Mapping Amphibian Distribution at National Scale, Using Species Environmental Models

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by

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Abstract

Amphibians are a key taxon of hydrobiont and, among the vertebrates, represent the link between the aquatic and terrestrial environment. As a result of environment pollution, many populations of amphibians have declined markedly throughout the world; some species have become extinct. China is a country which has abundant resource of amphibian; two thirds are Chinese endemic species. The species environmental models have been seldom introduced in amphibian researches before. This object is to test the species environmental models for amphibian at national scale in China and get the distribution maps for chosen species. This research used inductive and deductive approach to define the species-environment relationship. Four different methods were used to compare. They are BIOCLIM, DOMAIN, GARP, and MAXENT. The models ran by corresponding software (DIVA-GIS, GARP, MAXENT). Bioclimatic variables and other factors were used for modelling. Four methods give the prediction map with high accuracy. And DOMAIN gives the best one in most cases, followed by MAXENT and then BIOCLIM, GARP was the last. This approved that the species environmental models is a good approach for amphibian study.

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1. Introduction

1.1. Background

Amphibians are a key taxon of hydrobiont and, among the vertebrates, represent the link between the aquatic and terrestrial environment. Because of its specific biological and ecological character, amphibians are one of the key biological indicators(Xu Shixia 2004). The condition of amphibians indicates the environment degradation. As a result of environment pollution, many populations of amphibians have declined markedly throughout the world; some species have become extinct (Zhou, Xie et al. 2004).

China is located in the east of Asia, which has complex environment and wide variety of vegetation. It is a country which has abundant resource of amphibian; two thirds are Chinese endemic species (Fei, Ye et al. 1999; Fei, Ye et al. 2005). The situation of amphibians in China is serious, about 34 percent of the total 325 species(Zhou Zhou 2004) are in danger. The research on amphibian biodiversity conservation in China is inadequate. Most of the research is focused on the regional scale, and it is still mostly dealing with the quantification and evaluation of species checklist (Dong Wang 2004; Tao, Liu et al. 2004), which could not predict the trend of the species at national scale(Zhou, Xie et al. 2004).

Introduction of advanced approaches are in the urgent needs to support the research on amphibians in China. Modeling the amphibian distribution using species environment models is one of them.

Setting up a scientific and complete information system is another important issue for the conservation of amphibians (Zhou, Xie et al. 2004). Such tool could be used to integrate the information and to share it for future research. Although a species information system has already been set up (China species information service CSIS)(Zhou, Xie et al. 2004), the information collected is not complete.

The concept of modeling the environment with GIS and remote sensing has been widely explained in a number of scientific papers(e.g. Busby 2002; Leeuw J. 2002). A wide range of statistical techniques have been applied for predictive habitat distribution, such as multiple regressions, neural networks, and Bayesian models. Although statistics is critical in predictive models, the biological and ecological characteristics of the species will influence the quality and the accuracy of the models (Corsi F., Leeuw J. et al. 2000; Guisan and Zimmermann 2000; Austin 2002; Seoane, Carrascal et al. 2005). And limitation caused by species-specific characteristic can not be overcome in certain case(Seoane, Carrascal et al. 2005). In general, prediction models are limited by the ecological knowledge as a limiting factor. And different statistic models should be chosen based on the relationship between the species and the environment(Guisan and Zimmermann 2000; Austin 2002).

1.2 Objectives

1.2.1 General Objective

The objectives derived from the current status of amphibians in China:
• Testing the use of species-environment relationship models to map the distribution of a representative group of amphibian species at national scale.

1.2.2 Specific Objectives

• Find the most suitable species-environment techniques to map amphibian distribution using the published point localities.
• Provide a broad map of the species distribution of china using published localities data.
• Assess the accuracy of the distribution models.

1.3 Research questions

• Which environment variable(s) is/are functional to predict the distribution of each of the selected amphibian species?
• Which are the species environment requirements and how can they be described in terms of the available environmental variables?
• What is the distribution of the amphibian compared to decades ago?
• What is the accuracy of the species distribution model?
• Which is the best statistic model to predict the amphibian distribution using the available data?

2. Methods

2.1. Study Area

Based on the research objective and the data arability, the whole country was chosen as the study area. China(Peoples Republic of China) has abundant species of amphibians (3 order, 11 family, 59 genus (9 subgenus), 325 species (18 subspecies))(Fei, Ye et al. 2005). China is a country with a vast territory. The main species richness is in the south of QinLing Area, few in northeast, northwest, Huabei, Inner Mongolia and Xinjiang area. The picture in the left is the terrene of China.

2.2. Species

For ecological and economical aspect as well as for the data availability and the habitat requirement, the species whose distribution had been modelled were chosen from the three orders of the China's valuable and rare amphibian fauna (Ye, Fei et al. 1993). Although the species were expected to be chosen from each three order for the study, there is only one species of GYMNOPHIONA in China. This species was not chosen this time by reasons. Based on the data availability and the distribution, five species were chosen for the analysis from the rest two orders (Table 1). Those species could be check out from world amphibian websites and china species information system. Figure 2.1 gave the pictures of chosen species.
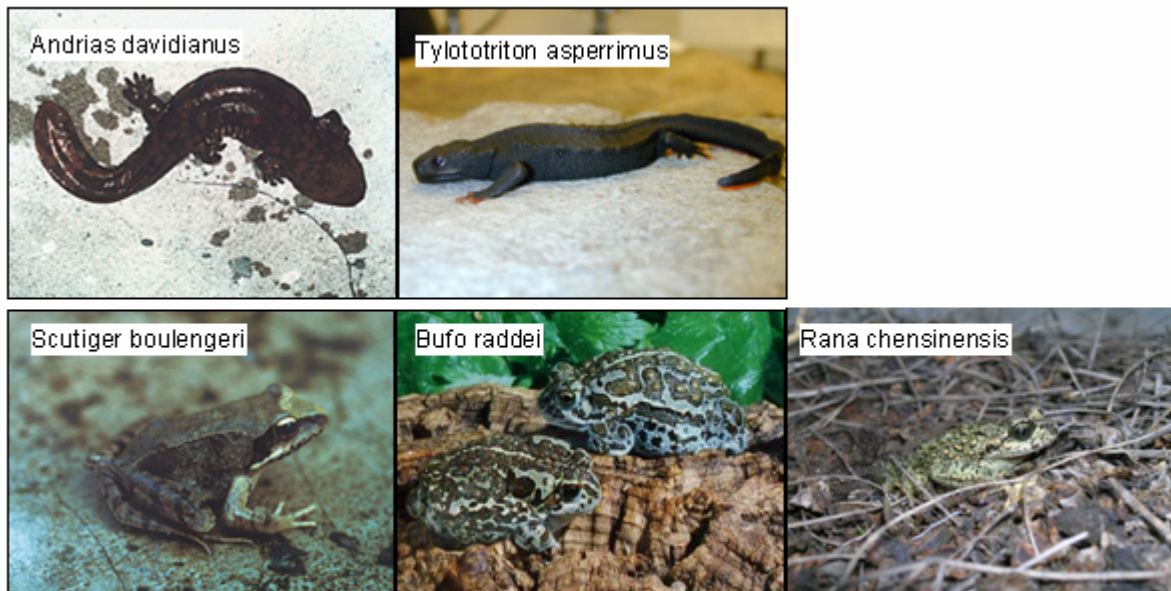
Figure 2.1 Chosen species pictures

2.3. Datasets

2.3.1. Observation data

The observation data was obtained from China species information service (CSIS). It is a website provides the species distribution data and species information online. All the basic data is public and free for the science research. The national observation data was available from the website. For more adequate and accurate dataset I required a full file (excel format) from the organization. All the species distribution data was given in high quality location data. Those datasets was gained by the works of the local workstation. And they were only present data.

Table 1 Studied species, with number of presence records

Latin Name	Latin Order	Latin Family	English Name	Samples
Andrias davidianus	URODELA	Cryptobranchidae	Chinese Giant Salamander	183
Tylototriton asperrimus	URODELA	Salamandridae	Black Knobby Newt	42
Scutiger boulengeri	ANURA	Megophryidae	Xizang Alpine Toad	69
Bufo raddei	ANURA	Bufonidae	Piebald Toad	132
Rana chensinensis	ANURA	Ranidae	Chinese Brown Frog	197

2.3.2. Environmental data

The environmental datasets were from public free global datasets (DIVA-GIS website). Those were high resolution global datasets (Hijmans J. R., et al., 2005). The datasets were list in Table 2. Although there were datasets, 19 variables were derived from for better prediction (Nix, 1986)(see Table 3).

Table 2 The environmental datasets

Datasets		Resolution	Source
Land cover	13 land cover type	30 seconds	U.S. Geological Survey, Global land cover characteristics data base. Legend: USGS Land Use/Land Cover System
Population	Persons per Km^2	2.5 minutes	CIESIN, Center for International Earth Science Information Network, Colombia University
Altitude	(elevation above sea level) (m)	30 seconds	GTOPO30 (U.S. Geological Survey)
Climate Data	average monthly mean temperature (°C * 10)	30 seconds	Worldclim, version 1.4
	average monthly minimum temperature (°C * 10)		
	average monthly maximum temperature (°C * 10)		
	average monthly precipitation (mm)		

Table 3 Bioclimatic variables derived from climate data

Code	Bioclimatic Variables

Code	Bioclimatic Variables
BIO1	Annual Mean Temperature
BIO2	Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIO3	Isothermality (P2/P7) (* 100)
BIO4	Temperature Seasonality (standard deviation *100)
BIO5	Max Temperature of Warmest Month
BIO6	Min Temperature of Coldest Month
BIO7	Temperature Annual Range (P5-P6)
BIO8	Mean Temperature of Wettest Quarter
BIO9	Mean Temperature of Driest Quarter
BIO10	Mean Temperature of Warmest Quarter
BIO11	Mean Temperature of Coldest Quarter
BIO12	Annual Precipitation
BIO13	Precipitation of Wettest Month
BIO14	Precipitation of Driest Month
BIO15	Precipitation Seasonality (Coefficient of Variation)
BIO16	Precipitation of Wettest Quarter
BIO17	Precipitation of Driest Quarter
BIO18	Precipitation of Warmest Quarter
BIO19	Precipitation of Coldest Quarter

2.3.3. Expert review

Data on the environment requirements of the species was get from the expert in China (Institute of Biology of the Chinese Academia of Science in Chengdu & Institute of Zoology of the Chinese academy of science) as well as from literature and website which tells about the characteristics of the species. The choice of the environmental variables was also considered based on these information.

2.4. Method for modeling

As for the species, the available data was only presence data. As the absence data is not generally available as the accuracy of it could not be sure. It could not tell that a species is not present only because it has not been observed. Maybe the species is hard to be found, or the living place is difficult for people get there, e.g. it hides in the stone gap in the stream. On contrary, a species has been observed could be said it lives there. So the species environmental methods were chosen from the approach could do the analysis without absence data. For another reason is that, the absence data is not as confident as presence data. We can not tell the species does not occur in one place only as they were not observed by people.
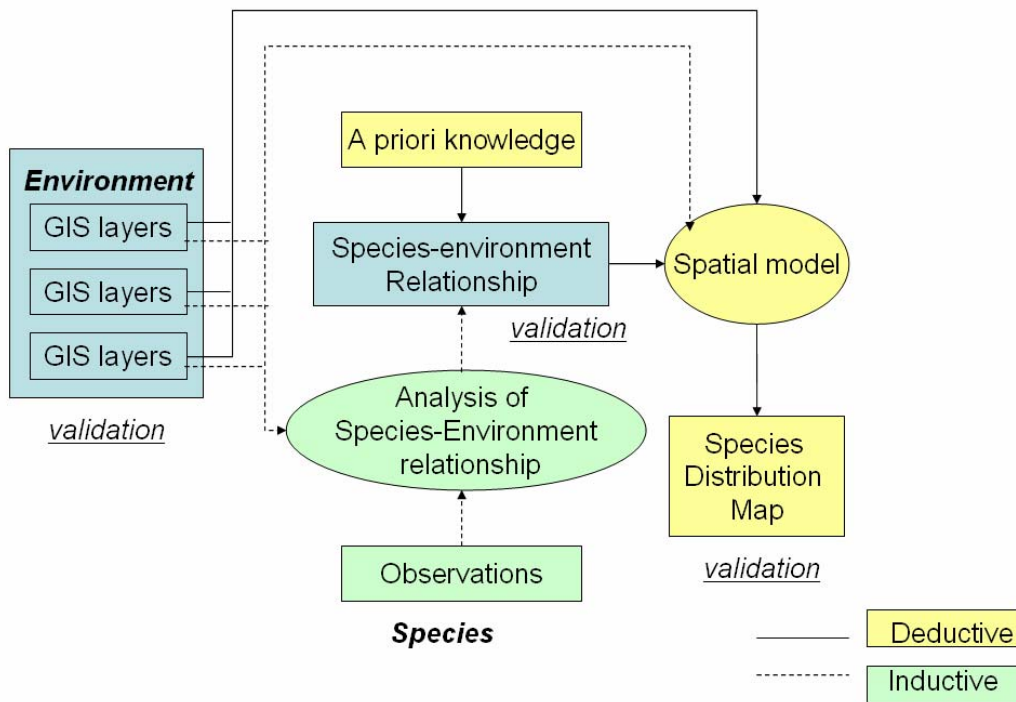
Figure 2.2 Idea flow diagram of building a species distribution model (Corsi F., Leeuw J. et al. 2000)

Both deductive and inductive approach was used to define the species-environment relationship. Deductive approach makes use of the known species' ecological requirement to define the suitable habitat. On contrary, inductive approach derive the ecological requirements from the species observation data(Corsi F., Leeuw J. et al. 2000). Figure 2.2 is the idea flow diagram of building a species distribution model. I assumed that the environmental layer had already been validated by the data provider. For the purpose of this research, the validation of the Species-Environment Relationship and the validation of the Distribution Map were combined into the measure of the performance of the final map. The methods that could predict species distribution without absence data was chosen (see below).

