eDNA Task

2023/11/06

Tosha Tang

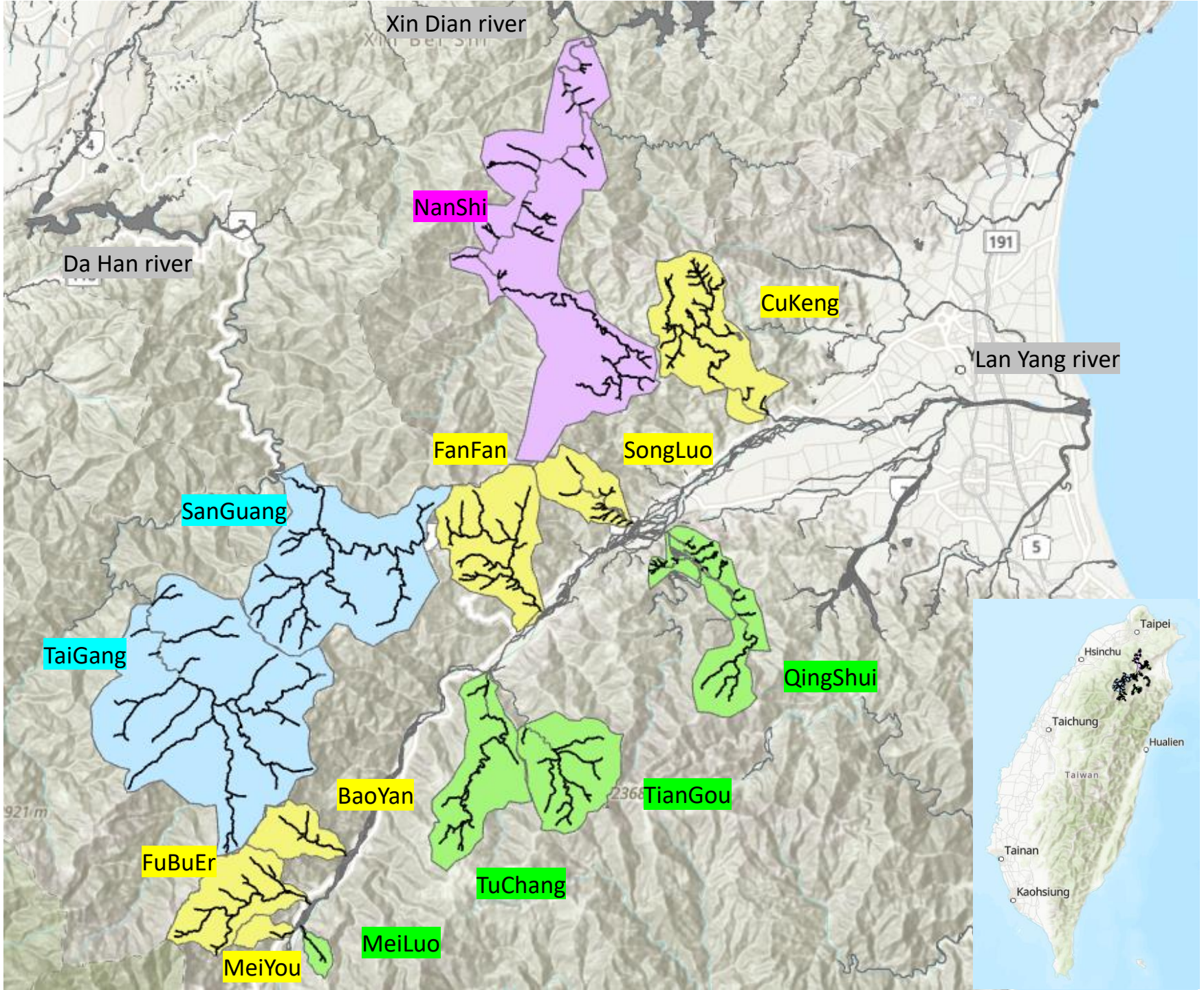
DATA

- Base Map: World Topographic Map + World Hillshade (ArcGIS pro default)
- Creatures: iNaturalist export
  - https://www.inaturalist.org/observations/export?flow_task_id=360235#export-372932
  - quality_grade=any&identifications=any&swlat=24.42&swlng=121.314&nelat=24.51&nelng=121.423
- River: Water Resources Agency, MOEA
  - https://gic.wra.gov.tw/Gis/Gic/API/Google/Index.aspx
- DTM: DATA.GOV.TW
  - https://data.gov.tw/dataset/160361

iNaturalist Export Fields

檔案大小	等待中	開始	完成	輸入	
14.1 MB	11月04日 11:12	11月04日 11:12	11月04日 12:40	**查詢** quality_grade=**any**&identifications=**any**&swlat=**24.41**&swlng=**121.266**&nelat=**24.92**&nelng=**121.678** **欄位** id, observed_on_string, observed_on, time_observed_at, time_zone, user_id, user_login, user_name, created_at, updated_at, quality_grade, license, url, image_url, sound_url, tag_list, description, num_identification_agreements, num_identification_disagreements, captive_cultivated, oauth_application_id, place_guess, latitude, longitude, positional_accuracy, private_place_guess, private_latitude, private_longitude, public_positional_accuracy, geoprivacy, taxon_geoprivacy, coordinates_obscured, positioning_method, positioning_device, species_guess, scientific_name, common_name, iconic_taxon_name, taxon_id, taxon_kingdom_name, taxon_phylum_name, taxon_subphylum_name, taxon_superclass_name, taxon_class_name, taxon_subclass_name, taxon_superorder_name, taxon_order_name, taxon_suborder_name, taxon_superfamily_name, taxon_family_name, taxon_subfamily_name, taxon_supertribe_name, taxon_tribe_name, taxon_subtribe_name, taxon_genus_name, taxon_genushybrid_name, taxon_species_name, taxon_hybrid_name, taxon_subspecies_name, taxon_variety_name, taxon_form_name	刪除

