibians, the `threat_details` output is a data frame listing threat processes for each Southeast Asia amphibian. By changing the input of `threat_details`, this function can generate threat data for all taxa listed on the IUCN Red List.

```r
iucn_data <- read.csv("export-89505.csv", header = TRUE)
new_species <- data.frame(A = iucn_data$Genus, B = iucn_data$Species)
iucn_data$new_species <- paste(new_species$A, new_species$B, sep=" ")
threat_details_output <- threat_details(iucn_data$new_species)
```

2) Species name and threat code (`threat_code`): Takes the output from `threat_details` and returns a data frame with species name and related threat codes. This function utilizes the package `dplyr` (Wickham et al., 2017), specifically the `filter` function.

```r
codes <- threat_code(threat_details_output)
```

3) Remove third level threats (`no_third_level`): `no_third_level` is embedded into `threat_tables`, below, and creates an empty table where each column represents a different threat, and each row represents a different species. In addition, third level threats are removed (Schulze et al. 2018).
4) Populate threat tables (threat_tables): threat_tables takes the output from threat_code and creates a table of threats for each species.

\[
\text{final_threats} <- \text{threat_tables(codes)}
\]

**Additional Functions**

5) Species habitat data (sp_habitats): Provides the habitat code for the habitats associated with each species. sp_habitats is utilized within pop_habitat_tables and in accordance with habitat_table. sp_habitats builds off of the function rl_habitats from rredlist. The result of this function is a data frame of the original species list and associated habitat codes.

\[
\text{sp_habitat_output} <- \text{sp_habitats(iucn_data$new_species)}
\]

6) Empty habitat table (habitat_table): Creates an empty habitat table based on the length of the parameter.

   Embedded in pop_habitat_tables

7) Populate habitat table (pop_habitat_tables): Populates empty habitat tables generated from habitat_table with the information from sp_habitats. The result is a data frame where each row represents a species, and each column is equal to a different type of threat.

\[
\text{pop_habitat_tables(sp_habitat_output)}
\]

In addition to accessing habitat and threat data, functions were also written to build off of the rredlist package that allows for further querying of the IUCN Red List.

8) Species only (sp_only): Separates species from subspecies, rank, and subpopulations, returning only species.

\[
\text{all_species} <- \text{sp_only(iucn_data$new_species)}
\]
9) Species taxonomic class (sp_class): Traverses through a vector of species and separates only amphibians.

   `amphibians <- sp_class(all_species$new_species)`

10) Species taxonomic family (sp_family): Returns only species from a desired family.

   `only_plethodontidae <- sp_family(all_species$new_species, "Plethodontidae")`

11) Species threat count (sp_threat_count): Counts the number of threat processes affecting each species. Third level threats were filtered out (Schulze et al. 2018).

   `number_threats <- sp_threat_count(iucn_data$new_species)`

12) Species and family (sp_all_family): Returns a data frame with species and respective family. The difference between sp_all_family and sp_family is for a species list, sp_all_family will return a data frame with the same length as the parameter input where all families for every species is listed. sp_family, however, requires an additional parameter that specifies the family that will be returned.

   `sp_and_family <- sp_all_family(iucn_data$new_species)`

For all of the functions specified above, the IUCN Red List key requirement was embedded into each function. The IUCN Red List key was saved to the global environment under the name token. For the functions to be able to access the IUCN Red List data, the key must be saved in the global environment as token.

   `token <- IUCN Red List Key`

**Code Dependencies and Limitations**
This code requires sqldf, dplyr, and rredlist. As described above, because the IUCN Red List has a rate-limiting requirement, extracting the data can take several hours, depending on the original size of the species list.

**Discussion**

Overall, the development of functions are a step towards robust analyses of the co-occurring threatening processes that are listed on the Red List. By having a three-part scripted code to analyze the threat data, there are ways of filtering the multifaceted threat details to extract only those threat titles with high threat scores, for example. On the Red List web database, filtering by threat scores (or other threat details) is not an available search option. In addition, all of the functions except `sp_class` can be applied to different taxonomies on the Red List. In other words, so long as there is a vector with species names saved as characters, this code can provide threat details for every species on the Red List with respective threat data. Therefore, the applications of this code extend beyond amphibians and give researchers the ability to conduct further assessments of Red List data in their fields of expertise.

Besides data analyses performed in R, having a large table of co-occurring threats by species also broadens mapping abilities. While this concept is applied and described further in Section III: IUCN Red List Threat Data Analyses for Southeast Asian amphibians, it is possible to map species where there are multiple corresponding threats, and analyze the landscape, set conservation priorities, and evaluate Red List threat assessments.

**Future Directions**

Future directions include embedding the Red List’s threatening processes ranking into the table so that threats with different ranking processes can have different weight when performing
analyses. While previous iterations have made the code faster, future directions also include making the code shorter and more efficient.

Appendix II: Reclassifying IUCN Red List Categories

<table>
<thead>
<tr>
<th>Red List Status</th>
<th>Classification</th>
</tr>
</thead>
<tbody>
<tr>
<td>Least Concern</td>
<td>Not Threatened</td>
</tr>
<tr>
<td>Near Threatened</td>
<td>Not Threatened</td>
</tr>
<tr>
<td>Vulnerable</td>
<td>Threatened</td>
</tr>
<tr>
<td>Endangered</td>
<td>Threatened</td>
</tr>
<tr>
<td>Critically Endangered</td>
<td>Threatened</td>
</tr>
</tbody>
</table>

Appendix III: Hierarchical clustering of Red List Threat Processes
### Appendix IV: Threat Data