• Environmental envelopes (BIOCLIM model) (using software DIVA-GIS)
• Environmental envelopes (DOMAIN model) (using software DIVA-GIS)
• Logistic regression models (Logit) (using software GARP)
• Maximum-entropy (MAXENT) (using software MAXENT)

2.4.1. BIOCLIM method

The first method was BIOCLIM, an approach to predict the potential distribution for species. This method used environmental envelop method to model the potential distribution of species (Busby, J.R. 1991; 1993). This method predicts the distribution bases on the climate variables. Based on the present species distribution data, a range of the variables which is suitable for the species living was derived. The place where the climatic variable falls in the range is considered suitable for the species (see Figure 2.3).

DIVA-GIS software of version 5.2.0.2 was used to do the prediction (available from DIVA-GIS Website).
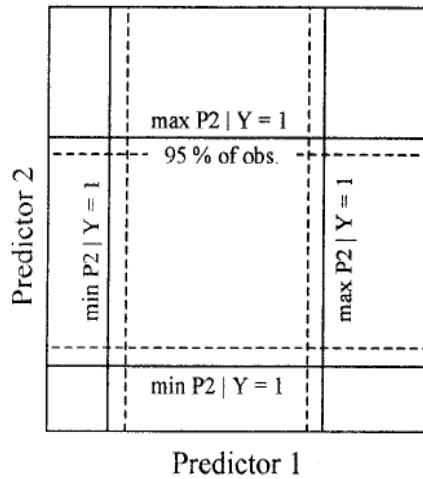
Figure 2.3 BIOCLIM Environmental envelop (Guisan and Zimmermann, 2000)

2.4.2. DOMAIN method

Carpenter G. et al. (1993) pointed out that BIOCLIM was not suitable for the species live in certain ecological and biological environment. They gave a simple example. A species live in hot-wet and cool-dry environment, the place with cool-wet environment could also be considered suitable for the species. Obviously, this classification does not well predict the distribution. Then DOMAIN method which overcomes the disadvantage of BIOCLIM was come out by Carpenter G. et al. (1993).
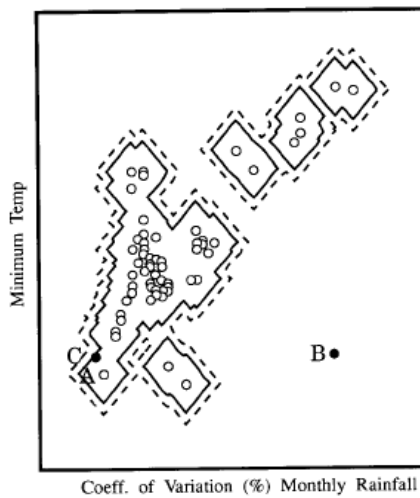
Figure 2.4 DOMAIN environmental envelope

The DOMAIN model uses "point-to-point similarity metric to assign a classification value to candidate site based on the proximity in environmental space of the most similar record site" (Carpenter G. et al., 1993) (Fig.). This method can do the prediction without absent data as well as BIOCLIM.

DIVA-GIS software of version 5.2.0.2 was used to do the prediction (available from DIVA-GIS Website).

2.4.3. GARP method

GARP is short for Genetic Algorithm for Rule Set Production and was originally conceived as a repository of ruled-based modelling approaches. The GARP software too integrates a number of rule-based approaches to modelling; for this study I chose logit rules to perform the models as it it the method that is complements the methods available in other software tools used.

Logit rules are an adaptation of logistic regression models to rules. "A logistic regression is a form of regression equation where the output is transformed into a probability". (Karen Payne and D. R. B. Stockwell, 2006)

GARP software of version 1.1.6.0 was used to do the prediction (available from GARP Website).

2.4.4. MAXENT method

MAXENT is short for maximum-entropy technique. This approach was proposed by Phillips S.J, et al. on a conference in 2004. This method is to model the probability distribution of the species from the species environmental variables. The maximum entropy distribution (maxent distribution) was considered the same as the maximum likelihood Gibbs distribution (Phillips S.J, et al., 2004; Phillips S.J, et al., 2006).

MAXENT software of version 2.1(February 2006) was used to do the prediction (available from MAXENT Website).

3. Results

3.1. Species Distribution Map

The predicted distribution maps were shown in group by species. Difference environmental variable were chosen for each species base on the ecological and biological characteristics (see Table 4). BIOCLIM and DOMAIN method operated the model only considered the bioclimatic variables. GARP and MAXENT considered land cover, population and altitude variables as well as the chosen bioclimatic variables to predicted the distribution map by GARP and MAXENT.

Table 4 Variables for prediction

Species	Method	Variables for Prediction
A. davidianus	BIOCLIM	bc7LR, bc9LR, bc11LR, bc14LR, bc15LR
	DOMAIN	bc7, bc9, bc11, bc12, bc14, bc15
	GARP	bc7, bc9, bc11, bc12, bc14, bc15, Alt, cov, pop
	MAXENT	worldclim_e30s(19 variables), Alt, cov, pop
T. asperrimus	BIOCLIM	bc5LR, bc7LR, bc8LR, bc14LR, bc15LR
	DOMAIN	bc5, bc7, bc8, bc14, bc15
	GARP	bc5, bc7, bc8, bc14, bc15, Alt, cov, pop
	MAXENT	worldclim_e30s(19 variables), Alt, lc, pop
S. boulengeri	BIOCLIM	bc1LR, bc5LR, bc9LR, bc12L, bc15LR, bc19LR
	DOMAIN	bc1, bc5, bc9, bc12, bc15, bc19
	GARP	bc1, bc5, bc9, bc12, bc15, bc19, Alt, cov, pop
	MAXENT	worldclim_e30s(19 variables), Alt, cov, pop
B. raddei	BIOCLIM	bc1LR, bc5LR, bc6LR, bc8LR, bc9LR, bc10LR, bc11LR, bc14LR
	DOMAIN	bc1, bc5, bc6, bc8, bc9, bc10, bc11, bc14
	GARP	bc1, bc5, bc6, bc8, bc9, bc10, bc11, bc14, Alt, cov, pop
	MAXENT	worldclim_e30s(19 variables), Alt, cov, pop
R. chensinensis	BIOCLIM	bc7, bc12, bc13, bc16
	DOMAIN	bc7LR, bc12LR, bc13LR, bc16LR
	GARP	bc7, bc12, bc13, bc16, Alt, cov, pop
	MAXENT	worldclim_e30s(19 variables), Alt, cov, pop

The environmental suitability for the species was ranked in five classes. The places not suitable for the species were displayed in white. Areas with various degree of environmental suitability for the species were showed from light green to dark green. The light green means lower suitability while darker indicates place with higher suitability. The classes were low, medium, high, very high and excellent.

The classification method was the same for all five species to allow for comparison. Base on the characteristic of each method, the class for the species was ranked as below. As the GARP only gives binary result, the zero means not suitable and one indicates suitable environments.

Table 5 Classification for each method

Legend	BIOCLIM	DOMAIN	GARP	MAXENT
Not suitable	0	<95	0	0
Low	0-2.5	95		0-12.5
Medium	2.5-5	96		12.5-50
high	5-10	97	1	25-50
Very high	10-20	98		50-75
excellent	Over 20	99,100		75-100

3.1.1. Andrias davidianus

Andrias davidianus is endemic to China. It is distributed in southwest and southeast of China. The number of individuals of this species has been decreased sharply. The rate of decrease was over 80% in the last three generation (Zhao, E., 1998). The distribution area has been reduced due to habitat destruction and degradation. *Andrias davidianus* was listed as the Critically Endangered (CR) (Wang, S. and Xie Y., 2004).

BIOCLIM
The vast area in southwest and southeast of China is suitable for the species. However, the area with higher suitability locates in the middle of the wide area. For BIOCLIM, Guizhou, Sichuan, Chongqing, Hubei, Shaanxi, Heinan, Anhui and Jiangsu are very suitable for *A. davidianus* by using bioclimatic environment variables. And Guizhou, Sichuan, Chongqing, Hubei are the excellent area for *A. davidianus*. Although there IS blankness from the main suitable area, the east of Shandong might be very suitable for the species. And there is a margin belt along the coast line in the south of mainland.

DOMAIN
The least suitable areas for the species are similar compared to the result of the BIOCLIM model; they are located in the southwest and southeast of China. But the place with higher suitability is a bit different. For DOMAIN, one of the most suitable places is located in main area of Guizhou and Chongqing. Other places are in Sichuan, Lanzhou, Shaanxi, Shanxi and Henan. There are relatively small high suitable areas for *A. davidianus* in Anhui, Zhejiang, Jiangxi, Hunan, Guangdong and Guangxi etc. Noticeably, Beijing and Qinghai are also figured as suitable place the where there should not suitable for *A. davidianus*. This was considered as the input data error.