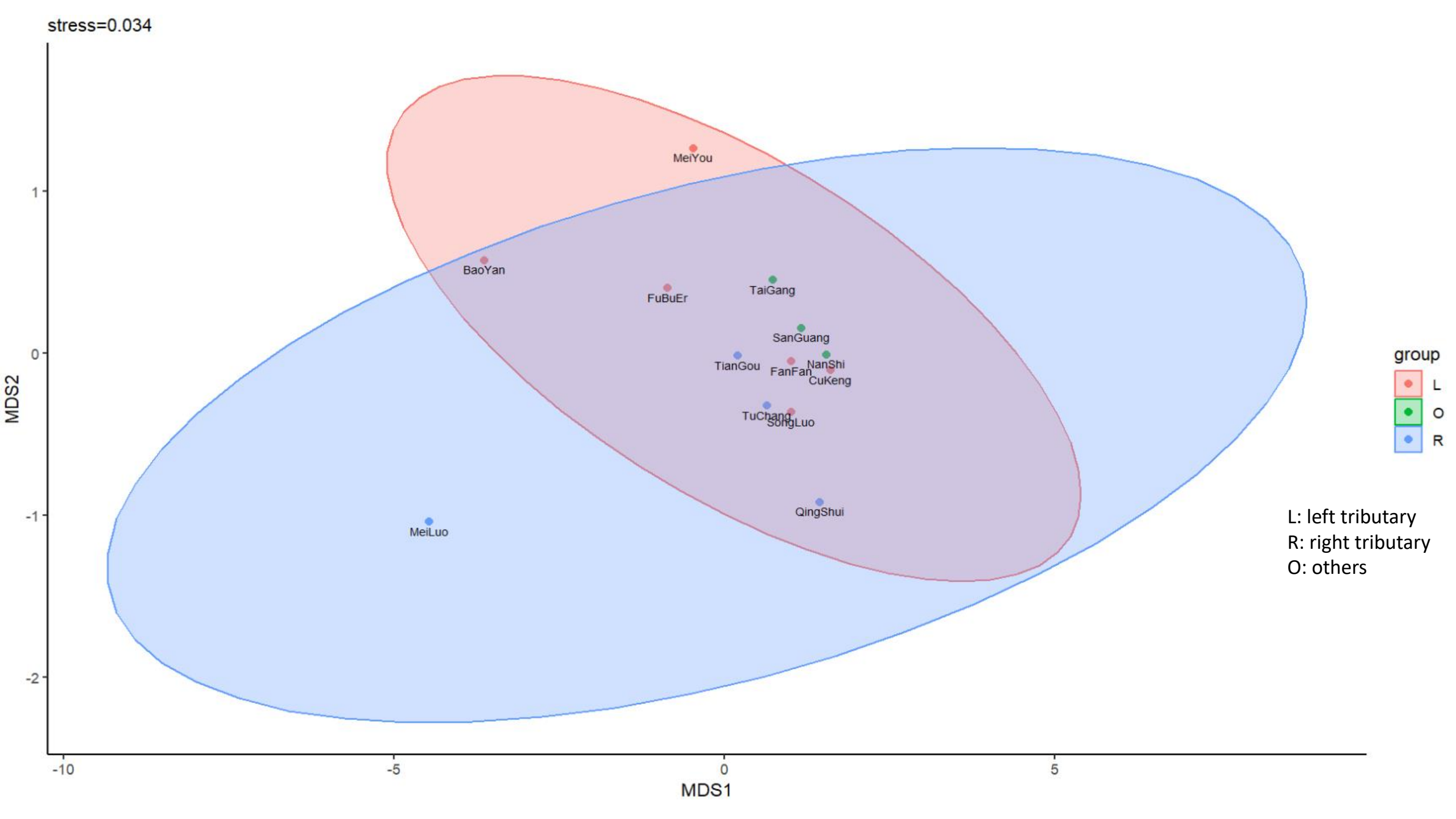
ArcGIS pro Project

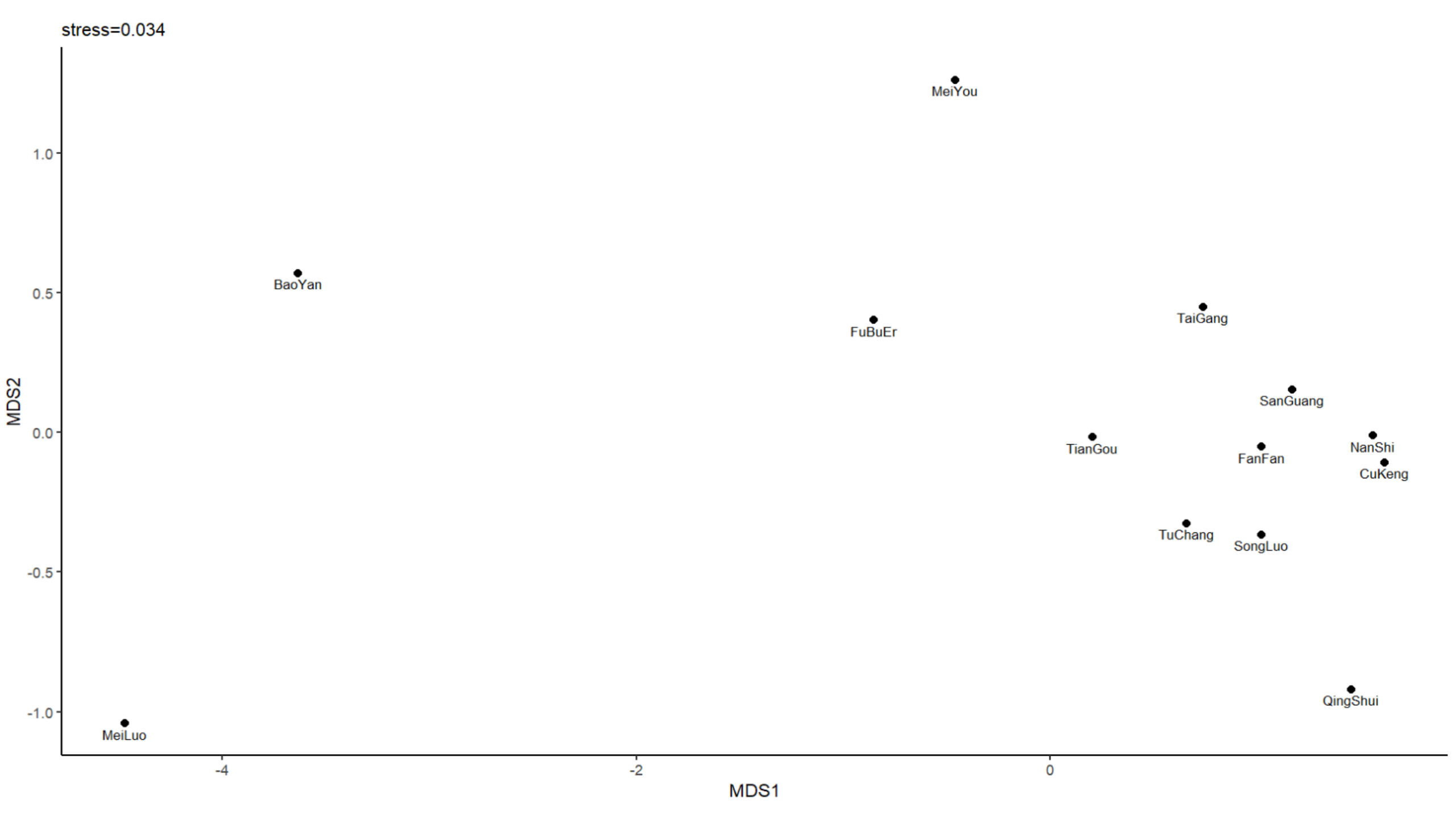


SUBRIVER LIST (13)

CuKeng
NanShi
SongLuo
FanFan
SanGuang
BaoYan
FuBuEr
MeiYou
QingShui
TianGou
TuChang
MeiLuo
TaiGang

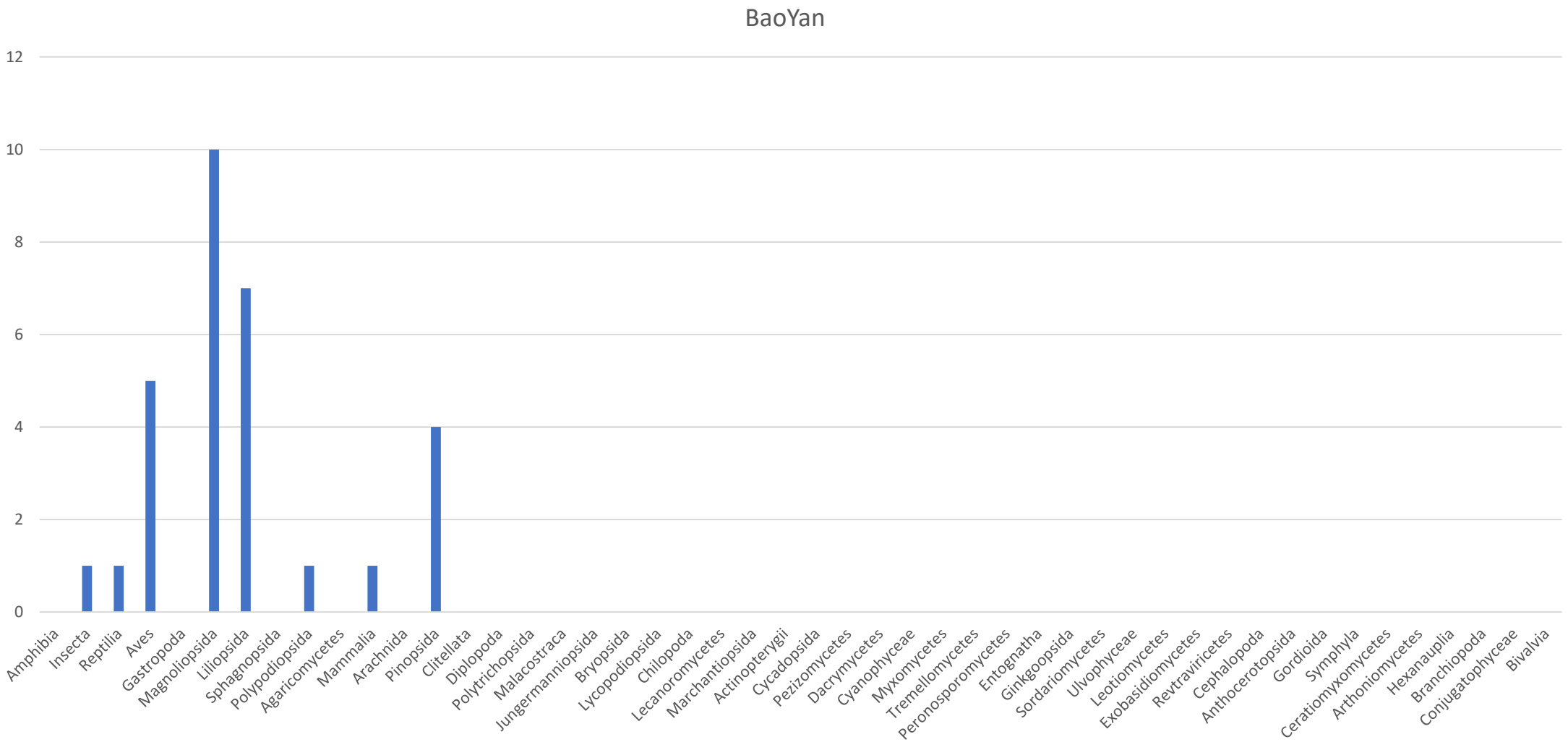
NMDS Result


stress=0.034
MeiYou
BaoYan
FuBuEr
TaiGang
SanGuang
TianGou
FanFan
NanShi
CuKeng
TuChang
SongLuo
QingShui
MeiLuo
MDS1
MDS2
-10
-5
0
5
1
0
-1
-2
group
L
O
R
L: left tributary
R: right tributary
O: others