<table>
<thead>
<tr>
<th>Title</th>
<th>Threat Code</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Residential &amp; commercial development</strong></td>
<td></td>
</tr>
<tr>
<td>Housing &amp; urban areas</td>
<td>1.1</td>
</tr>
<tr>
<td>Commercial &amp; industrial areas</td>
<td>1.2</td>
</tr>
<tr>
<td>Tourism &amp; recreation</td>
<td>1.3</td>
</tr>
<tr>
<td><strong>Agriculture &amp; Aquaculture</strong></td>
<td></td>
</tr>
<tr>
<td>Annual &amp; perennial non-timber crops</td>
<td>2.1</td>
</tr>
<tr>
<td>Wood &amp; pulp plantations</td>
<td>2.2</td>
</tr>
<tr>
<td>Livestock farming &amp; ranching</td>
<td>2.3</td>
</tr>
<tr>
<td>Marine &amp; freshwater aquaculture</td>
<td>2.4</td>
</tr>
<tr>
<td><strong>Energy production &amp; mining</strong></td>
<td></td>
</tr>
<tr>
<td>Oil &amp; gas drilling</td>
<td>3.1</td>
</tr>
<tr>
<td>Mining &amp; quarrying</td>
<td>3.2</td>
</tr>
<tr>
<td>Renewable energy</td>
<td>3.3</td>
</tr>
<tr>
<td><strong>Transportation &amp; service corridors</strong></td>
<td></td>
</tr>
<tr>
<td>Roads &amp; railroads</td>
<td>4.1</td>
</tr>
<tr>
<td>Utility &amp; service lines</td>
<td>4.2</td>
</tr>
<tr>
<td>Shipping lanes</td>
<td>4.3</td>
</tr>
<tr>
<td>Flight paths</td>
<td>4.4</td>
</tr>
<tr>
<td><strong>Biological resource use</strong></td>
<td></td>
</tr>
<tr>
<td>Hunting &amp; trapping terrestrial animals</td>
<td>5.1</td>
</tr>
<tr>
<td>Gathering terrestrial plants</td>
<td>5.2</td>
</tr>
<tr>
<td>Logging &amp; wood harvesting</td>
<td>5.3</td>
</tr>
<tr>
<td>Fishing &amp; harvesting aquatic resources</td>
<td>5.4</td>
</tr>
<tr>
<td><strong>Human intrusions &amp; disturbance</strong></td>
<td></td>
</tr>
<tr>
<td>Recreational activities</td>
<td>6.1</td>
</tr>
<tr>
<td>War, civil unrest &amp; military exercises</td>
<td>6.2</td>
</tr>
<tr>
<td>Work &amp; other activities</td>
<td>6.3</td>
</tr>
<tr>
<td><strong>Natural system modifications</strong></td>
<td></td>
</tr>
<tr>
<td>Fire &amp; fire suppression</td>
<td>7.1</td>
</tr>
<tr>
<td>Dams &amp; water management/use</td>
<td>7.2</td>
</tr>
<tr>
<td>Other ecosystem modifications</td>
<td>7.3</td>
</tr>
<tr>
<td><strong>Invasive and other problematic species, genes &amp; diseases</strong></td>
<td></td>
</tr>
</tbody>
</table>
Invasive non-native/alien species/diseases 8.1
Problematic native species/diseases 8.2
Introduced genetic material 8.3
Problematic species/diseases of unknown origin 8.4
Viral/prion-induced diseases 8.5
Diseases of unknown cause 8.6

Pollution
Domestic & urban waste water 9.1
Industrial & military effluents 9.2
Agricultural & forestry effluents 9.3
Garbage & solid waste 9.4
Air-born pollutants 9.5
Excess energy 9.6

Geological Events
Volcanoes 10.1
Earthquakes/tsunamis 10.2
Avalanches/landslides 10.3

Climate change & severe weather
Habitat shifting & alteration 11.1
Droughts 11.2
Temperature extremes 11.3
Storms & flooding 11.4
Other impacts 11.5

Other options
Other threat 12.1

Appendix IV: Red List Threat title and Threat Codes

Appendix V: Scripted Code
threat_details <- function(species_list){
  #Specifications:
  #Parameter: Iucndata$species
  #Note: IUCN export contains genus and species in separate columns.
  #These must be combined into one column before running this script.
  datalist <- list()
i <- 1
  for (species in species_list){
    threats <- rl_threats(species, key = token)
    df1 <- threats$result
    df1$species_name <- species
datalist[[i]] <- df1
    i <- i + 1
}
#Removes third level threats:
thirdlevel <- c("2.1.1", "2.1.2", "2.1.3", "2.1.4", "2.2.1", "2.2.2", "2.2.3",
   "2.3.1", "2.3.2", "2.3.3", "2.3.4", "2.4.1", "2.4.2", "2.4.3",
   "5.1.1", "5.1.2", "5.1.3", "5.1.4", "5.2.1", "5.2.2", "5.2.3",
   "5.2.4", "5.3.1", "5.3.2", "5.3.3", "5.3.4", "5.3.5", "5.4.1",
   "5.4.2", "5.4.3", "5.4.4", "5.4.5", "5.4.6", "7.1.1", "7.1.2",
   "7.1.3", "7.2.1", "7.2.2", "7.2.3", "7.2.4", "7.2.5", "7.2.6",
   "7.2.7", "7.2.8", "7.2.9", "7.2.10", "7.2.11", "8.1.1", "8.1.2",
   "8.2.1", "8.2.2", "8.4.1", "8.4.2", "8.5.1", "8.5.2", "9.1.1",
   "9.1.2", "9.1.3", "9.2.1", "9.2.2", "9.2.3", "9.3.1", "9.3.2",
   "9.3.3", "9.3.4", "9.5.1", "9.5.2", "9.5.3", "9.5.4", "9.6.1",
   "9.6.2", "9.6.3", "9.6.4")
library(dplyr)
big_data <- dplyr::bind_rows(datalist)
big_data <- as.data.frame(big_data)
final <- filter(big_data, !(code %in% thirdlevel))
reordered <-
final[,c("code","title","timing","scope","severity","score","invasive","species_name")]
return(reordered)