GARP
GARP method gives the widest prediction area compared to other methods. This method only gives the binary result. Almost the entire southwest and southeast province are considered as the suitable area. Further, the prediction area includes entire Hainan and three fourths of Taiwan province which are islands which separated from the mainland, and in which no *A. davidianus* has been observed.
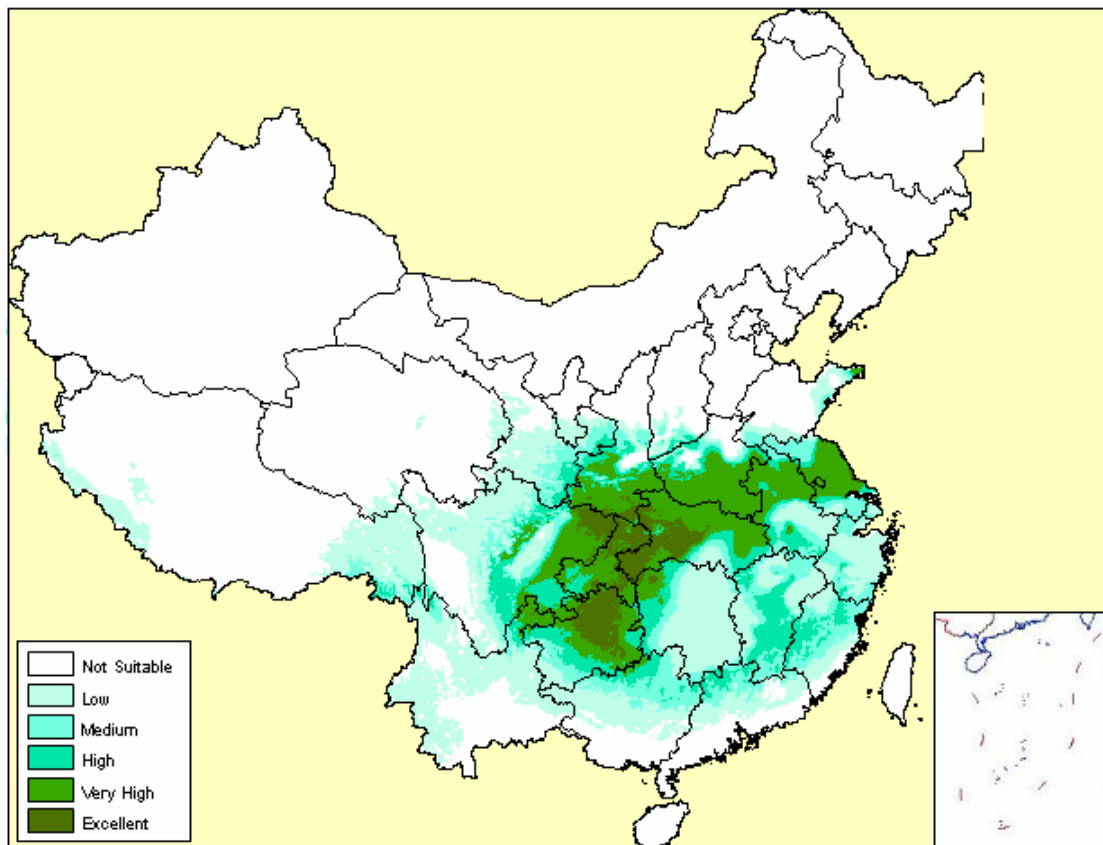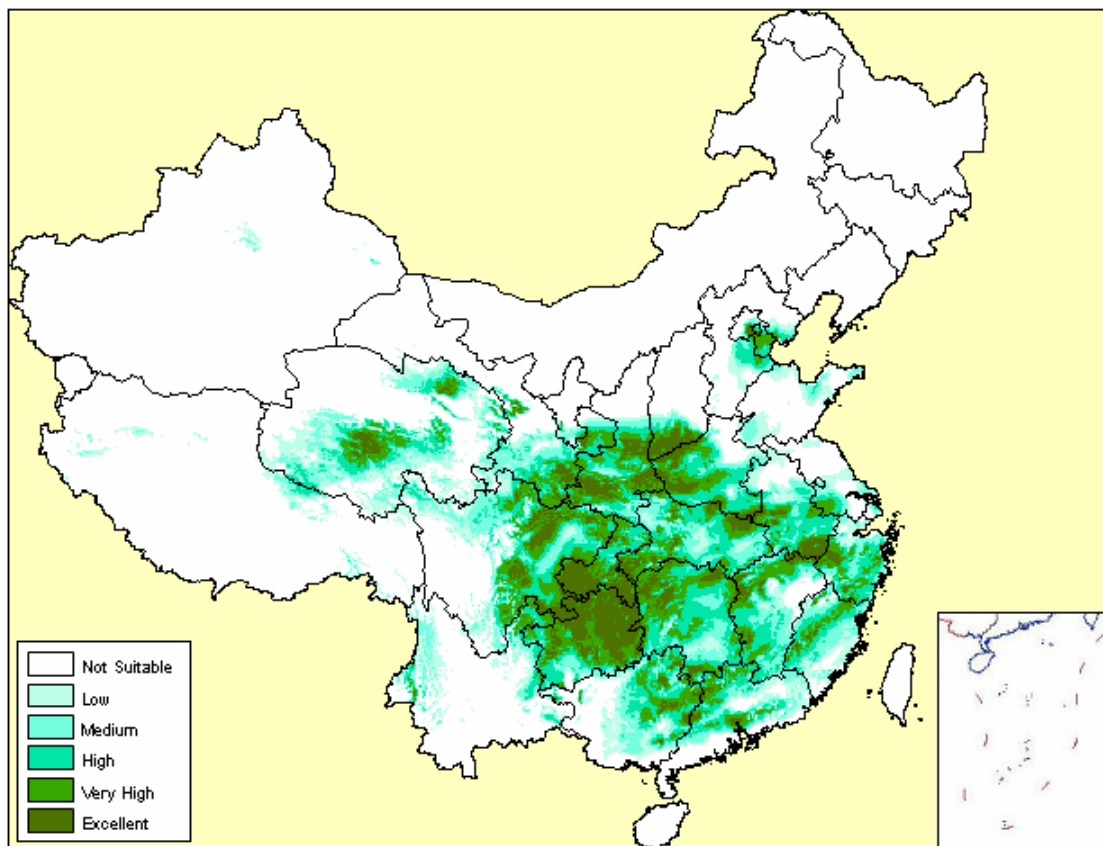
Figure 3.1 a BIOCLIM result for *A. davidianus.*
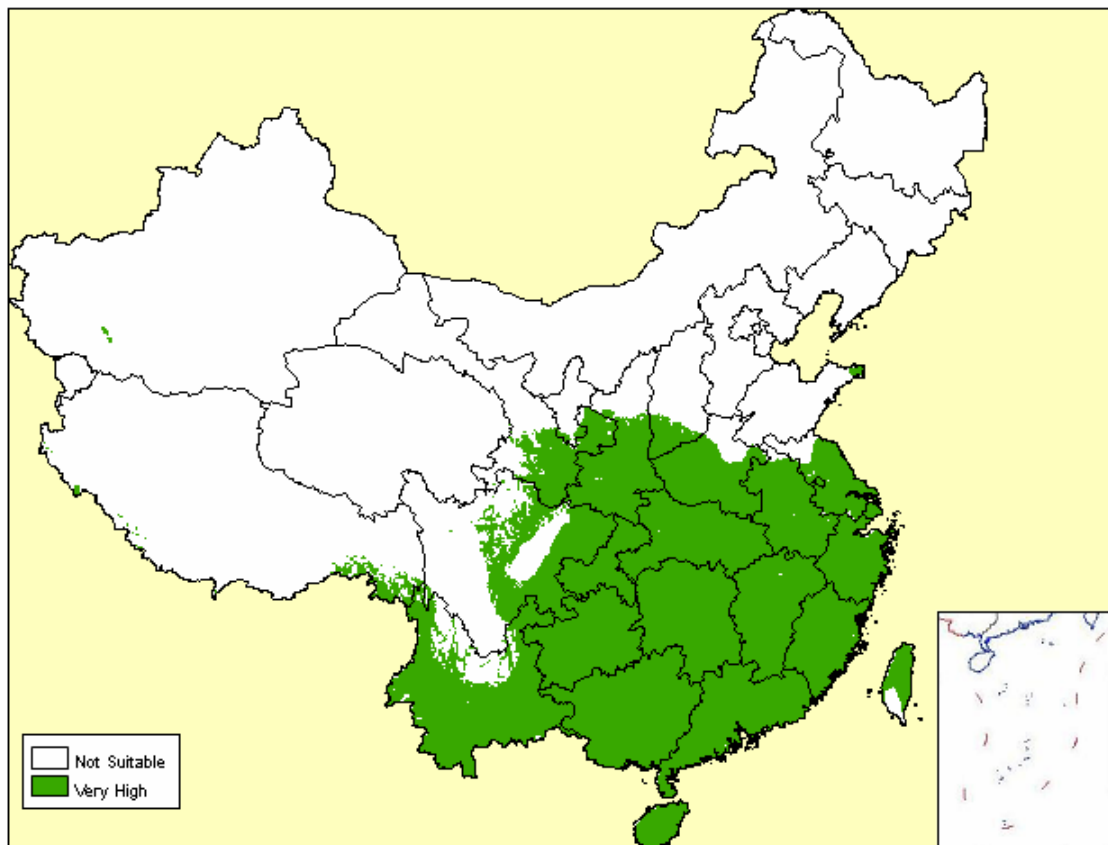

Figure 3.1 b DOMAIN result for *A. davidianus.*

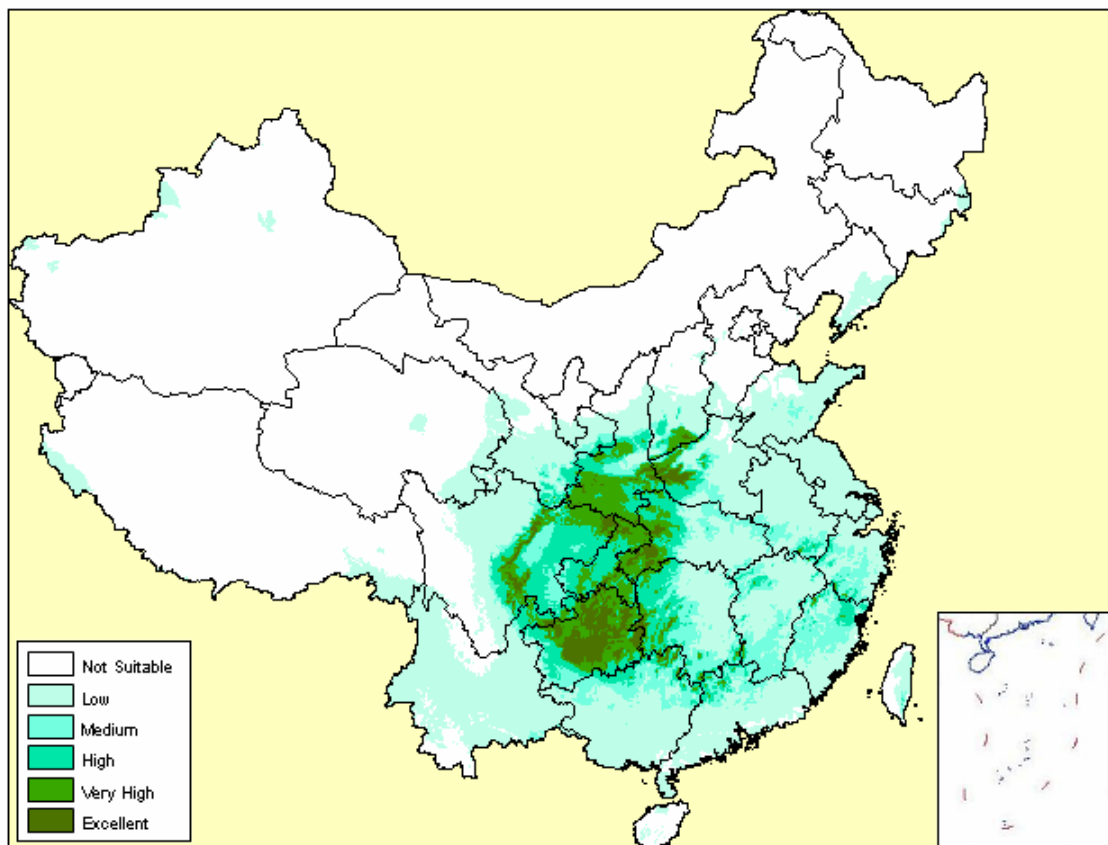Figure 3.1 c GARP result for *A. davidianus.*

Figure 3.1 d MAXENT result for *A. davidianus.*

MAXENT

The course prediction area is the same as the first three methods. However, the place with high suitability is relatively limited. The excellent suitable area given by MAXENT is located in the middle of China, mainly in the centre part of Guizhou. The place with very high suitability was in Guizhou, Chongqing, east Hubei, east Henan and south Shaanxi. The other provinces appear to be less suitable. Parts of Taiwan and Hainan are with low suitability for *A. davidianus* as well as the most province of south China.

3.1.2. Tylototriton asperrimus

Tylototriton asperrimus is also endemic to China, its known distribution is in Guangxi, Guangdong, Guizhou, Hunan, Anhui provinces (Zhao, E., 1998). Its category is listed as Near Threatened (NT), close measure up to Vulnerable (VU) (Wang, S. and Xie Y., 2004). The reason is that the distribution area is only 20,000km2, the fragmentation of habitat is high, there is a sharp decline of the area and the quality of the habitats, and the species over captured (Zhao, E., 1998).

BIOCLIM

The suitable areas for *T. asperrimus* are in the South of China. The major excellent area for *T. asperrimus* is in Guizhou, and almost the whole province is classified as excellent. Chongqing, part of Sichuan, Hainan, Guangdong, Fujian, Hubei, Hunan and Yunnan provinces have high suitability for *T. asperrimus*. Parts of island Taiwan is also considered very suitable for the species.

DOMAIN

The suitable areas for *T. asperrimus* is very small compared to other species. In particular the excellent area for the species is very small. The province and district with highest suitability and the vastest area for the species is Guizhou, followed by Guizhou and Hainan. Parts of Hunan, Jiangxi and Guangdong are also very suitable for *T. asperrimus* with medium suitable area. From the results map, we can see the fragmentation of this species is very serious. The results compares very well with the situation as described in (Zhao, E., 1998).

GARP

This method gives the largest prediction map for *T. asperrimus*. The suitable area for the species is quite vast, which do not show the actual known distribution. And it is difficult for further detailed study. The majority of the south China is suitable for the species.