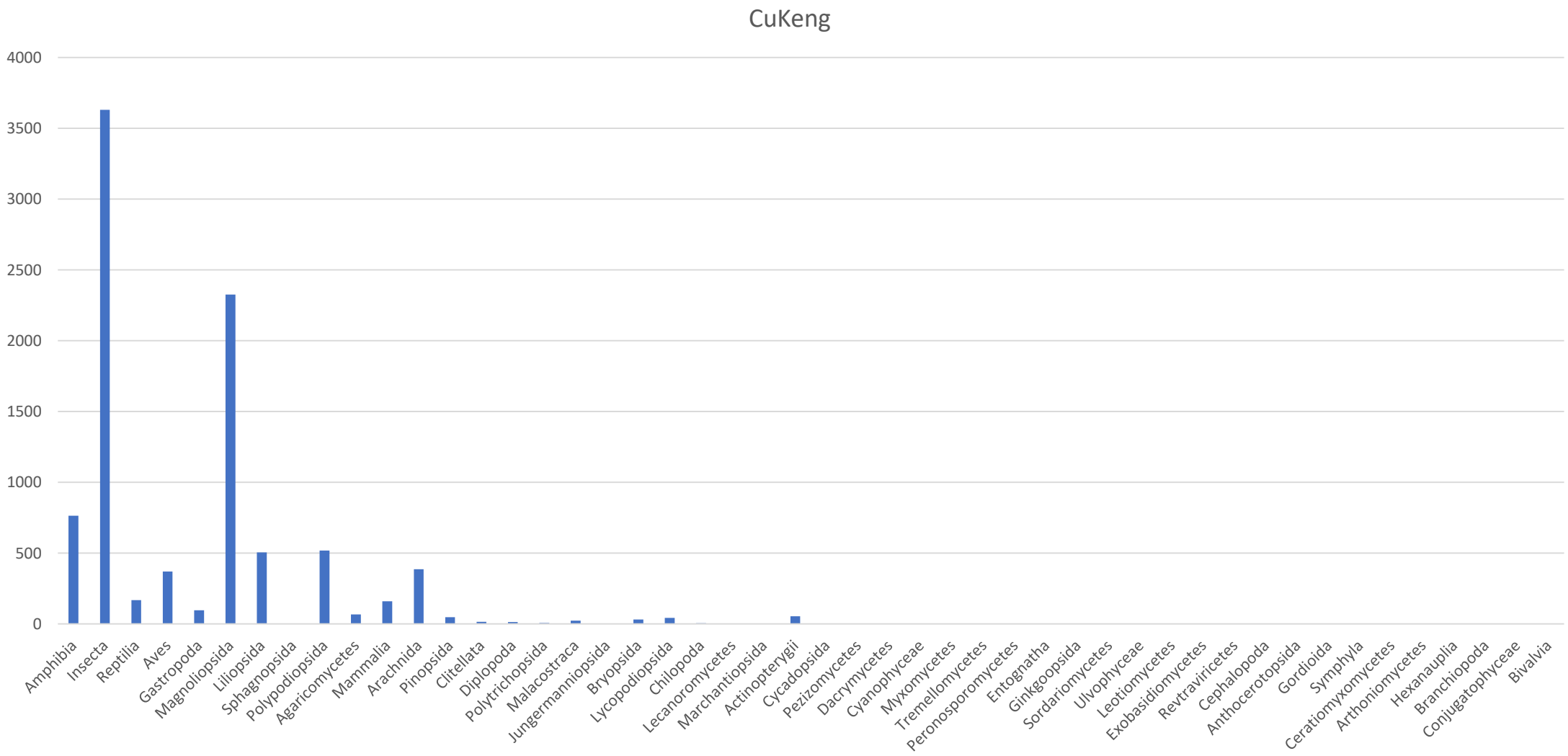

stress=0.034
MeiYou
BaoYan
FuBuEr
TaiGang
SanGuang
TianGou
FanFan
NanShi
CuKeng
TuChang
SongLuo
QingShui
MeiLuo
1.0
0.5
0.0
-0.5
-1.0
MDS2
-4
-2
0
MDS1

Creature Data in Every Tributary

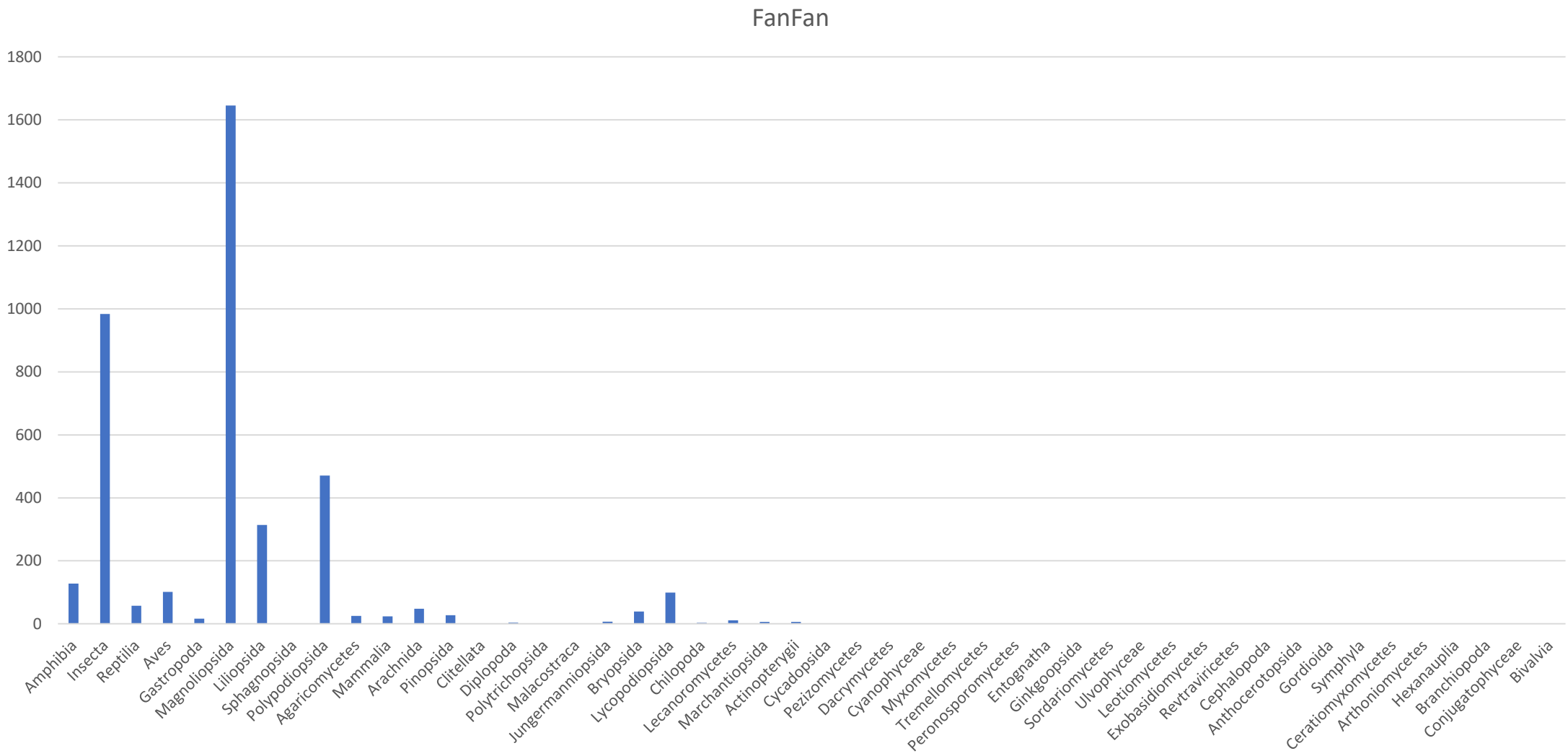
BaoYan - 30


BaoYan
12
10
8
6
4
2
0
Amphibia
Insecta
Reptilia
Aves
Gastropoda
Magnoliopsida
Liliopsida
Sphagnopsida
Polypodiopsida
Agaricomycetes
Mammalia
Arachnida
Pinopsida
Clitellata
Diplopoda
Polytrichopsida
Malacostraca
Jungermanniopsida
Bryopsida
Lycopodiopsida
Chilopoda
Lecanoromycetes
Marchantiopsida
Actinopterygii
Cycadopsida
Pezizomycetes
Dacrymycetes
Cyanophyceae
Myxomycetes
Tremellomycetes
Peronosporomycetes
Entognatha
Ginkgoopsida
Sordariomycetes
Ulvophyceae
Leotiomycetes
Exobasidiomycetes
Revtraviricetes
Cephalopoda
Anthocerotopsida
Gordioida
Symphyla
Ceratiomyxomycetes
Arthoniomycetes
Hexanauplia
Branchiopoda
Conjugatophyceae
Bivalvia