\textbf{threat\_code} <- function(threat\_details\_output){
  #Parameter: threat\_details\_output
  # Output: data is a dataframe with the species\_list
  # as one column and the threat\_code as the other.
  species\_list <- names(table(threat\_details\_output$species\_name))
  threat\_code <- vector(mode = "character", length = length(species\_list))
  i <- 1
  library(dplyr)
  for (species in species\_list){
    subset\_species <- filter(threat\_details\_output, threat\_details\_output$species\_name == species)
    code <- names(table(subset\_species$code))
    threat\_code[i] <- paste(code, collapse = " ")
    i <- 1 + i
  }
  threat\_df <- data.frame(species\_list, threat\_code)
  return(threat\_df)
}

\textbf{no\_third\_level}<- function(species\_list){
R1.1 <- rep(c(0), each = length(species\_list))
R1.2 <- rep(c(0), each = length(species\_list))
R1.3 <- rep(c(0), each = length(species_list))

#Agriculture and Aquaculture
A2.1 <- rep(c(0), each = length(species_list))
A2.2 <- rep(c(0), each = length(species_list))
A2.3 <- rep(c(0), each = length(species_list))
A2.4 <- rep(c(0), each = length(species_list))

#Energy Production and mining
E3.1 <- rep(c(0), each = length(species_list))
E3.2 <- rep(c(0), each = length(species_list))
E3.3 <- rep(c(0), each = length(species_list))

#Transportation and service corridors
T4.1 <- rep(c(0), each = length(species_list))
T4.2 <- rep(c(0), each = length(species_list))
T4.3 <- rep(c(0), each = length(species_list))
T4.4 <- rep(c(0), each = length(species_list))

#Biological Resource use
B5.1 <- rep(c(0), each = length(species_list))
B5.2 <- rep(c(0), each = length(species_list))
B5.3 <- rep(c(0), each = length(species_list))
B5.4 <- rep(c(0), each = length(species_list))

#Human intrusions and disturbance
H6.1 <- rep(c(0), each = length(species_list))
H6.2 <- rep(c(0), each = length(species_list))
H6.3 <- rep(c(0), each = length(species_list))

#Natural system modifications
N7.1 <- rep(c(0), each = length(species_list))
N7.2 <- rep(c(0), each = length(species_list))
N7.3 <- rep(c(0), each = length(species_list))

#Invasive and other problematic species, genes and disease
I8.1 <- rep(c(0), each = length(species_list))
I8.2 <- rep(c(0), each = length(species_list))
I8.3 <- rep(c(0), each = length(species_list))
I8.4 <- rep(c(0), each = length(species_list))
I8.5 <- rep(c(0), each = length(species_list))
I8.6 <- rep(c(0), each = length(species_list))

#Pollution
P9.1 <- rep(c(0), each = length(species_list))
P9.2 <- rep(c(0), each = length(species_list))
P9.3 <- rep(c(0), each = length(species_list))
P9.4 <- rep(c(0), each = length(species_list))
P9.5 <- rep(c(0), each = length(species_list))
P9.6 <- rep(c(0), each = length(species_list))

# Geological Events
G10.1 <- rep(c(0), each = length(species_list))
G10.2 <- rep(c(0), each = length(species_list))
G10.3 <- rep(c(0), each = length(species_list))

# Climate Change and severe weather
C11.1 <- rep(c(0), each = length(species_list))
C11.2 <- rep(c(0), each = length(species_list))
C11.3 <- rep(c(0), each = length(species_list))
C11.4 <- rep(c(0), each = length(species_list))
C11.5 <- rep(c(0), each = length(species_list))

# Other options
O12.1 <- rep(c(0), each = length(species_list))

threat_df <- data.frame(species_list, R1.1, R1.2, R1.3, A2.1, A2.2, A2.3, A2.4, E3.1, E3.2,
                         E3.3, T4.1, T4.2, T4.3, T4.4, B5.1, B5.2, B5.3, B5.4,
                         C11.3, C11.4, C11.5)
return(threat_df)
}

threat_tables <- function(data){
  # Parameter: thread_code output
  # Output: Dataframe with binary values for each threat (0,1)
  threatdf <- no_third_level(data$species_list)
  i <- 1
  for (strings in data$threat_code){
    many_strings <- strsplit(strings, split = " ")
    for (elem in many_strings){
      for(code in elem){
        #### Residential
        if (code == "1.1"){
          threatdf$R1.1[i] <- 1
        } else if (code == "1.2"){
          threatdf$R1.2[i] <- 1
        } else if (code == "1.3"){
          threatdf$R1.3[i] <- 1
        }
      }
    }
  }
  return(threatdf)
}
threatdf$R1.3[i] <- 1