MAXENT

The same as GARP, MAXENT gives similar wide predicted areas for *T. asperrimus*. However, the place with medium and high suitability is much smaller. The excellent area is still Guizhou and Hainan. The high suitable province and district which are partially good for the species are Chongqing, Fujian and Hubei. This prediction map also shows the habitat fragmentation although not as bad as evidenced by DOMAIN.
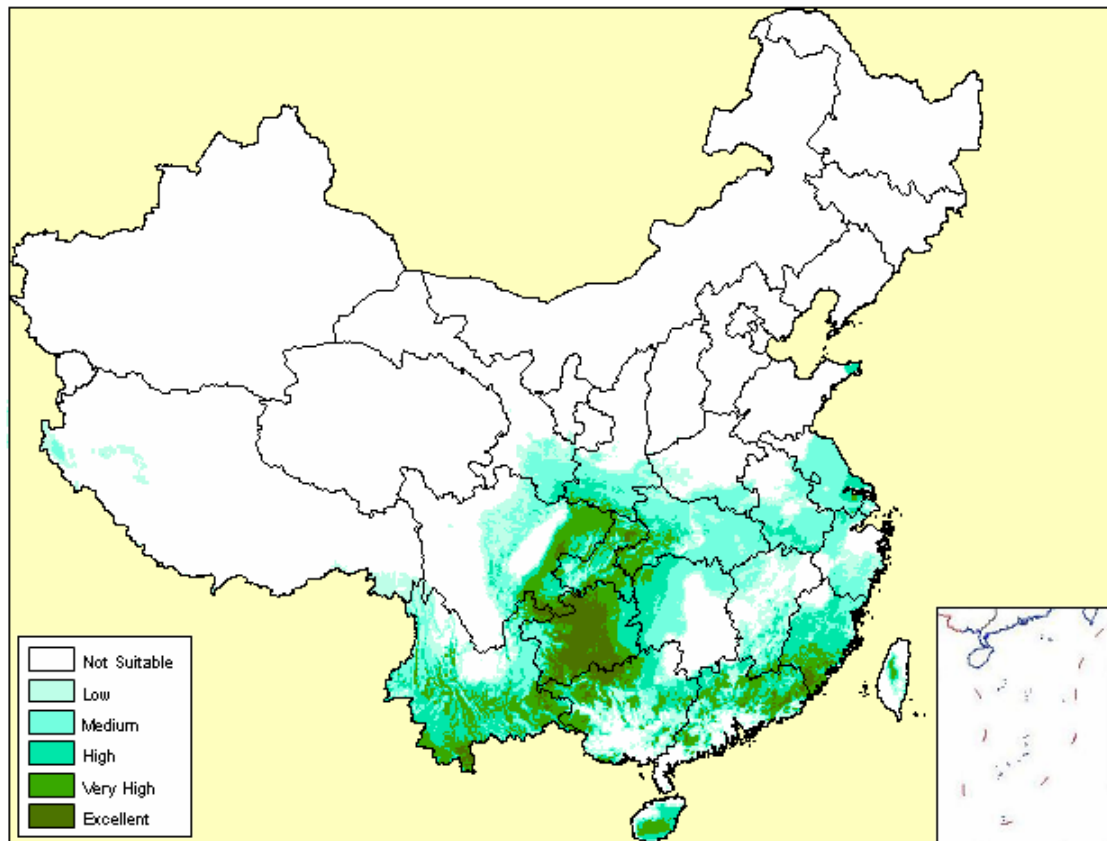
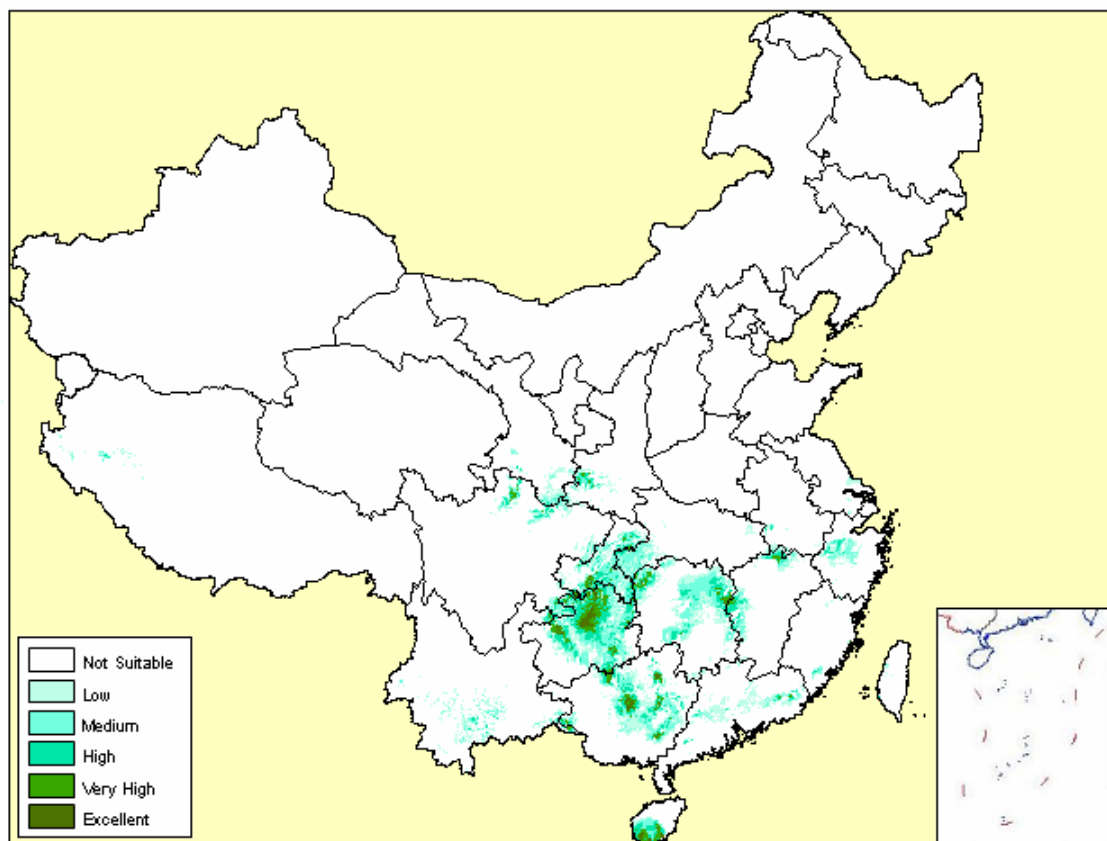Figure 3.2 a BIOCLIM result for *T. asperrimus*

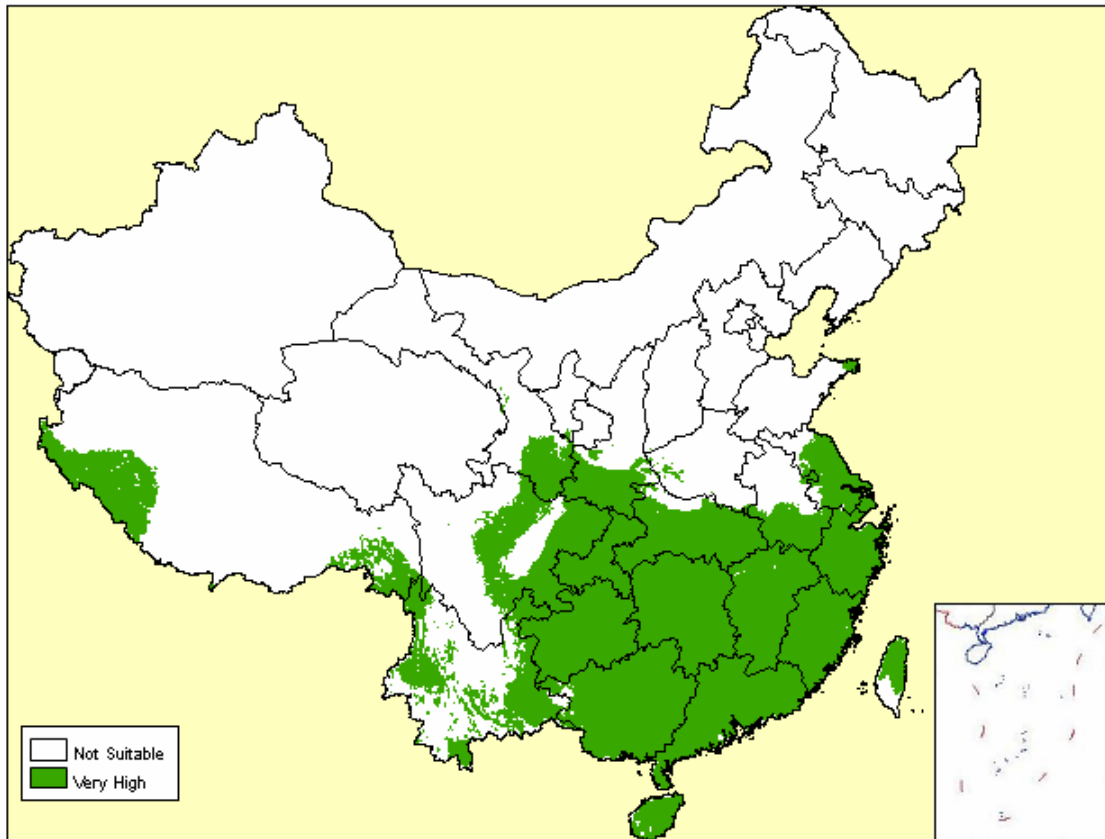Figure 3.2 b DOMAIN results for *T. asperrimus*
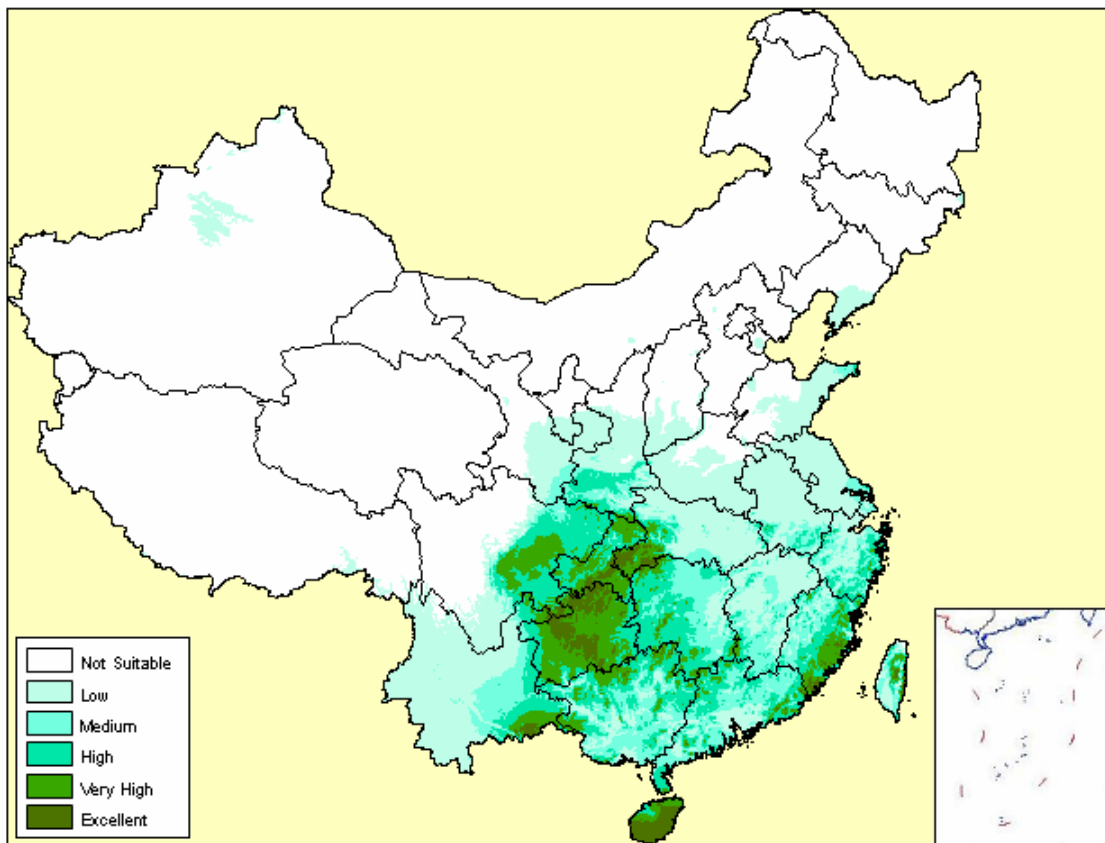
Figure 3.2 c GARP result for *T. asperrimus*

Figure 3.2 d MAXENT result for *T. asperrimus*

3.1.3. Scutiger boulengeri

Scutiger boulengeri is endemic to China, mainly distributes in Qinghai, Xizang, and Sichuan (Zhao, E., 1998). This species is Least Concern (LC) species (Wang, S. and Xie Y., 2004).

BIOCLIM

The suitable areas for *S. boulengeri* are located in the southwest to the middle of China. There are five provinces suitable for the species, Xizang, Sichuan, Qinghai, Gansu and Ningxia. The areas with the highest class of suitability are in the east Xizang and west Sichuan and between the east boundary of Qinghai. Shanxi and part of north Shaanxi are areas with potential medium suitability for the species although there was not record found.

DOMAIN

The prediction area is slightly different from BIOCLIM. The suitable areas are smaller. They only lie in part of west China. The best place is also smaller. There are two major places with high suitability for *S. boulengeri*: one is located on the boundary of Xizang, Sichuan and Qinghai, the other one is west of Gansu, with smaller area in west Qinghai and north Sichuan.

GARP

The potential area is much larger than both BIOCLIM and DOMAIN. The great majority of Xizang, Qinghai, Gansu, and the West part of Sichuan, part of Xinjiang, Shaanxi and Shanxi are suitable area for the species. As the prediction area is quite large, it might have less meaning than other methods.