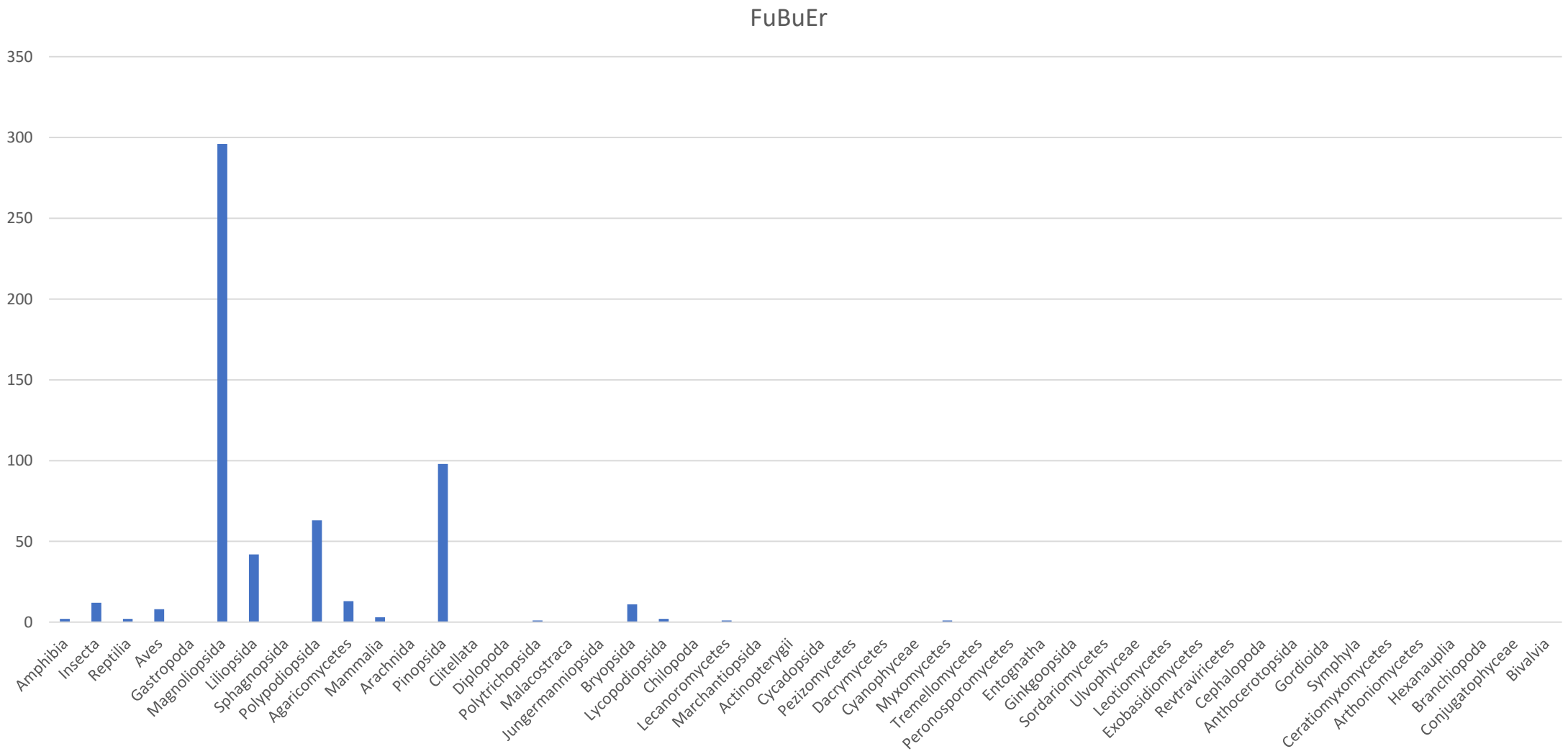
CuKeng - 9626


CuKeng
4000
3500
3000
2500
2000
1500
1000
500
0
Amphibia
Insecta
Reptilia
Aves
Gastropoda
Magnoliopsida
Liliopsida
Sphagnopsida
Polypodiopsida
Agaricomycetes
Mammalia
Arachnida
Pinopsida
Clitellata
Diplopoda
Polytrichopsida
Malacostraca
Jungermanniopsida
Bryopsida
Lycopodiopsida
Chilopoda
Lecanoromycetes
Marchantiopsida
Actinopterygii
Cycadopsida
Pezizomycetes
Dacrymycetes
Cyanophyceae
Myxomycetes
Tremellomycetes
Peronosporomycetes
Entognatha
Ginkgoopsida
Sordariomycetes
Ulvophyceae
Leotiomycetes
Exobasidiomycetes
Revtraviricetes
Cephalopoda
Anthocerotopsida
Gordioida
Symphyla
Ceratiomyxomycetes
Arthoniomycetes
Hexanauplia
Branchiopoda
Conjugatophyceae
Bivalvia