### Agriculture
} else if (code == "2.1"){
    threatdf$A2.1[i] <- 1
} else if (code == "2.1.1"){
    threatdf$A2.1.1[i] <- 1
} else if (code == "2.1.2"){
    threatdf$A2.1.2[i] <- 1
} else if (code == "2.1.3"){
    threatdf$A2.1.3[i] <- 1
} else if (code == "2.1.4"){
    threatdf$A2.1.4[i] <- 1
} else if (code == "2.2"){
    threatdf$A2.2[i] <- 1
} else if (code == "2.2.1"){
    threatdf$A2.2.1[i] <- 1
} else if (code == "2.2.2"){
    threatdf$A2.2.2[i] <- 1
} else if (code == "2.2.3"){
    threatdf$A2.2.3[i] <- 1
} else if (code == "2.3"){
    threatdf$A2.3[i] <- 1
} else if (code == "2.3.1"){
    threatdf$A2.3.1[i] <- 1
} else if (code == "2.3.2"){
    threatdf$A2.3.2[i] <- 1
} else if (code == "2.3.3"){
    threatdf$A2.3.3[i] <- 1
} else if (code == "2.3.4"){
    threatdf$A2.3.4[i] <- 1
} else if (code == "2.4"){
    threatdf$A2.4[i] <- 1
} else if (code == "2.4.1"){
    threatdf$A2.4.1[i] <- 1
} else if (code == "2.4.2"){
    threatdf$A2.4.2[i] <- 1
} else if (code == "2.4.3"){
    threatdf$A2.4.3[i] <- 1

### Energy
} else if (code == "3.1"){
    threatdf$E3.1[i] <- 1

} else if (code == "3.2"){
    threatdf$E3.2[i] <- 1
} else if (code == "3.3"){
    threatdf$E3.3[i] <- 1

#### Transportation and service corridors
} else if (code == "4.1"){
    threatdf$T4.1[i] <- 1
} else if (code == "4.2"){
    threatdf$T4.2[i] <- 1
} else if (code == "4.3"){
    threatdf$T4.3[i] <- 1
} else if (code == "4.4"){
    threatdf$T4.4[i] <- 1

#### Biological resource use
} else if (code == "5.1"){
    threatdf$B5.1[i] <- 1
} else if (code == "5.1.1"){
    threatdf$B5.1.1[i] <- 1
} else if (code == "5.1.2"){
    threatdf$B5.1.2[i] <- 1
} else if (code == "5.1.3"){
    threatdf$B5.1.3[i] <- 1
} else if (code == "5.1.4"){
    threatdf$B5.1.4[i] <- 1
} else if (code == "5.2"){
    threatdf$B5.2[i] <- 1
} else if (code == "5.2.1"){
    threatdf$B5.2.1[i] <- 1
} else if (code == "5.2.2"){
    threatdf$B5.2.2[i] <- 1
} else if (code == "5.2.3"){
    threatdf$B5.2.3[i] <- 1
} else if (code == "5.2.4"){
    threatdf$B5.2.4[i] <- 1
} else if (code == "5.3"){
    threatdf$B5.3[i] <- 1
} else if (code == "5.3.1"){
    threatdf$B5.3.1[i] <- 1
} else if (code == "5.3.2"){
    threatdf$B5.3.2[i] <- 1
} else if (code == "5.3.3"){
threatdf$B5.3.3[i] <- 1
} else if (code == "5.3.4"){
    threatdf$B5.3.4[i] <- 1
} else if (code == "5.3.5"){
    threatdf$B5.3.5[i] <- 1
} else if (code == "5.4"){
    threatdf$B5.4[i] <- 1
} else if (code == "5.4.1"){
    threatdf$B5.4.1[i] <- 1
} else if (code == "5.4.2"){
    threatdf$B5.4.2[i] <- 1
} else if (code == "5.4.3"){
    threatdf$B5.4.3[i] <- 1
} else if (code == "5.4.4"){
    threatdf$B5.4.4[i] <- 1
} else if (code == "5.4.5"){
    threatdf$B5.4.5[i] <- 1
} else if (code == "5.4.6"){
    threatdf$B5.4.6[i] <- 1

### Human intrusions
} else if (code == "6.1"){
    threatdf$H6.1[i] <- 1
} else if (code == "6.2"){
    threatdf$H6.2[i] <- 1
} else if (code == "6.3"){
    threatdf$H6.3[i] <- 1

### Natural system modifications
} else if (code == "7.1"){
    threatdf$N7.1[i] <- 1
} else if (code == "7.1.1"){
    threatdf$N7.1.1[i] <- 1
} else if (code == "7.1.2"){
    threatdf$N7.1.2[i] <- 1
} else if (code == "7.1.3"){
    threatdf$N7.1.3[i] <- 1
} else if (code == "7.2"){
    threatdf$N7.2[i] <- 1
} else if (code == "7.2.1"){
    threatdf$N7.2.1[i] <- 1
} else if (code == "7.2.2"){
threatdf$N7.2.2[i] <- 1
} else if (code == "7.2.3"){
    threatdf$N7.2.3[i] <- 1
} else if (code == "7.2.4"){
    threatdf$N7.2.4[i] <- 1
} else if (code == "7.2.5"){
    threatdf$N7.2.5[i] <- 1
} else if (code == "7.2.6"){
    threatdf$N7.2.6[i] <- 1
} else if (code == "7.2.7"){
    threatdf$N7.2.7[i] <- 1
} else if (code == "7.2.8"){
    threatdf$N7.2.8[i] <- 1
} else if (code == "7.2.9"){
    threatdf$N7.2.9[i] <- 1
} else if (code == "7.2.10"){
    threatdf$N7.2.10[i] <- 1
} else if (code == "7.2.11"){
    threatdf$N7.2.11[i] <- 1
}

} else if (code == "7.3"){
    threatdf$N7.3[i] <- 1

#### Invasive species/disease/introduced genes
} else if (code == "8.1"){
    threatdf$I8.1[i] <- 1
} else if (code == "8.1.1"){
    threatdf$I8.1.1[i] <- 1
} else if (code == "8.1.2"){
    threatdf$I8.1.2[i] <- 1
}

} else if (code == "8.2"){
    threatdf$I8.2[i] <- 1
} else if (code == "8.2.1"){
    threatdf$I8.2.1[i] <- 1
} else if (code == "8.2.2"){
    threatdf$I8.2.2[i] <- 1
}