MAXENT

The suitable areas predicted by MAXENT are relatively smaller compared to GARP. There is only one main large highly suitable zone for *S. boulengeri*: the common boundary of Gansu and Sichuan. There are fragmented areas with high suitability in Xizang and Sichuan. The real suitable place for *S. boulengeri* is very limited.
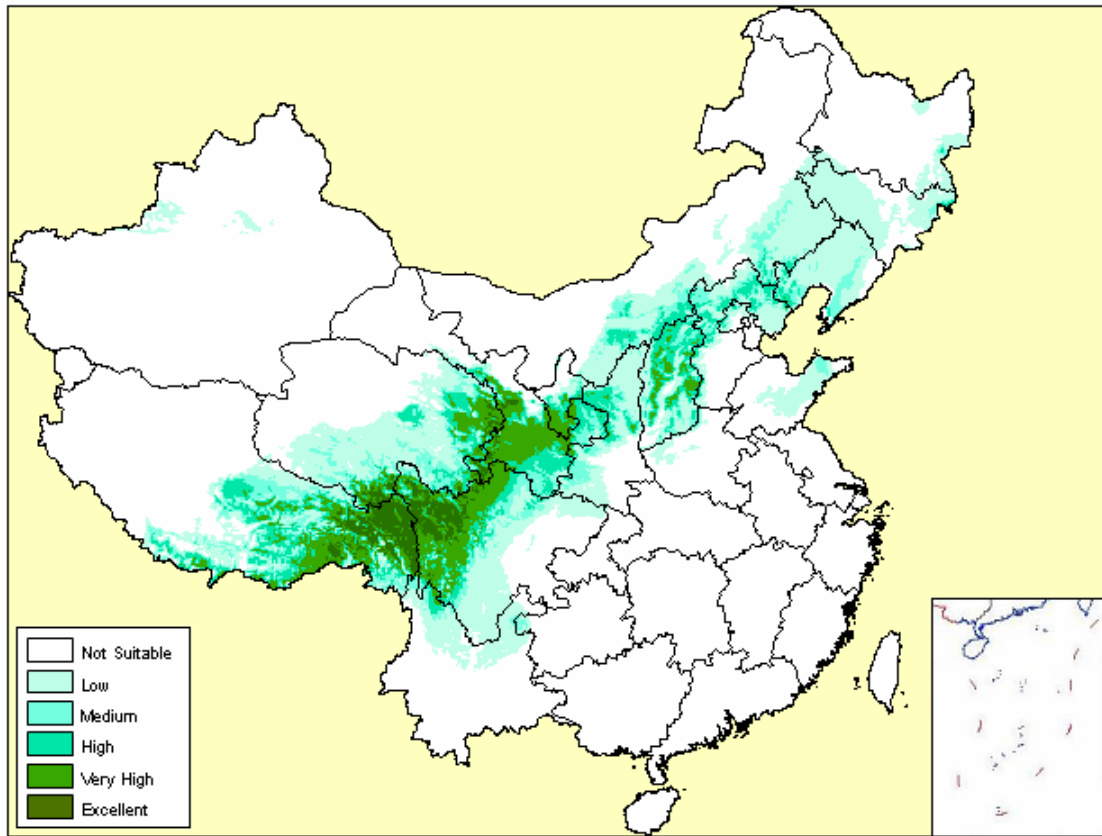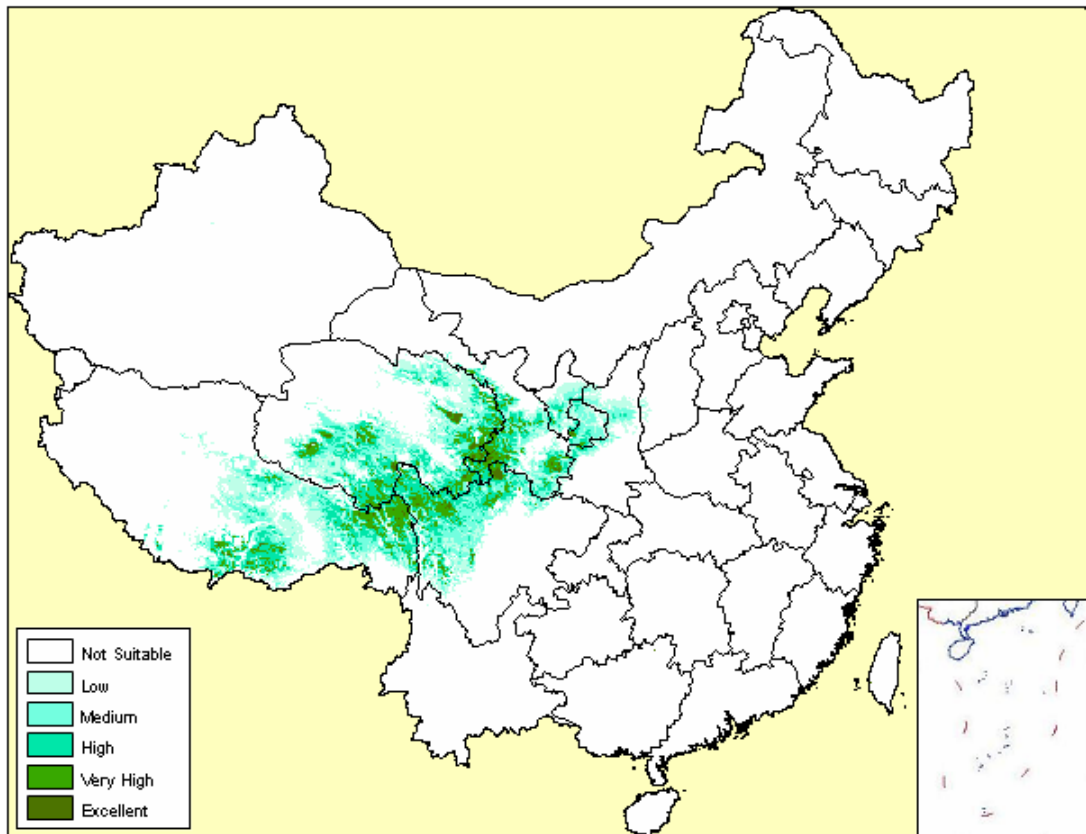
Figure 3.3 a BIOCLIM result for S.boulengeri

Figure 3.3 b DOMAIN result for S. boulengeri
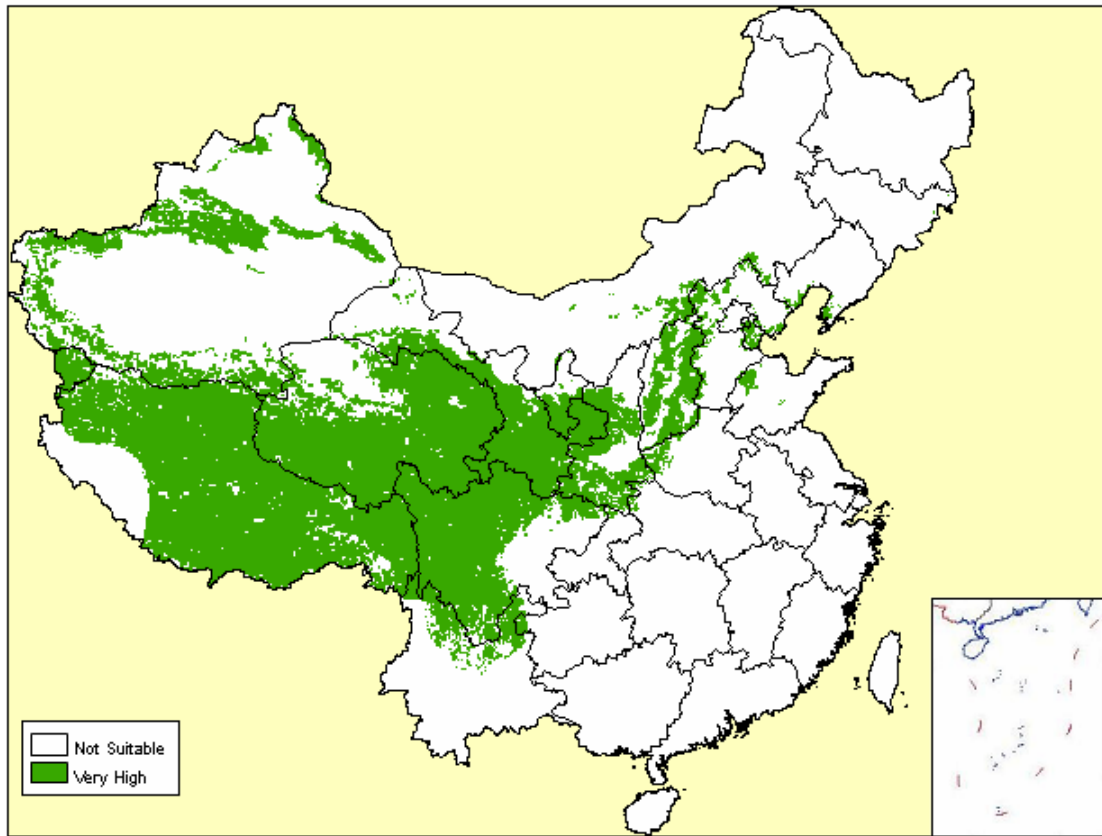
Figure 3.3 a GARP result for S. boulengeri
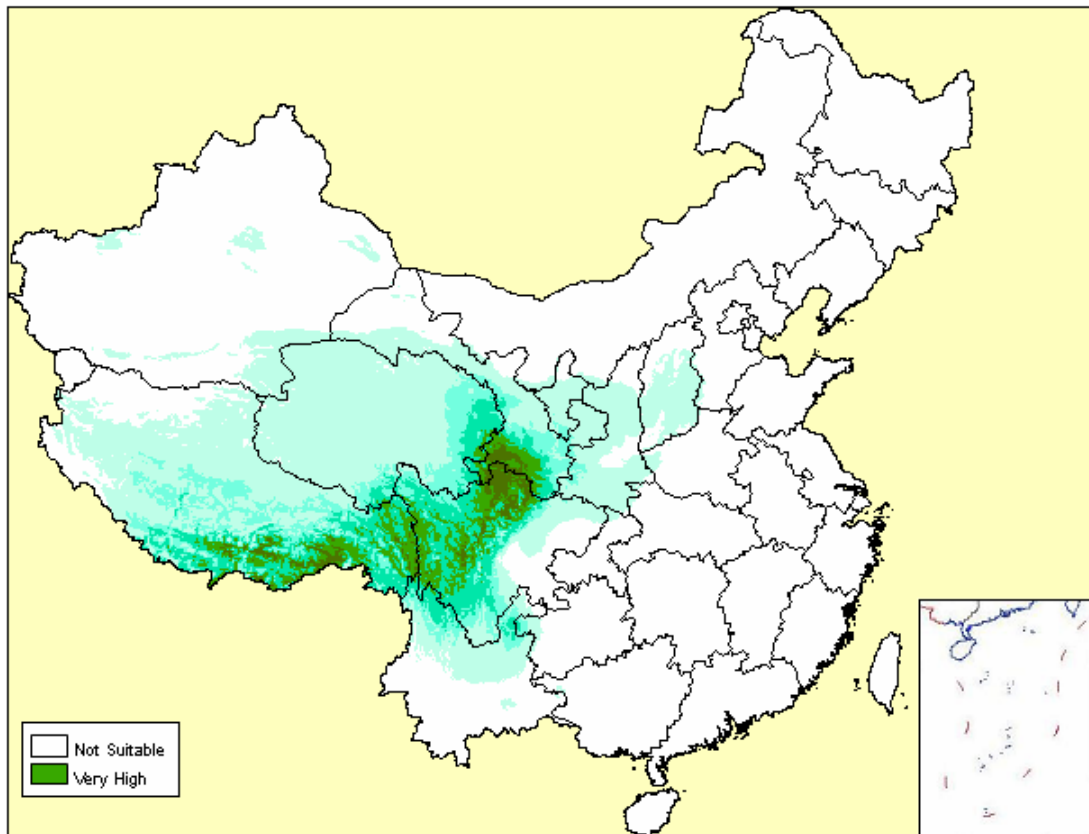
Figure 3.3 d MAXENT result for S. boulengeri

3.1.4. Bufo raddei

Bufo raddei is found in China, Mongolia, Russia and Democratic People's Republic of Korea, minor range in China (Zhao, E., 1998). The species main distributes in northeast, northwest and north China. The species was set as Least Concern (LC) (Wang, S. and Xie Y., 2004).

BIOCLIM

Considering the lower suitability classes almost the entire north China appears to be suitable for *B. raddei*,. Excellent areas for the species are located in Shaanxi, Ningxia, Gansu, Shanxi, Hebei and Liaoning. The provinces which have very high suitability for the species, are Qinghai and Inner Mongolia. etc.

DOMAIN

The areas suitable for the species are less vast compared to BIOCLIM. The excellent areas are in Ningxia, Inner Mongolia, Gansu, Shaanxi, Shanxi, Henan and Shandong etc., although these areas seem under fragmentation treat. The predicted areas are not continuously distributed; it might mean that the situation for *B. raddei* is not good, and the species needs attention for protection.