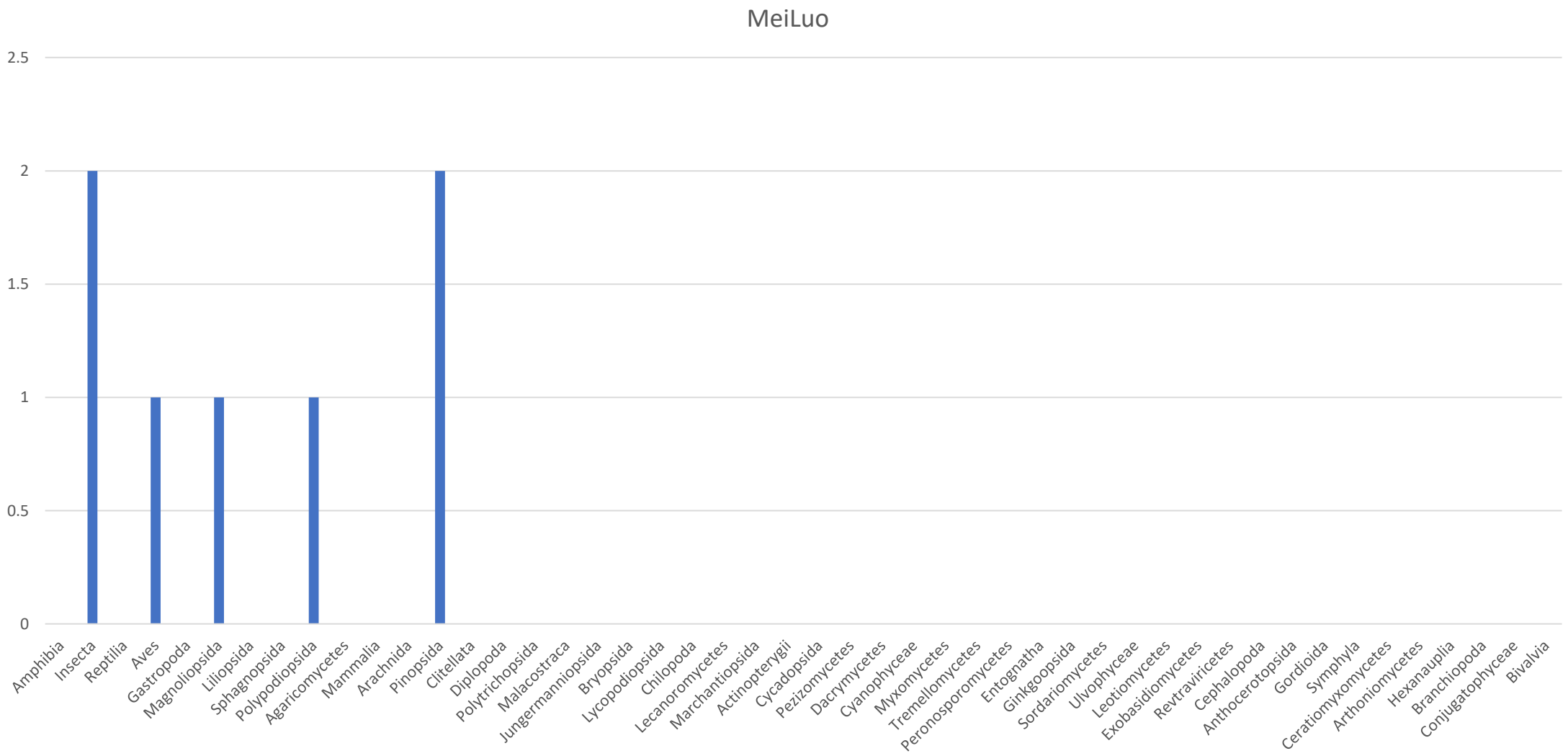
FanFan - 4351


FanFan
1800
1600
1400
1200
1000
800
600
400
200
0
Amphibia
Insecta
Reptilia
Aves
Gastropoda
Magnoliopsida
Liliopsida
Sphagnopsida
Polypodiopsida
Agaricomycetes
Mammalia
Arachnida
Pinopsida
Clitellata
Diplopoda
Polytrichopsida
Malacostraca
Jungermanniopsida
Bryopsida
Lycopodiopsida
Chilopoda
Lecanoromycetes
Marchantiopsida
Actinopterygii
Cycadopsida
Pezizomycetes
Dacrymycetes
Cyanophyceae
Myxomycetes
Tremellomycetes
Peronosporomycetes
Entognatha
Ginkgoopsida
Sordariomycetes
Ulvophyceae
Leotiomycetes
Exobasidiomycetes
Revtraviricetes
Cephalopoda
Anthocerotopsida
Gordioida
Symphyla
Ceratiomyxomycetes
Arthoniomycetes
Hexanauplia
Branchiopoda
Conjugatophyceae
Bivalvia

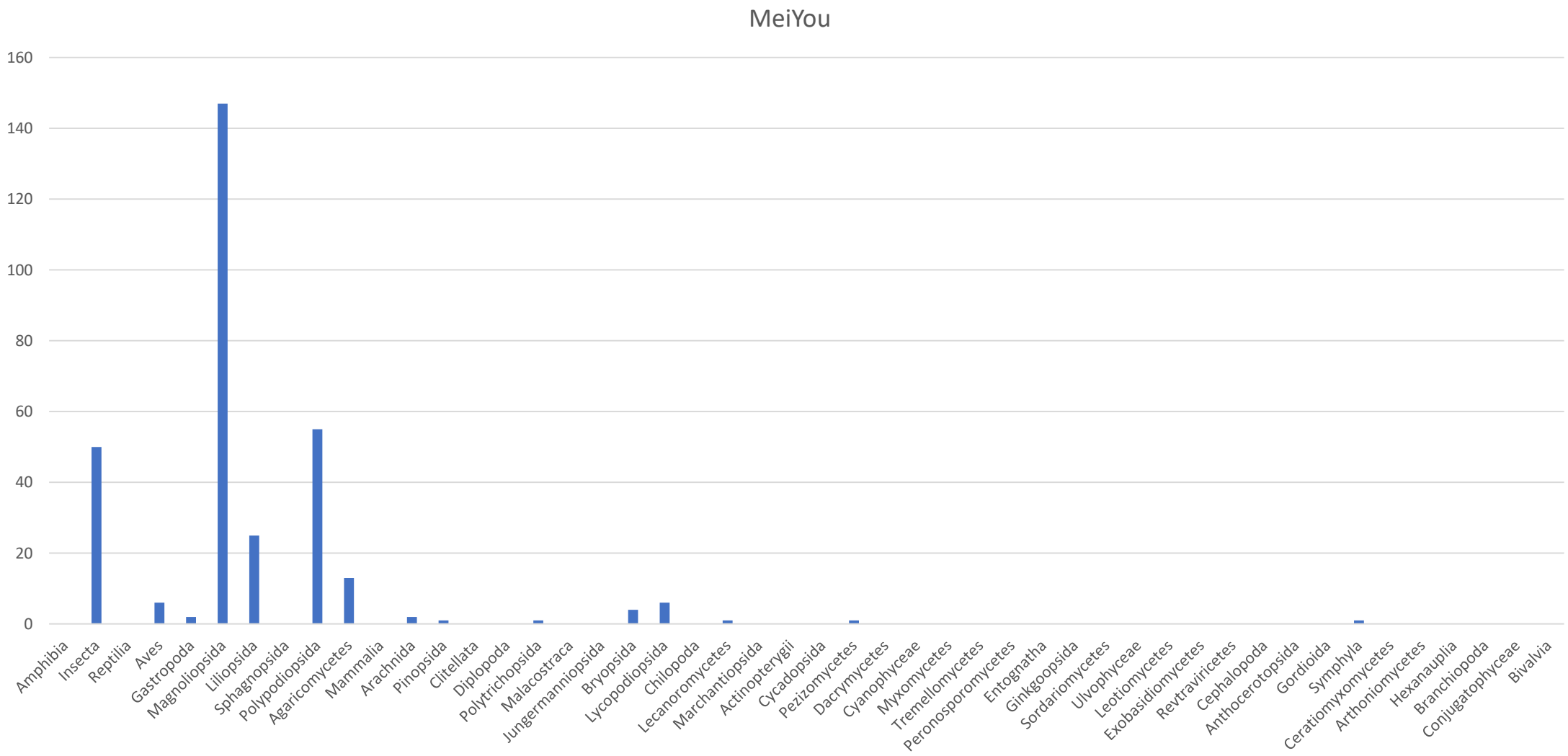
FuBuEr - 606


FuBuEr
350
300
250
200
150
100
50
0
Amphibia
Insecta
Reptilia
Aves
Gastropoda
Magnoliopsida
Liliopsida
Sphagnopsida
Polypodiopsida
Agaricomycetes
Mammalia
Arachnida
Pinopsida
Clitellata
Diplopoda
Polytrichopsida
Malacostraca
Jungermanniopsida
Bryopsida
Lycopodiopsida
Chilopoda
Lecanoromycetes
Marchantiopsida
Actinopterygii
Cycadopsida
Pezizomycetes
Dacrymycetes
Cyanophyceae
Myxomycetes
Tremellomycetes
Peronosporomycetes
Entognatha
Ginkgoopsida
Sordariomycetes
Ulvophyceae
Leotiomycetes
Exobasidiomycetes
Revtraviricetes
Cephalopoda
Anthocerotopsida
Gordioida
Symphyla
Ceratiomyxomycetes
Arthoniomycetes
Hexanauplia
Branchiopoda
Conjugatophyceae
Bivalvia