} else if (code == "8.3"){
    threatdf$I8.3[i] <- 1
}

} else if (code == "8.4"){
    threatdf$I8.4[i] <- 1
```r
} else if (code == "8.4.1"){
  threatdf$I8.4.1[i] <- 1
} else if (code == "8.4.2"){
  threatdf$I8.4.2[i] <- 1
}

} else if (code == "8.5"){
  threatdf$I8.5[i] <- 1
} else if (code == "8.5.1"){
  threatdf$I8.5.1[i] <- 1
} else if (code == "8.5.2"){
  threatdf$I8.5.2[i] <- 1
} else if (code == "8.6"){
  threatdf$I8.6[i] <- 1

#### Pollution
} else if (code == "9.1"){
  threatdf$P9.1[i] <- 1
} else if (code == "9.1.1"){
  threatdf$P9.1.1[i] <- 1
} else if (code == "9.1.2"){
  threatdf$P9.1.2[i] <- 1
} else if (code == "9.1.3"){
  threatdf$P9.1.3[i] <- 1
}

} else if (code == "9.2"){
  threatdf$P9.2[i] <- 1
} else if (code == "9.2.1"){
  threatdf$P9.2.1[i] <- 1
} else if (code == "9.2.2"){
  threatdf$P9.2.2[i] <- 1
} else if (code == "9.2.3"){
  threatdf$P9.2.3[i] <- 1
}

} else if (code == "9.3"){
  threatdf$P9.3[i] <- 1
} else if (code == "9.3.1"){
  threatdf$P9.3.1[i] <- 1
} else if (code == "9.3.2"){
  threatdf$P9.3.2[i] <- 1
} else if (code == "9.3.3"){
  threatdf$P9.3.3[i] <- 1
} else if (code == "9.3.4"){
```
threatdf$P9.3.4[i] <- 1

} else if (code == "9.4"){
threatdf$P9.4[i] <- 1

} else if (code == "9.5"){
threatdf$P9.5[i] <- 1
} else if (code == "9.5.1"){
threatdf$P9.5.1[i] <- 1
} else if (code == "9.5.2"){
threatdf$P9.5.2[i] <- 1
} else if (code == "9.5.3"){
threatdf$P9.5.3[i] <- 1
} else if (code == "9.5.4"){
threatdf$P9.5.4[i] <- 1

} else if (code == "9.6"){
threatdf$P9.6[i] <- 1
} else if (code == "9.6.1"){
threatdf$P9.6.1[i] <- 1
} else if (code == "9.6.2"){
threatdf$P9.6.2[i] <- 1
} else if (code == "9.6.3"){
threatdf$P9.6.3[i] <- 1
} else if (code == "9.6.4"){
threatdf$P9.6.4[i] <- 1

#### Geological Events
} else if (code == "10.1"){
threatdf$G10.1[i] <- 1
} else if (code == "10.2"){
threatdf$G10.2[i] <- 1
} else if (code == "10.3"){
threatdf$G10.3[i] <- 1

#### Climate Change
} else if (code == "11.1"){
threatdf$C11.1[i] <- 1
} else if (code == "11.2"){
threatdf$C11.2[i] <- 1
} else if (code == "11.3"){
threatdf$C11.3[i] <- 1
} else if (code == "11.4"){
threatdf$C11.4[i] <- 1
} else if (code == "11.5"){
    threatdf$C11.5[i] <- 1
}

i <- 1 + i

return(threatdf)


sp_habitats <- function(species_list){
    #Description: Takes a vector of species names (that are characters) and traverses through the vector. For each species, the habitat(s) are identified. The corresponding habitat code is then collected.
    #Parameter: species_list.
    habitat_code <- vector(length = length(species_list), mode = "character")
    i <- 1
    for (species in species_list){
        habitat <- rl_habitats(species, key = token)
        code <- habitat$result$code
        habitat_code[i] <- paste(code, collapse = " ")
        i <- i + 1
    }
    final_results <- data.frame(species_list, habitat_code)
    return(final_results)
}

habitat_table <- function(species_list){
    #Parameters: species_list
    #Forest
    F1.1 <- rep(c(0), each = length(species_list))
    F1.2 <- rep(c(0), each = length(species_list))
    F1.3 <- rep(c(0), each = length(species_list))
    F1.4 <- rep(c(0), each = length(species_list))
    F1.5 <- rep(c(0), each = length(species_list))
    F1.6 <- rep(c(0), each = length(species_list))
    F1.7 <- rep(c(0), each = length(species_list))
    F1.8 <- rep(c(0), each = length(species_list))
    #Savanna
    Sa2.1 <- rep(c(0), each = length(species_list))
    Sa2.2 <- rep(c(0), each = length(species_list))
    #Shrubland
    Sh3.1 <- rep(c(0), each = length(species_list))
Sh3.2 <- rep(c(0), each = length(species_list))
Sh3.3 <- rep(c(0), each = length(species_list))
Sh3.4 <- rep(c(0), each = length(species_list))
Sh3.5 <- rep(c(0), each = length(species_list))
Sh3.6 <- rep(c(0), each = length(species_list))
Sh3.7 <- rep(c(0), each = length(species_list))
Sh3.8 <- rep(c(0), each = length(species_list))

# Grassland
G4.1 <- rep(c(0), each = length(species_list))
G4.2 <- rep(c(0), each = length(species_list))
G4.3 <- rep(c(0), each = length(species_list))
G4.4 <- rep(c(0), each = length(species_list))
G4.5 <- rep(c(0), each = length(species_list))
G4.6 <- rep(c(0), each = length(species_list))
G4.7 <- rep(c(0), each = length(species_list))