GARP

B. raddei is given relative small suitable area by GARP compared to other species. The suitable areas are almost the same as DOMAIN results, which were Ningxia, Inner Mongolia, Gansu, Shaanxi, Shanxi, Henan and Shandong.

MAXENT

The area with low suitability for *B. raddei* is wide and it is larger than the one obtained with GARP. However, with this model this species is given smallest highest suitable area, comprising a belt from Gansu, Ningxia and Shanxi. The area with very high and high suitability is Shanxi, north Shaanxi and Liaoning.

Figure 3.4 a BIOCLIM result for *B. raddei*

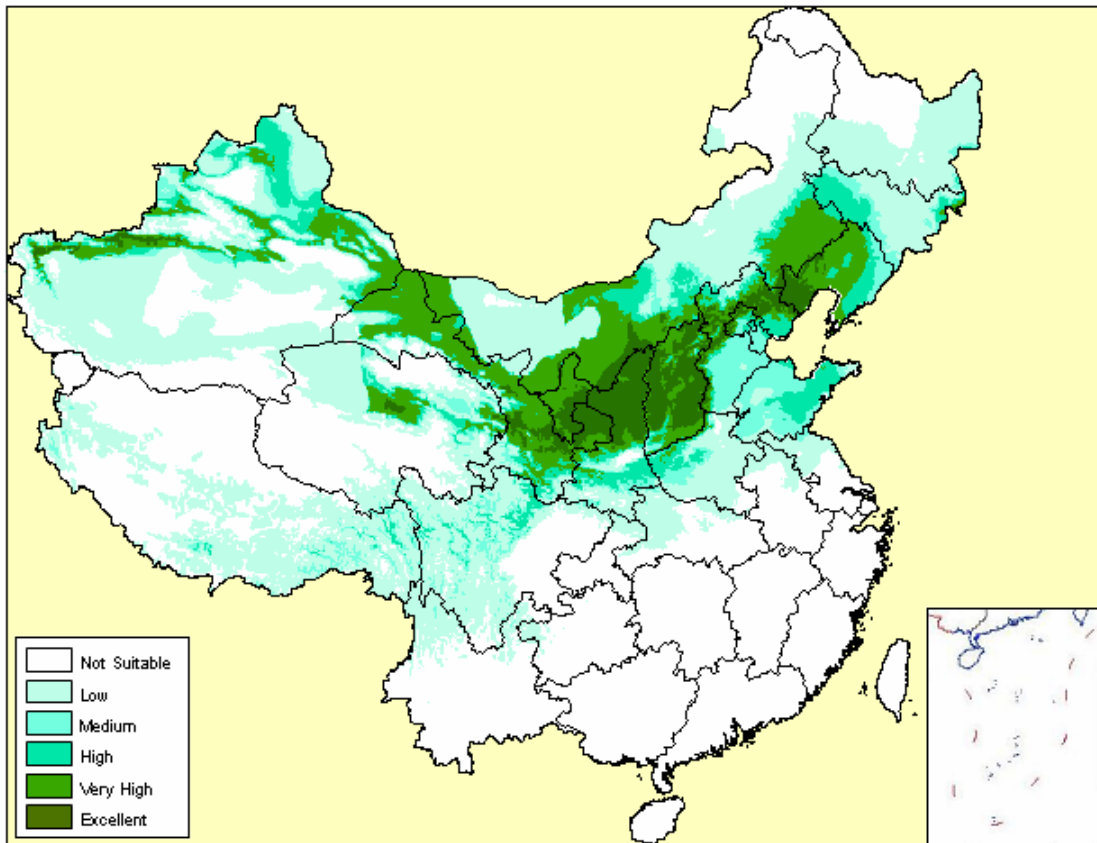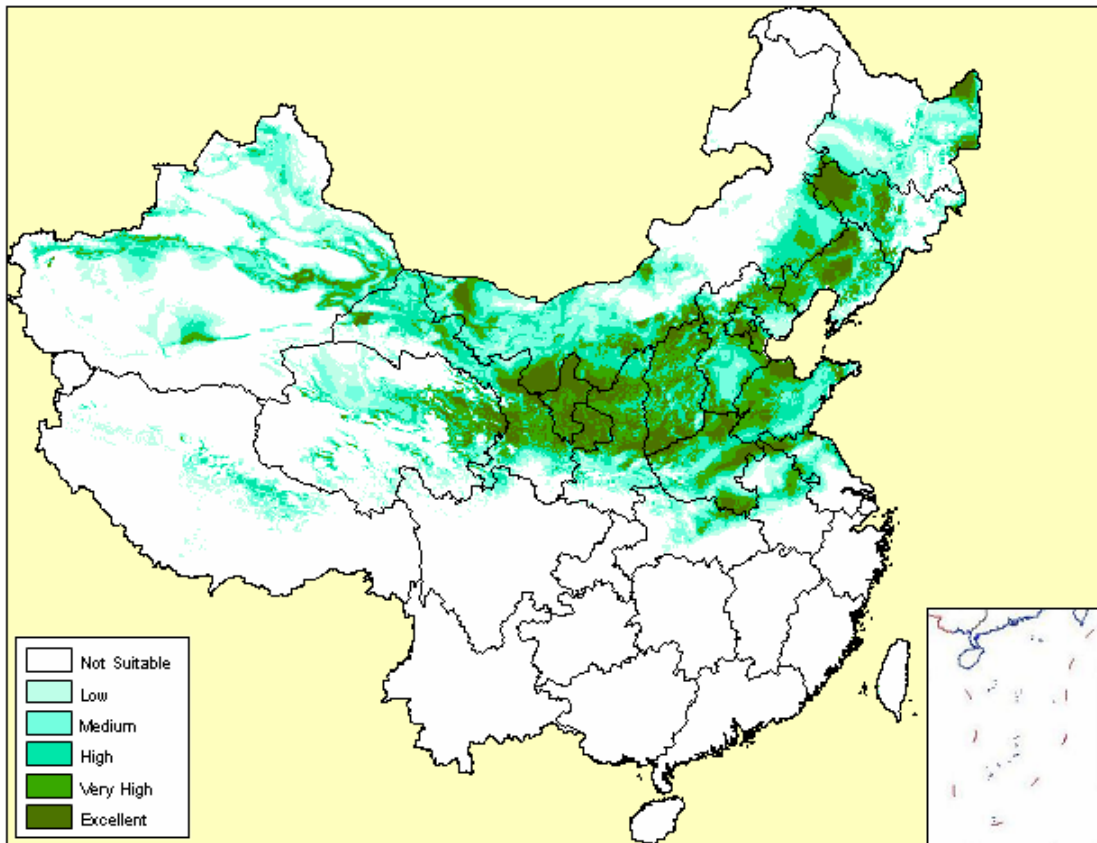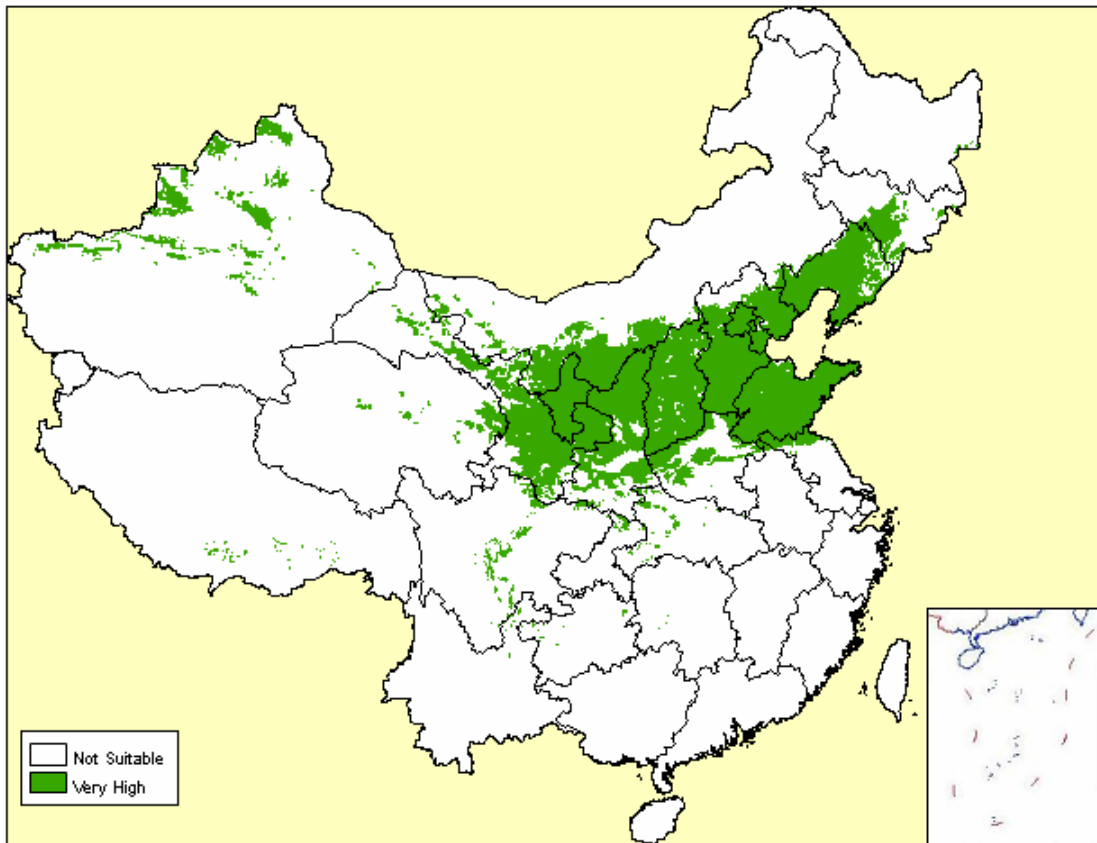Figure 3.4 b DOMAIN result for *B. raddei*

Figure 3.4 c GARP result for *B. raddei*
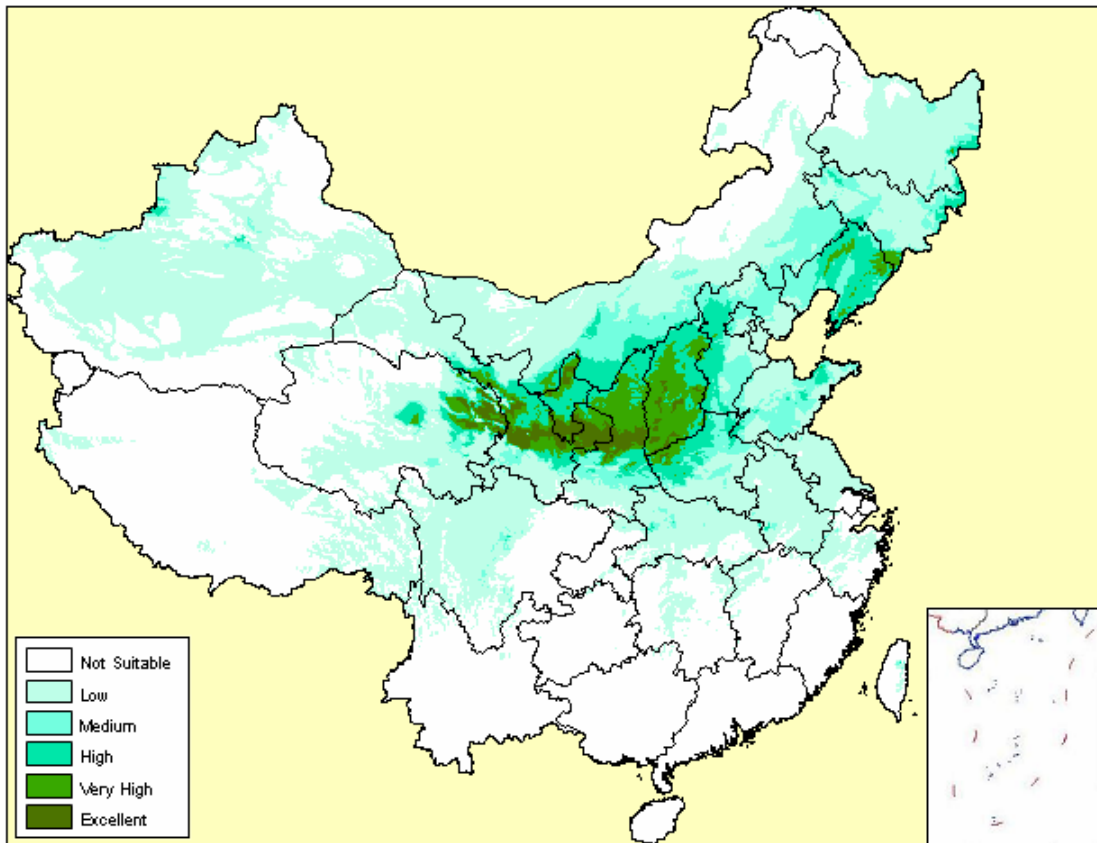
Figure 3.4 d MAXENT result for *B. raddei*

3.1.5. Rana chensinensis

Rana chensinensis is a common species in China. This species mainly appears in the northern China, southward to Jiangsu in the east and Sichuan in the west (Zhao, E., 1998). The species was set as Least Concern (LC) (Wang, S. and Xie Y., 2004).