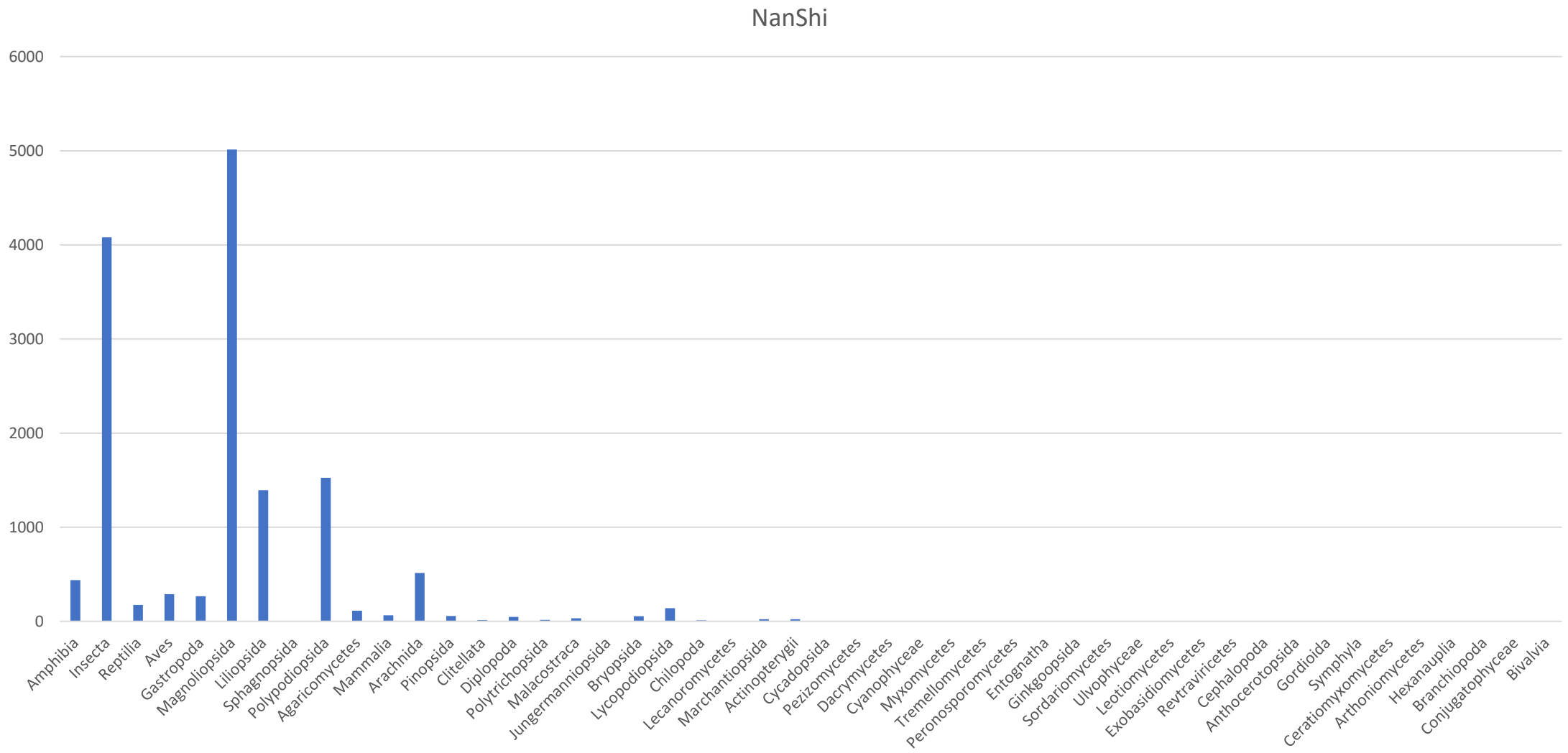
MeiLuo - 7


MeiLuo
2.5
2
1.5
1
0.5
0
Amphibia
Insecta
Reptilia
Aves
Gastropoda
Magnoliopsida
Liliopsida
Sphagnopsida
Polypodiopsida
Agaricomycetes
Mammalia
Arachnida
Pinopsida
Clitellata
Diplopoda
Polytrichopsida
Malacostraca
Jungermanniopsida
Bryopsida
Lycopodiopsida
Chilopoda
Lecanoromycetes
Marchantiopsida
Actinopterygii
Cycadopsida
Pezizomycetes
Dacrymycetes
Cyanophyceae
Myxomycetes
Tremellomycetes
Peronosporomycetes
Entognatha
Ginkgoopsida
Sordariomycetes
Ulvophyceae
Leotiomycetes
Exobasidiomycetes
Revtraviricetes
Cephalopoda
Anthocerotopsida
Gordioida
Symphyla
Ceratiomyxomycetes
Arthoniomycetes
Hexanauplia
Branchiopoda
Conjugatophyceae
Bivalvia

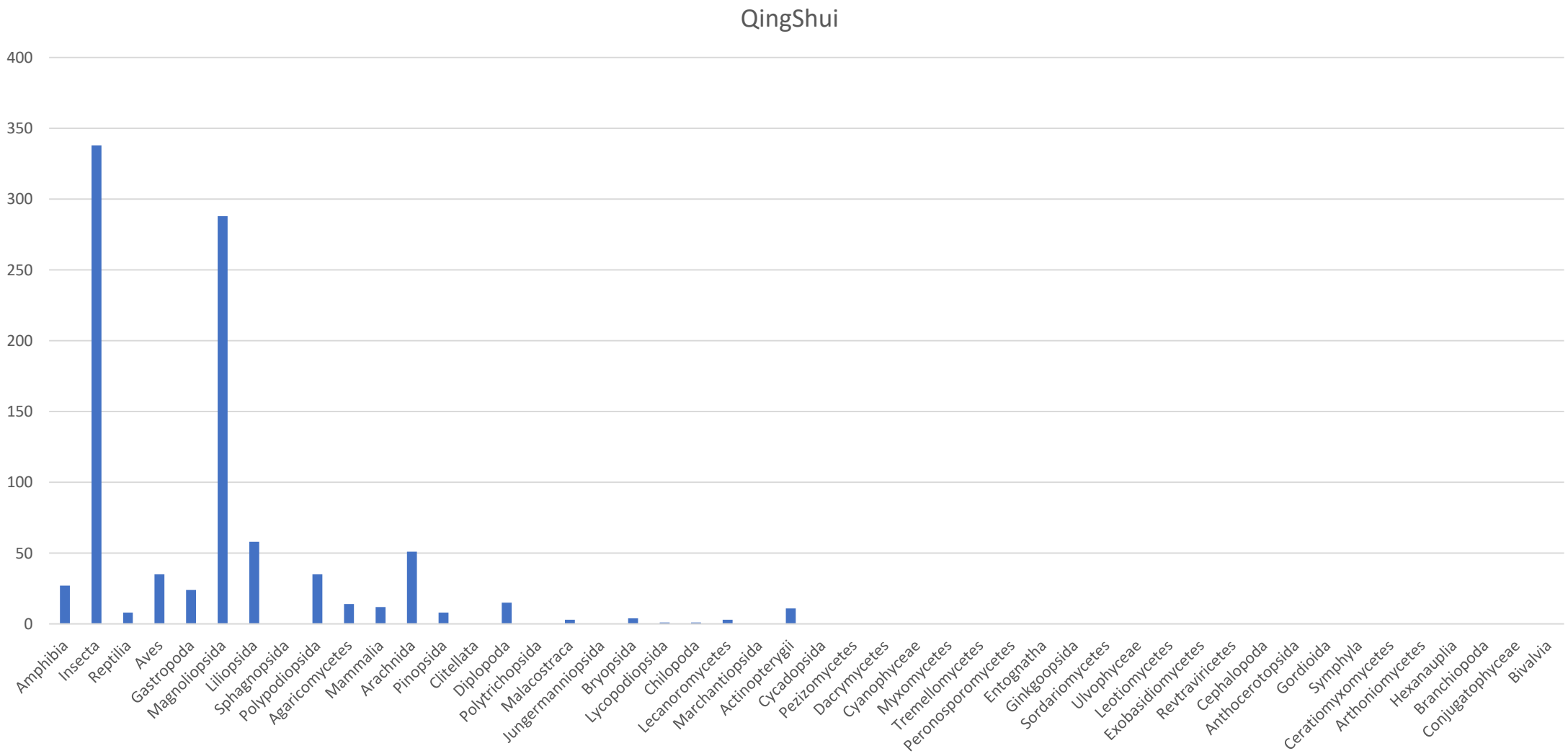
MeiYou - 322


MeiYou
160
140
120
100
80
60
40
20
0
Amphibia
Insecta
Reptilia
Aves
Gastropoda
Magnoliopsida
Liliopsida
Sphagnopsida
Polypodiopsida
Agaricomycetes
Mammalia
Arachnida
Pinopsida
Clitellata
Diplopoda
Polytrichopsida
Malacostraca
Jungermanniopsida
Bryopsida
Lycopodiopsida
Chilopoda
Lecanoromycetes
Marchantiopsida
Actinopterygii
Cycadopsida
Pezizomycetes
Dacrymycetes
Cyanophyceae
Myxomycetes
Tremellomycetes
Peronosporomycetes
Entognatha
Ginkgoopsida
Sordariomycetes
Ulvophyceae
Leotiomycetes
Exobasidiomycetes
Revtraviricetes
Cephalopoda
Anthocerotopsida
Gordioida
Symphyla
Ceratiomyxomycetes
Arthoniomycetes
Hexanauplia
Branchiopoda
Conjugatophyceae
Bivalvia