# Wetlands
W5.1 <- rep(c(0), each = length(species_list))
W5.2 <- rep(c(0), each = length(species_list))
W5.3 <- rep(c(0), each = length(species_list))
W5.4 <- rep(c(0), each = length(species_list))
W5.5 <- rep(c(0), each = length(species_list))
W5.6 <- rep(c(0), each = length(species_list))
W5.7 <- rep(c(0), each = length(species_list))
W5.8 <- rep(c(0), each = length(species_list))
W5.9 <- rep(c(0), each = length(species_list))
W5.10 <- rep(c(0), each = length(species_list))
W5.11 <- rep(c(0), each = length(species_list))
W5.12 <- rep(c(0), each = length(species_list))
W5.13 <- rep(c(0), each = length(species_list))
W5.14 <- rep(c(0), each = length(species_list))
W5.15 <- rep(c(0), each = length(species_list))
W5.16 <- rep(c(0), each = length(species_list))
W5.17 <- rep(c(0), each = length(species_list))
W5.18 <- rep(c(0), each = length(species_list))

# Rocky
R6 <- rep(c(0), each = length(species_list))

# Caves
C7.1 <- rep(c(0), each = length(species_list))
C7.2 <- rep(c(0), each = length(species_list))

# Desert
D8.1 <- rep(c(0), each = length(species_list))
D8.2 <- rep(c(0), each = length(species_list))
D8.3 <- rep(c(0), each = length(species_list))
MN9.1 <- rep(c(0), each = length(species_list))
MN9.2 <- rep(c(0), each = length(species_list))
MN9.3 <- rep(c(0), each = length(species_list))
MN9.4 <- rep(c(0), each = length(species_list))
MN9.5 <- rep(c(0), each = length(species_list))
MN9.6 <- rep(c(0), each = length(species_list))
MN9.7 <- rep(c(0), each = length(species_list))
MN9.8 <- rep(c(0), each = length(species_list))
MN9.9 <- rep(c(0), each = length(species_list))
MN9.10 <- rep(c(0), each = length(species_list))

#Marine Oceanic
MO10.1 <- rep(c(0), each = length(species_list))
MO10.2 <- rep(c(0), each = length(species_list))
MO10.3 <- rep(c(0), each = length(species_list))
MO10.4 <- rep(c(0), each = length(species_list))

#Marine Benthic
M11.1 <- rep(c(0), each = length(species_list))
M11.2 <- rep(c(0), each = length(species_list))
M11.3 <- rep(c(0), each = length(species_list))
M11.4 <- rep(c(0), each = length(species_list))
M11.5 <- rep(c(0), each = length(species_list))
M11.6 <- rep(c(0), each = length(species_list))

#Marine Intertidal
MI12.1 <- rep(c(0), each = length(species_list))
MI12.2 <- rep(c(0), each = length(species_list))
MI12.3 <- rep(c(0), each = length(species_list))
MI12.4 <- rep(c(0), each = length(species_list))
MI12.5 <- rep(c(0), each = length(species_list))
MI12.6 <- rep(c(0), each = length(species_list))
MI12.7 <- rep(c(0), each = length(species_list))

#Marine Coastal
MC13.1 <- rep(c(0), each = length(species_list))
MC13.2 <- rep(c(0), each = length(species_list))
MC13.3 <- rep(c(0), each = length(species_list))
MC13.4 <- rep(c(0), each = length(species_list))
MC13.5 <- rep(c(0), each = length(species_list))

#Artificial/Terrestrial
AT14.1 <- rep(c(0), each = length(species_list))
AT14.2 <- rep(c(0), each = length(species_list))
AT14.3 <- rep(c(0), each = length(species_list))
AT14.4 <- rep(c(0), each = length(species_list))
AT14.5 <- rep(c(0), each = length(species_list))
AT14.6 <- rep(c(0), each = length(species_list))

#Artificial/Aquatic
AA15.1 <- rep(c(0), each = length(species_list))
AA15.2 <- rep(c(0), each = length(species_list))
AA15.3 <- rep(c(0), each = length(species_list))
AA15.4 <- rep(c(0), each = length(species_list))
AA15.5 <- rep(c(0), each = length(species_list))
AA15.6 <- rep(c(0), each = length(species_list))
AA15.7 <- rep(c(0), each = length(species_list))
AA15.8 <- rep(c(0), each = length(species_list))
AA15.9 <- rep(c(0), each = length(species_list))
AA15.10 <- rep(c(0), each = length(species_list))
AA15.11 <- rep(c(0), each = length(species_list))
AA15.12 <- rep(c(0), each = length(species_list))
AA15.13 <- rep(c(0), each = length(species_list))

###Introduced Vegetation
Veg16 <- rep(c(0), each = length(species_list))

###Other
O17 <- rep(c(0), each = length(species_list))

###Unknown
U18 <- rep(c(0), each = length(species_list))

habitat_df <- data.frame(species_list, F1.1, F1.2, F1.3, F1.4, F1.5, F1.6, F1.7, F1.8,
                          Sa2.1, Sa2.2, Sh3.1, Sh3.2, Sh3.3, Sh3.4, Sh3.5, Sh3.6,
                          Sh3.7, Sh3.8, G4.1, G4.2, G4.3, G4.4, G4.5, G4.6,
                          G4.7, W5.1, W5.2, W5.3, W5.4, W5.5, W5.6, W5.7,
                          W5.8, W5.9, W5.10, W5.11, W5.12, W5.13, W5.14, W5.15,
                          W5.16, W5.17, W5.18, R6, C7.1, C7.2, D8.1, D8.2, D8.3,
                          MN9.9, MN9.10, MO10.1, MO10.2, MO10.3, MO10.4, M11.1,
                          M11.2, M11.3, M11.4, M11.5, M11.6, MI12.1, MI12.2, MI12.3,
                          AA15.1, AA15.2, AA15.3, AA15.4, AA15.5, AA15.6, AA15.7,
                          AA15.8, AA15.9, AA15.10, AA15.11, AA15.12, AA15.13,
                          Veg16, O17, U18)