BIOCLIM

The predicted distribution area is in the north of the country. *R. Chensinensis* could live from the west part of China, Qinghai and Xizang, to the east most provinces Heilongjiang, although the condition of the three northern most provinces is not very nice for the species. There are about nice provinces could provide excellent and very high suitable environment for the species to live, Xizang, Qinghai, Sichuan, Gansu, Ningxia, Shaanxi, Shanxi, Heibei and Henan form the northern to the eastern China.

DOMAIN

In the mass, DOMAIN provided very similar results of *R. Chensinensis* compared to BIOCLIOM. However, the species is given larger suitable place than BIOLCIM and the grade of the suitability is higher. The excellent and very high suitable distribution areas were very wide too. They were Xizang, Qinghai, Gansu, Chongqing, Shaanxi, Shanxi etc. And parts of northeast part of China are very suitable for the species. Parts middle land are high suitable for the species.

GARP

According to GARP, *R. Chensinensis* should locate in the middle of China. Those places are Sichuan, Gansu, Ningxia, Shaanxi, Shanxi, Henan, Hebei and Shandong. The northeast part is not suitable for the species at all, though there are at least twenty present records. The suitable place is not much discrepancy with BIOCLIM and DOMAIN results, except Shandong is considered as a suitable area.

MAXENT

Although the place with low suitability is wide, the place with high suitable value is relatively small compared to other three methods. The place with highest suitability is only located in Gansu and the neighbourhood provinces of Gansu. Shanxi is with medium suitability. Jilin is with medium suitability in the three northeast provinces, the suitability of other province is even lower.

Figure 3.5 a BIOCLIM result for *R. Chensinensis*

Figure 3.5 b DOMAIN result for *R. Chensinensis*
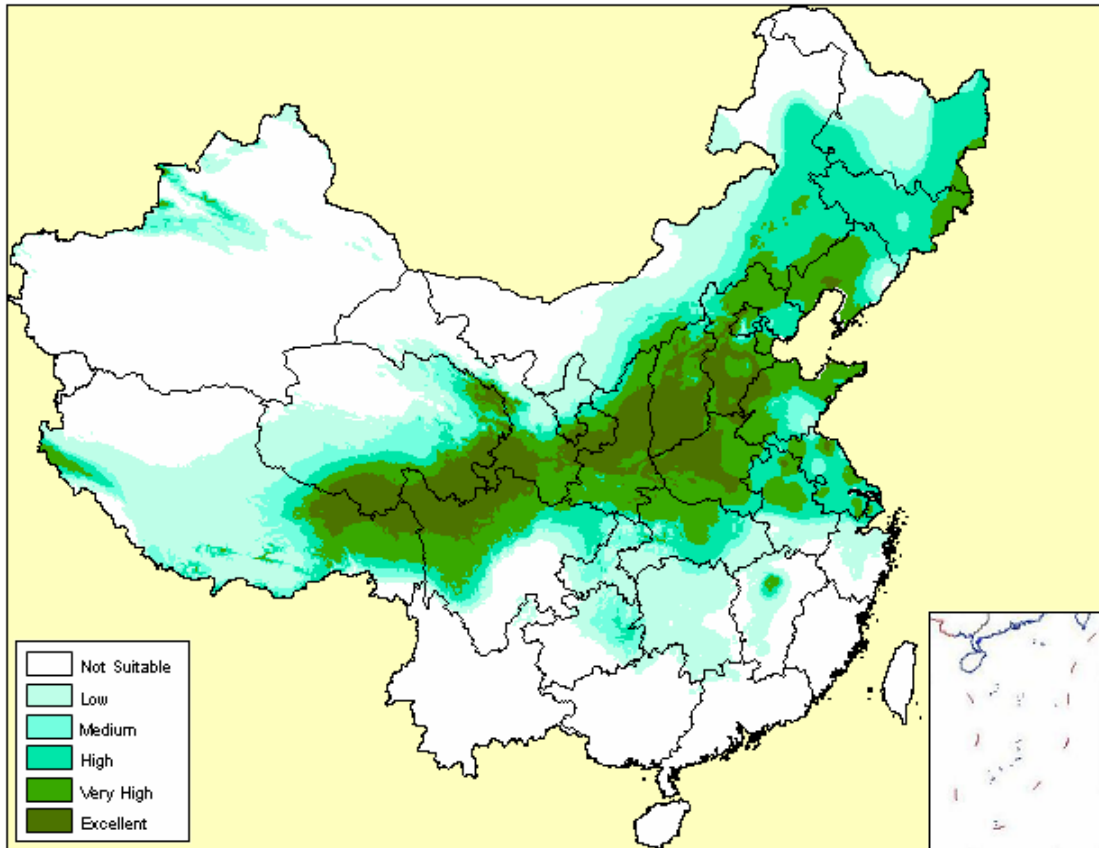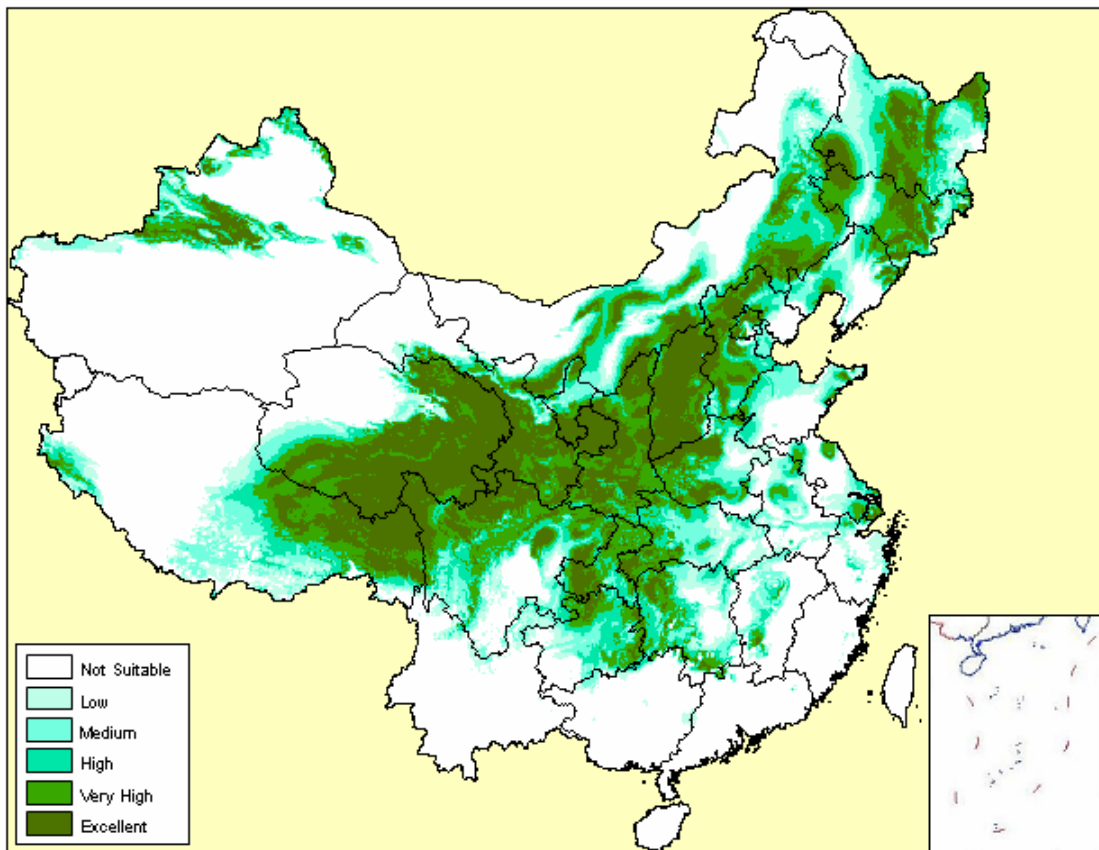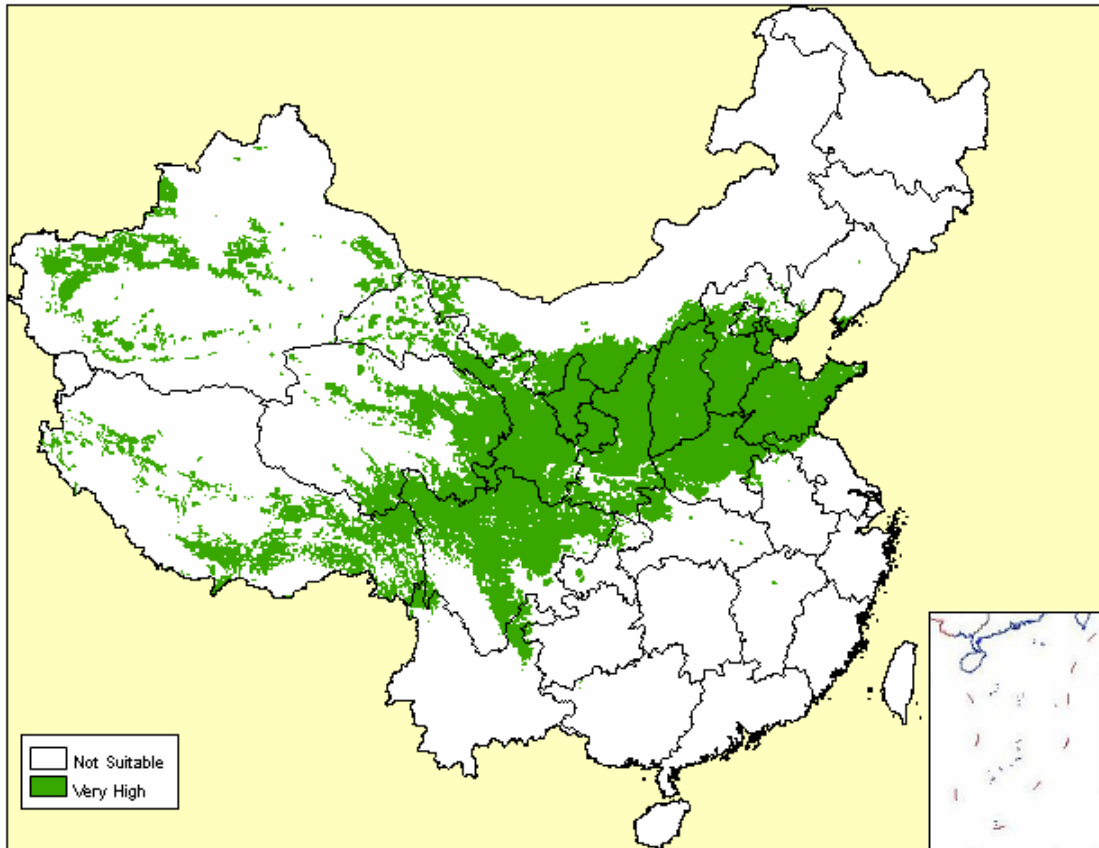
Figure 3.5 c GARP result for *R. Chensinensis*
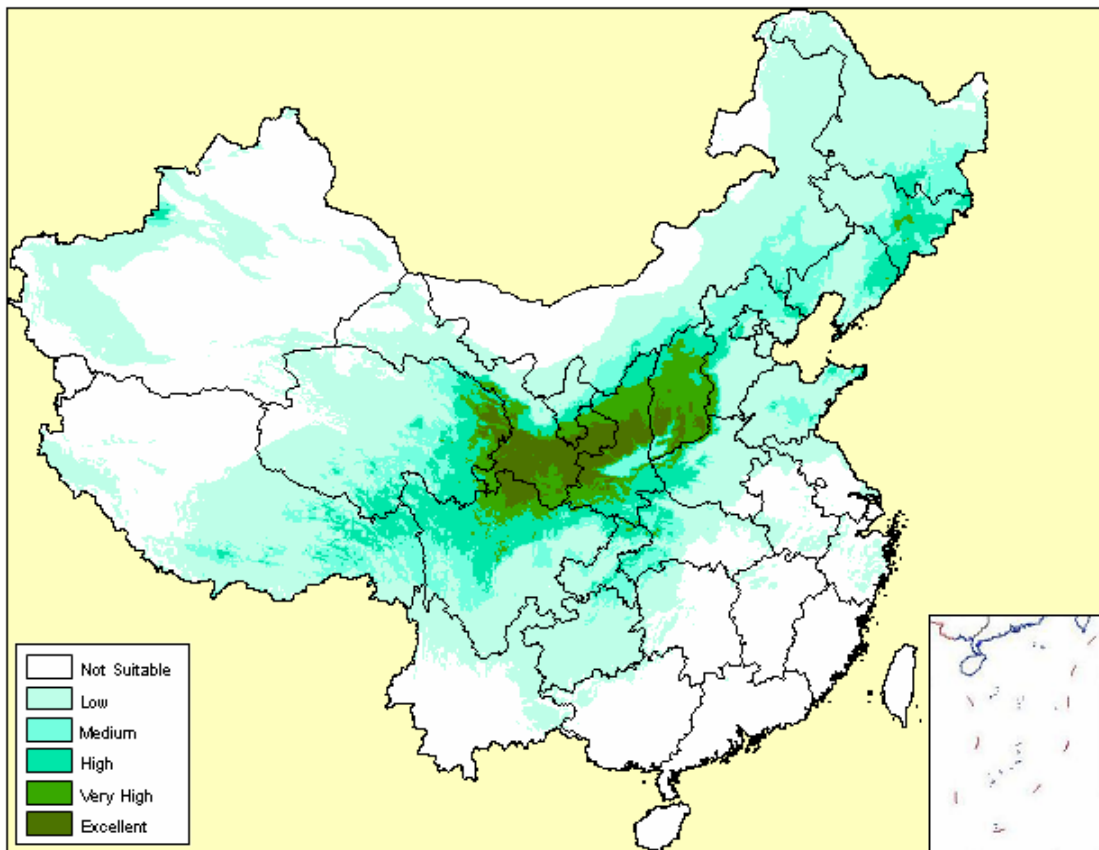
Figure 3.5 d MAXENT result for *R. Chensinensis*

3.2.　　Accuracy Assessment

The validation data was split from the presence datasets. Two thirds were used for training datasets, with the condition that at least 20 samples were used for running the models. The test data was the remaining one thirds of the datasets. Points falling exactly on the same locality of an existing point were removed. For comparing the accuracy of the models, the models were run 10 time to randomise the data.