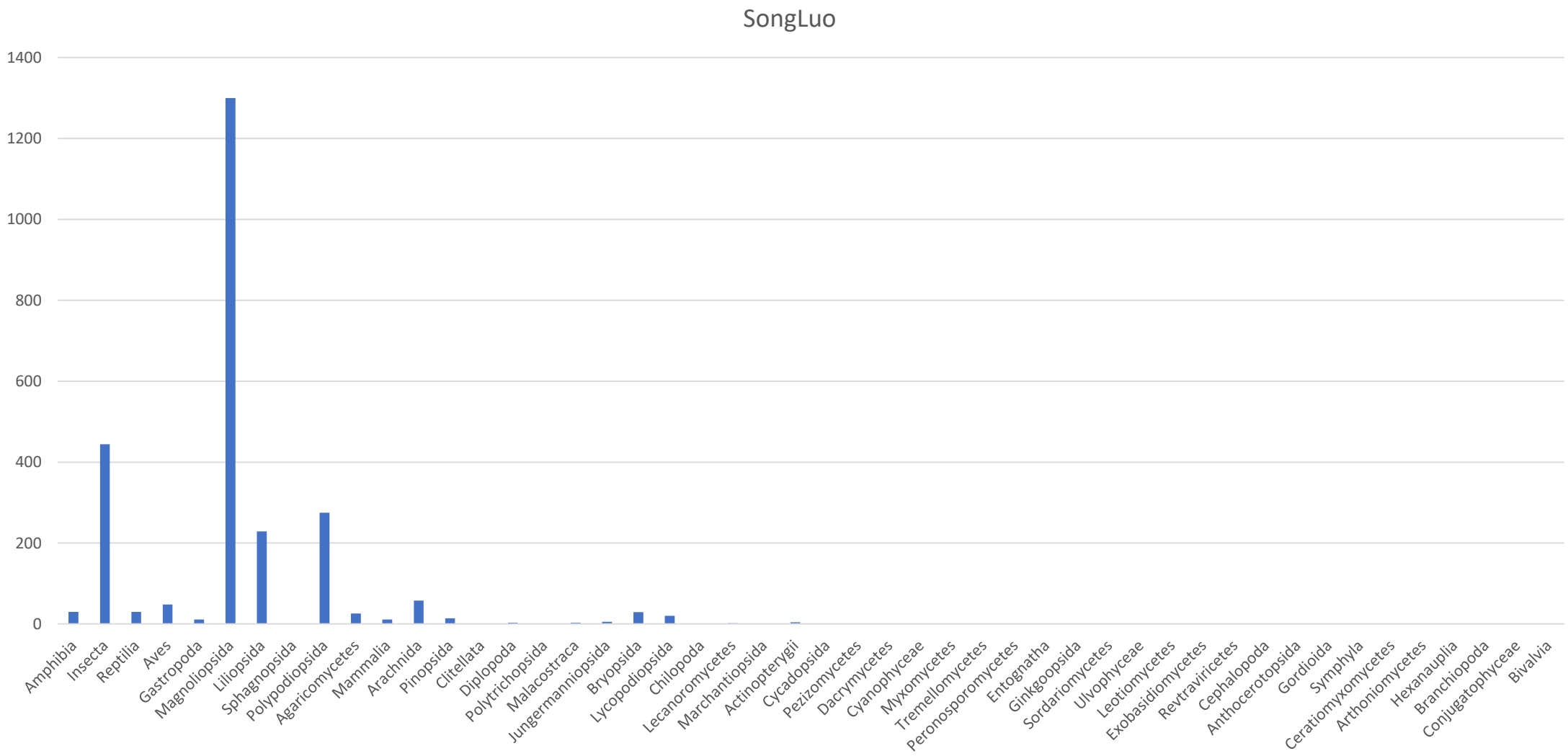
NanShi - 14641



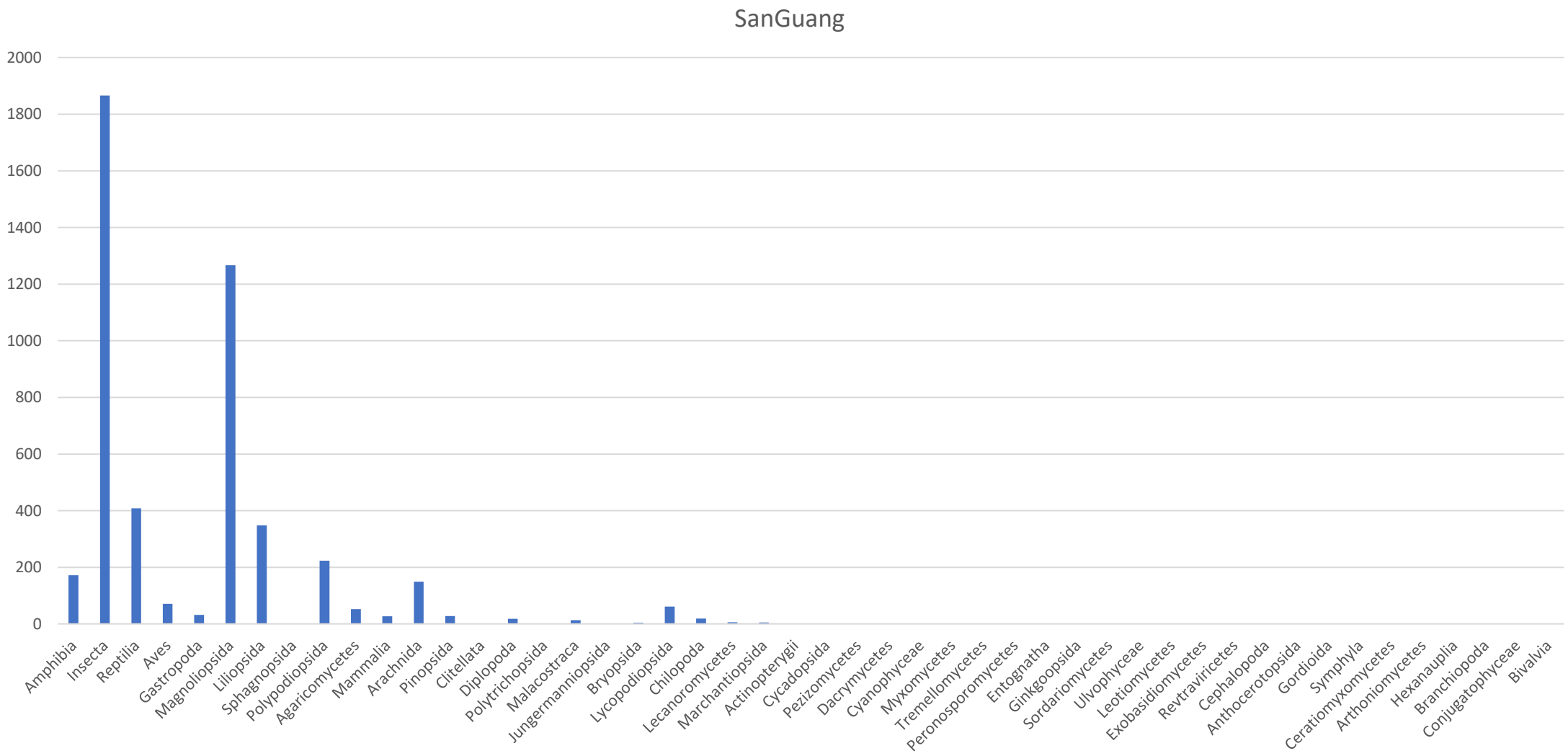
QingShui - 985



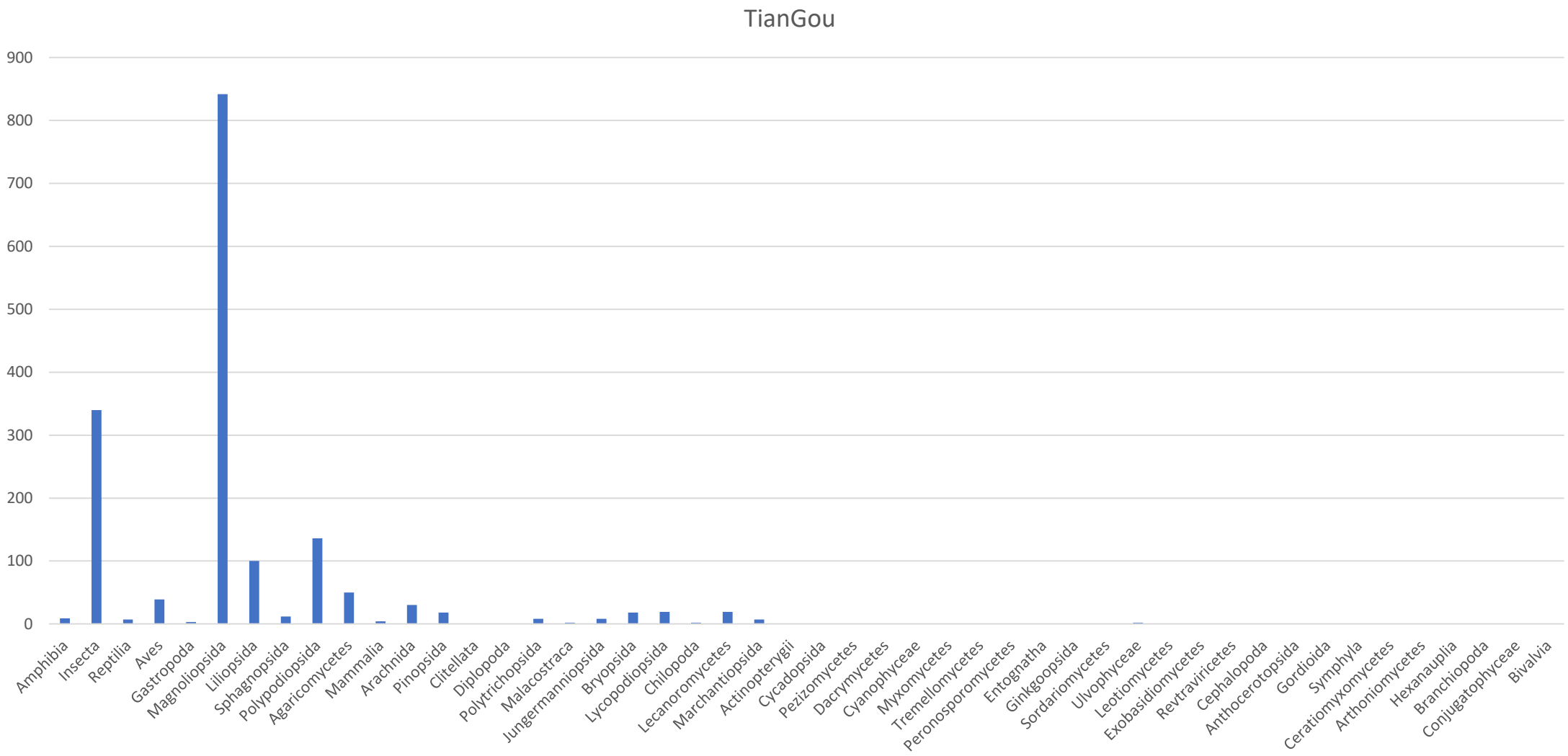