return(habitat_df)
}

pop_habitat_tables <- function(data){
  ### data is a dataframe with the species_list as one column and the habitat_code as the other
  ### works directly with sp_habitats and habitat_tables
  habitatdf <- habitat_table(data$species_list)
i <- 1
  for (strings in data$habitat_code){
    # Your code here
  }
}


many_strings <- strsplit(strings, split = " ")
for (elem in many_strings){
for(code in elem){
    #### Forest
    if (code == "1.1"){
        habitatdf$F1.1[i] <- 1
    } else if (code == "1.2"){
        habitatdf$F1.2[i] <- 1
    } else if (code == "1.3"){
        habitatdf$F1.3[i] <- 1
    } else if (code == "1.4"){
        habitatdf$F1.4[i] <- 1
    } else if (code == "1.5"){
        habitatdf$F1.5[i] <- 1
    } else if (code == "1.6"){
        habitatdf$F1.6[i] <- 1
    } else if (code == "1.7"){
        habitatdf$F1.7[i] <- 1
    } else if (code == "1.8"){
        habitatdf$F1.8[i] <- 1
    } else if (code == "5.1"){
        habitatdf$W5.1[i] <- 1
    } else if (code == "2.1"){
        habitatdf$Sa2.1[i] <- 1
    } else if (code == "2.2"){
        habitatdf$Sa2.2[i] <- 1
    } else if (code == "3.1"){
        habitatdf$Sh3.1[i] <- 1
    } else if (code == "3.2"){
        habitatdf$Sh3.2[i] <- 1
    } else if (code == "3.3"){
        habitatdf$Sh3.3[i] <- 1
    } else if (code == "3.4"){
        habitatdf$Sh3.4[i] <- 1
    } else if (code == "3.5"){
        habitatdf$Sh3.5[i] <- 1
    } else if (code == "3.6"){
        habitatdf$Sh3.6[i] <- 1
    } else if (code == "3.7"){
        habitatdf$Sh3.7[i] <- 1
    } else if (code == "3.8"){
        habitatdf$Sh3.8[i] <- 1
}
#### Grassland

```r
else if (code == "4.1") {
  habitatdf$G4.1[i] <- 1
```

```r
else if (code == "4.2") {
  habitatdf$G4.2[i] <- 1
```

```r
else if (code == "4.3") {
  habitatdf$G4.3[i] <- 1
```

```r
else if (code == "4.4") {
  habitatdf$G4.4[i] <- 1
```

```r
else if (code == "4.5") {
  habitatdf$G4.5[i] <- 1
```

```r
else if (code == "4.6") {
  habitatdf$G4.6[i] <- 1
```

```r
else if (code == "4.7") {
  habitatdf$G4.7[i] <- 1
```

#### Wetland

```r
else if (code == "5.1") {
  habitatdf$W5.1[i] <- 1
```

```r
else if (code == "5.2") {
  habitatdf$W5.2[i] <- 1
```

```r
else if (code == "5.3") {
  habitatdf$W5.3[i] <- 1
```

```r
else if (code == "5.4") {
  habitatdf$W5.4[i] <- 1
```

```r
else if (code == "5.5") {
  habitatdf$W5.5[i] <- 1
```

```r
else if (code == "5.6") {
  habitatdf$W5.6[i] <- 1
```

```r
else if (code == "5.7") {
  habitatdf$W5.7[i] <- 1
```

```r
else if (code == "5.8") {
  habitatdf$W5.8[i] <- 1
```

```r
else if (code == "5.9") {
  habitatdf$W5.9[i] <- 1
```

```r
else if (code == "5.10") {
  habitatdf$W5.10[i] <- 1
```

```r
else if (code == "5.11") {
  habitatdf$W5.11[i] <- 1
```

```r
else if (code == "5.12") {
  habitatdf$W5.12[i] <- 1
```

```r
else if (code == "5.13") {
  habitatdf$W5.13[i] <- 1
```

```r
else if (code == "5.14") {
  habitatdf$W5.14[i] <- 1
```
} else if (code == "5.15"){
    habitatdf$W5.15[i] <- 1
    #Rocky
} else if (code == "6"){
    habitatdf$R6[i] <- 1
    #### Caves
} else if (code == "7.1"){
    habitatdf$C7.1[i] <- 1
} else if (code == "7.2"){
    habitatdf$C7.2[i] <- 1
    #### Desert
} else if (code == "8.1"){
    habitatdf$D8.1[i] <- 1
} else if (code == "8.2"){
    habitatdf$D8.2[i] <- 1
} else if (code == "8.3"){
    habitatdf$D8.3[i] <- 1
    ### Marine Neritic
} else if (code == "9.1"){
    habitatdf$MN9.1[i] <- 1
} else if (code == "9.2"){
    habitatdf$MN9.2[i] <- 1
} else if (code == "9.3"){
    habitatdf$MN9.3[i] <- 1
} else if (code == "9.4"){
    habitatdf$MN9.4[i] <- 1
} else if (code == "9.5"){
    habitatdf$MN9.5[i] <- 1
} else if (code == "9.6"){
    habitatdf$MN9.6[i] <- 1
} else if (code == "9.7"){
    habitatdf$MN9.7[i] <- 1
} else if (code == "9.8.1" | code == "9.8.2" | code == "9.8.3"| code == "9.8.4" | code == "9.8.5"){
    habitatdf$MN9.8[i] <- 1
} else if (code == "9.9"){
    habitatdf$MN9.9[i] <- 1
} else if (code == "9.10"){
    habitatdf$MN9.10[i] <- 1
    #### Marine Oceanic
} else if (code == "10.1"){
    habitatdf$MO10.1[i] <- 1
} else if (code == "10.2"){
    habitatdf$MO10.2[i] <- 1
} else if (code == "10.3"){
    habitatdf$MO10.3[i] <- 1
} else if (code == "10.4"){
    habitatdf$MO10.4[i] <- 1