AUC (area under an ROC curve) and Kappa analysis were used for comparing the performance of those four methods.

3.2.1.　ROC Analysis

The receiver operating characteristic (ROC) was used to compared. The area under an ROC curve (AUC) shows the statistical interpretation of the prediction. The prefect AUC value should be 1(range 0.5-1, when 0.5 is equal to random prediction). Using the same dataset for the analysis, the value was calculated (see Table 6).

Table 6 AUC value of each method

Species \AUC	BIOCLIM	DOMAIN	GARP	MAXENT
A. davidianus	0.922	0.988	0.810	0.950
T. asperrimus	0.940	0.997	0.892	0.951
S. boulengeri	0.954	0.989	0.853	0.954
B. raddei	0.910	0.982	0.808	0.951
R. chensinensis	0.878	0.979	0.745	0.913

The DOMAIN method had the highest AUC value for all five selected species. And the performance was very good as the AUC was among 0.979 to 0.997. Then the method with second highest AUC was MAXENT, whose value was over 0.95 except *R. chensinensis*. BIOCLIM also had relative high value though it was not as high as DOMAIN nor MAXENT. For *S. boulengeri*, BIOCLIM did as well as MAXENT. However, the performance of GARP was not as good as the other three methods. The AUC value was much lower. The highest AUC value of GARP was below 0.90 while the lowest one was under 0.75.

From ROC comparison, the method gave the best prediction was DOMAIN. The second one was MAXENT, and then followed by BIOCLIM. The last one was GARP.

3.2.2.　Kappa analysis

Kappa, a widely useful evaluating measure was also used for judging the methods (range 0-1). The kappa results are showed in Table 7. The difference is sharp. The method which had the best kappa value was DOMAIN again. The kappa value was very high compared to other three methods. The kappa value was all above 0.85 and for three species the value above 0.9. Those showed DOMAIN did

very good job for prediction the distribution of species. The performance of BIOCLIM and MAXENT was almost the same, while MAXENT slightly better than BIOCLIM. MAXENT gave higher value than BIOCLIM in three predictions and BIOCLIM did a little better in the other two species. The same as ROC analysis case, GARP was the one which gave lowest value. And the value was relatively low. And for *R. chensinensis* the kappa value was quite low compared to other prediction, even BIOCLIM and MAXENT did not gave good results. It showed that GARP did not have advantage for those species predictions.

For kappa analysis, DOMAIN was the first choice for the prediction. MAXENT and BIOCLIM methods was suggest to consider for comparison. GAPR method was not suggested as it did not give high accuracy as the other three methods.

Table 7 Kappa value of each method

Species\Kappa	BIOCLIM	DOMAIN	GARP	MAXENT
A. davidianus	0.765	0.908	0.621	0.802
T. asperrimus	0.829	0.963	0.785	0.778
S. boulengeri	0.856	0.914	0.706	0.851
B. raddei	0.724	0.855	0.617	0.802
R. chensinensis	0.615	0.866	0.489	0.709

4. Discussion

4.1. Suggested methods for amphibian modelling

All four methods have their advantage for species distribution. From the accuracy analysis, the performance of those four methods was clear. DOMAIN methods gave the best results for all five species. It was approved by the AUV and kappa value. So it is a good choice to do prediction for other amphibian species. DOMAIN gave the distribution results in a ranked way. For different species, the suitability classes might be different.

For the approach of DOMAIN, this method always gives the results quite close to the sample points. The place where the presence record locates usually has the excellent suitability (100 percent value, at least over 95). This is very nice for getting the main distribution data when the data is adequate. The probability for DOMAIN to give wider range for the species is not very exciting. It is even the case where limited presence data is available. This method somewhat overfits to getting the distribution models, especially when the sample is not adequate, e.g. *T. asperrimus* and *S. boulengeri*. Although the biological and ecological reasons cause this result, the DOMAIN approach might be one factor.

Software DIVA-GIS provide an easy way to do the species distribution. There is distinct difference among the suitable place, even the difference of the value is only one. One advantage for this is that it could predict the individual habitat places or fragmentation compared to BIOCLIM.

Although the software does the prediction based on the bioclimatic variables, the other variables as Elevation and Landover etc. can be used in. The idea is to mask the place where the probability is very rare for the species to live. It could improve the accuracy for the models when error presence data was calculated. The case that Beijing is suitable place for *A. davidianus* would be avoided.

MAXENT is also a good prediction approach. One the one hand, it gives very similar results compared to DOMAIN. Especially for the "excellent" suitable areas, MAXENT and DOMAIN locate them in the same area. And MAXENT could give the signal of individual habitat or alarm for fragmentation as well as DOMAIN. An advantage for MAXENT approach is that the range of MAXENT predicted value is much wider than DOMAIN. The value of suitable place given by DOMAIN is often at least over 95. MAXENT has a range of 100. This makes classification much more flexible by the user. On the other hand, when summing up all of the suitability classes into one single class, the predicted area is very similar to the one generated by GARP. One cause might be both MAXENT and GARP not only consider the bioclimatic variables but also other environmental variables, such as altitude and land use. It can be seemed from the result map that the gap between low and medium suitability is sharp. The place where the suitability is above medium is much smaller than that above low. This shows that, to a certain extent, MAXENT give conservative result in certain extent, but it might be helpful for finding the potential species habitat places.

BOCLIM is an option for predicting the harsh distribution for the species. It gives wider range than DOMIAN. From the calculating perspective, DOMAIN is capable of describing the species-environmental relationship more precisely than BIOCLIM. However, BIOCLIM does a good job in most cases. There are differences between these two methods but they give similar main area for the species. And BIOCLIM predict the higher suitability place in a more positive way.

GARP was the method which gave the widest suitable place in most cases. One reason is the GARP result is binary data. This might make GARP give positive result when the there are still instable factors. And it proved the widest positive results, this might make people consider the real situation in an over optimistic way.

4.2.   Species distribution and protection suggestion

When we compare predicted distribution map compared to the known species range, the difference between them shows the changing situation and might give some insight.

A. davidianus
The *A. davidianus* prediction map is consistent to the known distribution for the general range. This species mainly live in middle and lower tributaries of Changjiang (the Yangtze River), Huang He (the Yellow River). And the species is abundant in Hunan, Hubei, Sichuan, Guizhou, Shaanxi, and Henan provinces (Zhao, E., 1998). All the methods confirms that Guizhou is the best place for the species, which the over half of the province is perfect for the species. Hubei, Hunan, Henan, Chongqing, Shanxi and Gansu are classified as high suitability. It convinced the real distribution. However, its category is critically endangered. The situation does not reflect the situation in the map as worse as Zhao E. (1998) described. It means that despite the bioclimatic influence, human influence is serious. Population reduction of the species should belong to it.

One reason for this is the over collecting by people. *A. davidianus* was described as tasteful and edible, in the book "Species Index of Amphibian in China" published in 1977 (Sichuan Biology Institute and A. R. Institute). Thirty years have past, and the situation of the species has been changed a lot. Although it is forbidden to eat *A. davidianus* in China, it is not easy to eliminate the bad habits in a short time. Another reason is that the species lives in the river or streamlet etc. The construction of the dams is destroying their habitats (Zhao, E., 1998), which is also affected by the third reason which is water pollution

To well predict the species, more factors should be considered. Like the industry locations, the influence range of industry waste and human activity. However, DOMIAN, MAXENT, BIOCLIM can give a better prediction in areas where there are less human activities.

T. asperrimus
The situation of *T. asperrimus* is not very good. From DOMAIN result, the suitable habitat for it is really limited. There are only small areas in few provinces. BIOCLIM and MAXENT gave larger area. Still, the suitable areas are not extensive for the species. It shows why this species was Vulnerable. In the past thee species was widely distributed and had a large populations (Sichuan Biology Institute and

A. R. Institute, 1997; Zhao, E., 1998; etc.). Now both the range and the population size have degraded sharply.

But the predicted distribution map is larger than the known range map. The influence factor to *T. asperrimus* is the degradation of the habitat, the environment has been changed. The other reason is illegal collecting. As the situation for this species is vulnerable, it is set as Ⅱ Protection Species. It has been suggested that putting the species under nearby nature reserves of protection (Zhao, E., 1998).

S. boulengeri

For *S. boulengeri*, the one method whose outputs is perfectly consistent with the known distribution map is MAXENT. However, the other three methods predictions still give similar results. For domain, the species habitat is fragmentation. One reason for *S. boulengeri* categorized as Least Concern species is its distribution area. The area is located in Gansu and southwest of China, provinces which are less populated, thus the species is less influence by human activity.

B. raddei

According to the know distribution range, *B. raddei* should be found in the Northeast, northwest and north of China. All four models predict areas with higher suitability that are smaller than known distribution area. An interesting case is that the northeast three provinces, where there are observation for the species, does not classify as suitable in the models. This might means that the real good distribution area is not as good as preciously believed. On contrary, the bioclimatic variables as well as other factors does not influence this species much.

R. chensinensis

The prediction results of *R. chensinensis* are wider than *B. raddei.* But it has a similar problem as *B. raddei*. The distribution range is different from the known map. The prediction area is less northerly than the known distribution map in the north and southerly in the south. Most areas of the three northeast provinces are not considered as good habitat for *R. chensinensis,* though they are the main distribution areas for the species. It shows the suitability for the species in the north part is declined.

Furthermore, *R. chensinensis* is an economical species used for nourishing drug. Over exploitation makes the situation even worse (Zhao, E., 1998). That is why this species was set as Vulnerable in 1998 (Zhao, E.). However, It was set as set as Least Concern (LC) (Wang, S. and Xie Y., 2004). It is suggested to consider setting this species as Vulnerable again.

As a developing country, the law for environmental protection is adequate in China. Also it is hard to implement them. However, the government has already taken notice into those problems. But we need time and energy to improve the situation and slow down the decline.

5. Conclusions and Recommendations

The species environmental models give the prediction maps showed in Chapter 3. The models perform well to the chosen species. The species environmental models show their powerful in amphibian distribution prediction. The models will give great help in amphibian distribution in national scale.

The functional environmental variables for each species are given in Chapter 3. The bioclimatic variables played an important role in the prediction. And the non-bioclimatic variables（e.g. landcover, latitude, population) give additional information which bioclimatic variables could not provided.

The distribution area of chosen species, compared to decades ago, most had been declined in different scale. Human activities give negative influence to the species, especially those high economy species. It suggests government put more attention to the environmental conservation and the species protection.

DOMAN method has the highest accuracy for modelling. The second one is MAXENT followed by BIOCLIM. The last one is GARP one. DOMAIN, MAXENT and BIOCLIM all have high accuracy in most case.

DOMAIN is considered as the best method to do the prediction with only bioclimatic variables. And it could be improved by adding other factors in a certain way. MAXENT could be used as a complement as well as BIOCLIM. GARP is not suggested as the first choice though it still could be used for coarse modelling

New species datasets should be set up. The species locality data are relatively old. The source was observed since thirty years ago. Some species was extinct as the environment has been totally changed. Those information does not match the reality should be deleted in the datasets.

For more detailed regional data research, the more detail data set is recommended. (E.g. High resolution landcover map, the latest population density map etc.)

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