#### Marine Deep Benthic
} else if (code == "11.1" | code == "11.1.2" | code == "11.1.2"){
    habitatdf$M11.1[i] <- 1
} else if (code == "11.2"){
    habitatdf$M11.2[i] <- 1
} else if (code == "11.3"){
    habitatdf$M11.3[i] <- 1
} else if (code == "11.4"){
    habitatdf$M11.4[i] <- 1
} else if (code == "11.5"){
    habitatdf$M11.5[i] <- 1
} else if (code == "11.6"){
    habitatdf$M11.6[i] <- 1

#### Marine Intertidal
} else if (code == "12.1"){
    habitatdf$MI12.1[i] <- 1
} else if (code == "12.2"){
    habitatdf$MI12.2[i] <- 1
} else if (code == "12.3"){
    habitatdf$MI12.3[i] <- 1
} else if (code == "12.4"){
    habitatdf$MI12.4[i] <- 1
} else if (code == "12.5"){
    habitatdf$MI12.5[i] <- 1
} else if (code == "12.6"){
    habitatdf$MI12.6[i] <- 1
} else if (code == "12.7"){
    habitatdf$MI12.7[i] <- 1

#### Marine Coastal
} else if (code == "13.1"){
    habitatdf$MC13.1[i] <- 1
} else if (code == "13.2"){
    habitatdf$MC13.2[i] <- 1
} else if (code == "13.3"){
    habitatdf$MC13.3[i] <- 1
} else if (code == "13.4"){
    habitatdf$MC13.4[i] <- 1
} else if (code == "13.5"){
    habitatdf$MC13.5[i] <- 1

#### Artificial/Terrestrial
} else if (code == "14.1"){
    habitatdf$AT14.1[i] <- 1
} else if (code == "14.2"){
    habitatdf$AT14.2[i] <- 1
} else if (code == "14.3"){
    habitatdf$AT14.3[i] <- 1
} else if (code == "14.4"){
    habitatdf$AT14.4[i] <- 1
} else if (code == "14.5"){
    habitatdf$AT14.5[i] <- 1
} else if (code == "14.6"){
    habitatdf$AT14.6[i] <- 1

#### Introduced Vegetation
} else if (code == "16"){
    habitatdf$Veg16[i] <- 1

#### Other
} else if (code == "17"){
    habitatdf$O17[i] <- 1

#### Unknown
} else if (code == "18"){
    habitatdf$U18[i] <- 1

} }
}
i <- 1 + i
}
return(habitat)

sp_only <- function(species_list)
{
    #parameter name is confusing - takes a list of everything,
    #returns species. filters out subpopulations, rank, etc.
    df<- as.data.frame(species_list)
    df[is.na(df)] <- 0
    only species <- subset(df, (df$result.subspecies == 0) &
                            (df$result.rank == 0) & (df$result.subpopulation == 0))
    only species <- only_species$result.scientific_name
    return(only species)
}

sp_class <- function (species_list)
{
    #Des.: Traverses through a list, and pulls out Class = AMPHIBIA
#Input: species_list is any list of species w/ and w/o amphibians
#Output: Vector of Amphibians
amphibian_list <- vector(length = length(species_list),
    mode = "character")
failed <- vector(length = length(species_list), mode = "character")
i <- 1
for (species in species_list){
general_info <- rl_search(species, key = token)
tax <- general_info$result$class
Sys.sleep(2)
if (general_info[1] == "0"){
    failed[i] <- species
}else if (tax == "AMPHIBIA"){
    amphibian_list[i] <- species
}
i <- i+1
}
amph <- amphibian_list[amphibian_list != ""]
return(amph)

sp_family <- function (species_list, desired.family){
    #Des.: Traverses through a list, and pulls out selected taxa
    #Input: species_list is any list of species w/ and w/o amphibians
    #Input: desired.family = name of family you'd like to pull species names
    #Output: Vector of amphibian species of desired family
    amphibian_list <- vector(length = length(species_list),
        mode = "character")
i <- 1
for (species in species_list){
general_info <- rl_search(species, key = token)
Sys.sleep(2)
family <- general_info$result$family
if (family == desired.family){
    amphibian_list[i] <- species
}
i <- i+1
}
return(amphibian_list[amphibian_list != ""])
}

sp_threat_count <- function(threat_details_output){

}
### data is a dataframe with the species_list
### as one column and the threat_code as the
### other aims to work directly with sp_threats
### and threat_tables

```r
species_list <- names(table(threat_details_output$species_name))
threat_count <- vector(mode = "character", length = length(species_list))
i <- 1
library(dplyr)
for (species in species_list){
  subset_species <- filter(threat_details_output, threat_details_output$species_name == species)
  count <- length(subset_species$code)
  threat_count[i] <- count
  i <- 1 + i
}
threatdf <- data.frame(species_list, threat_count)
return(threatdf)
}
```

```r
sp_all_family <- function(species_list){
  #returns a dataframe with species name and family name
  family_list <- vector(length = length(species_list), mode = "character")
i <- 1
  for (species in species_list){
    general_info <- rl_search(species, key = token)
    family_list[i] <- general_info$result$family
    i <- i + 1
  }
  spfamily <- data.frame(species_list, family_list)
  return(spfamily)
}
```