SongLuo - 2786



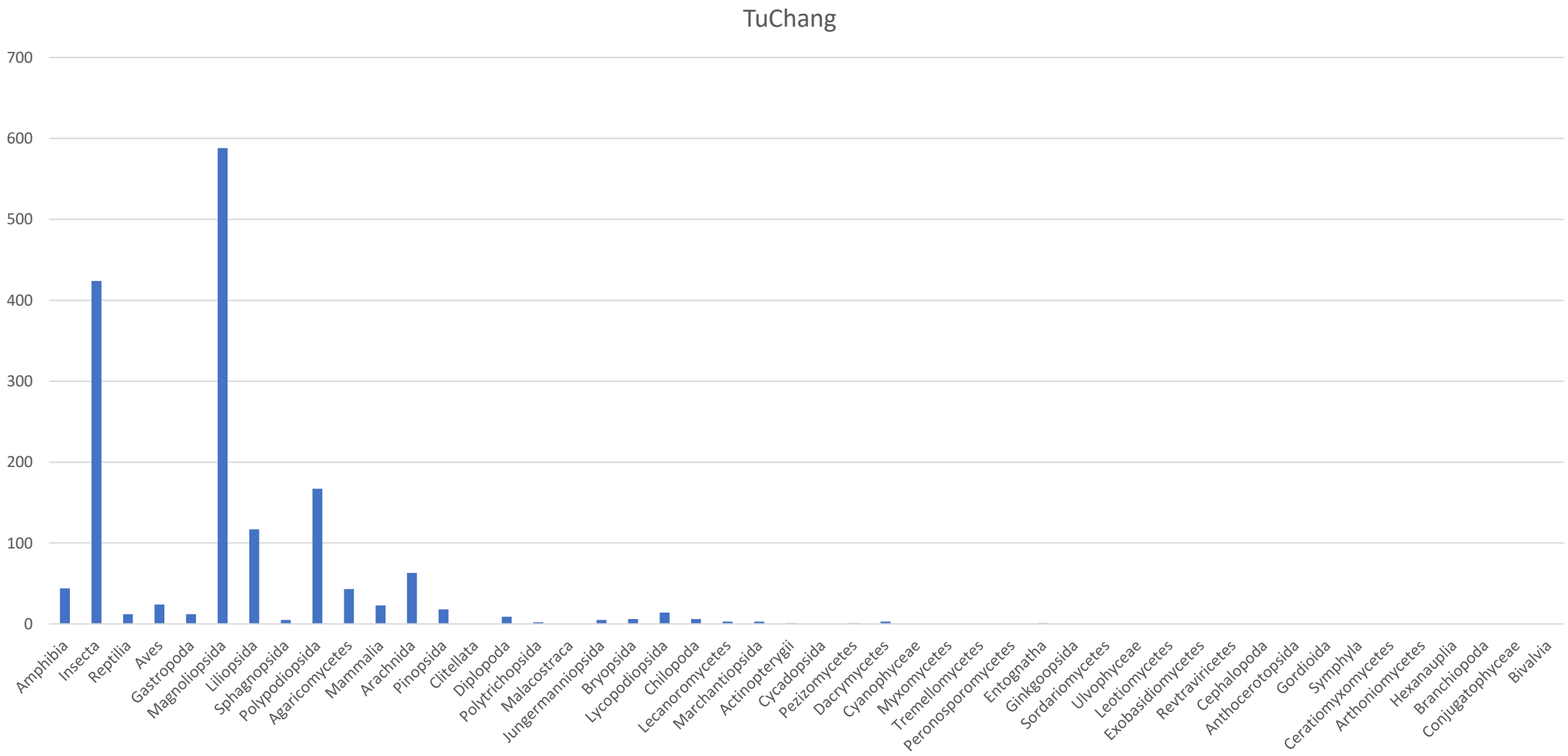
SanGuang - 5068



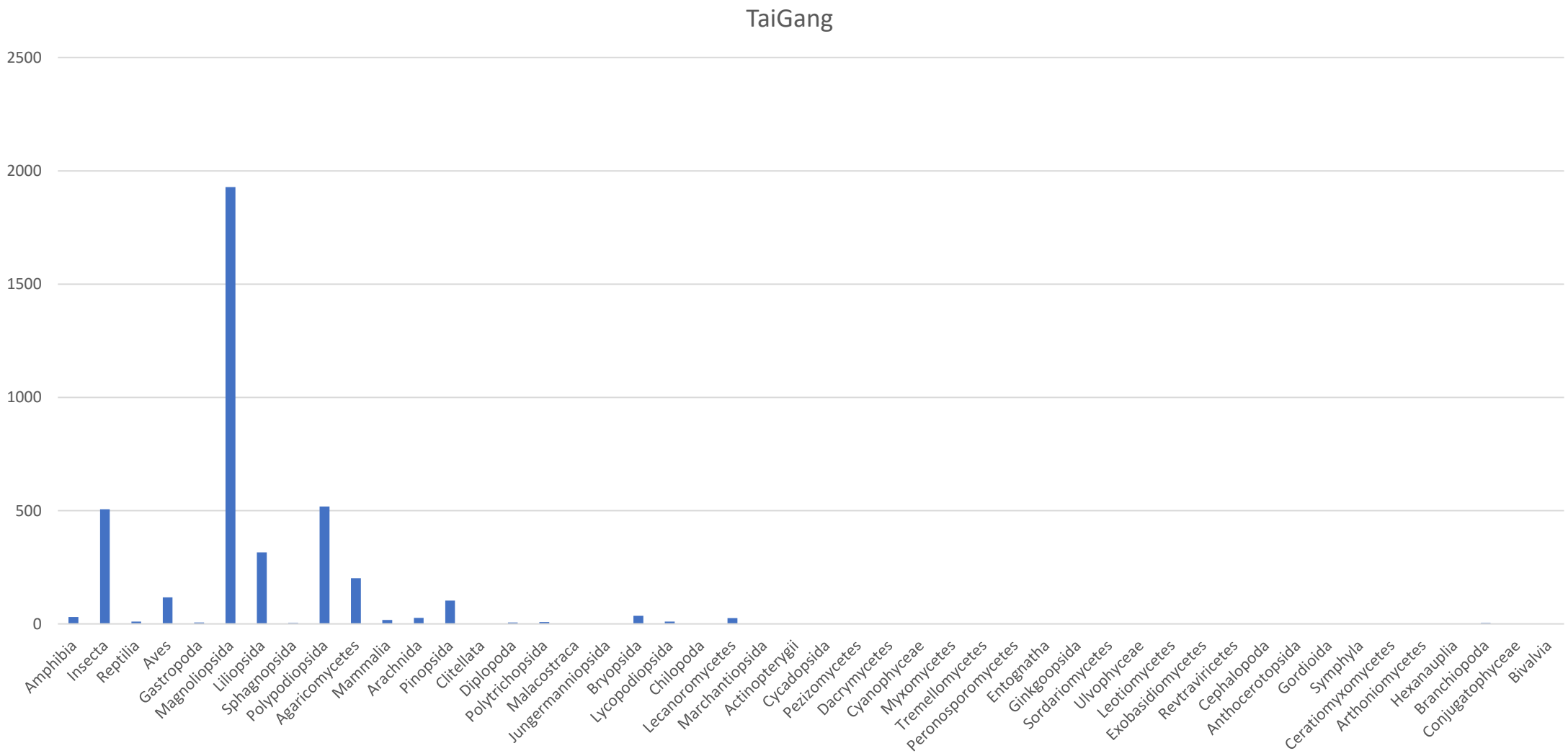
TianGou - 1825



TuChang - 1728



TaiGang - 4077

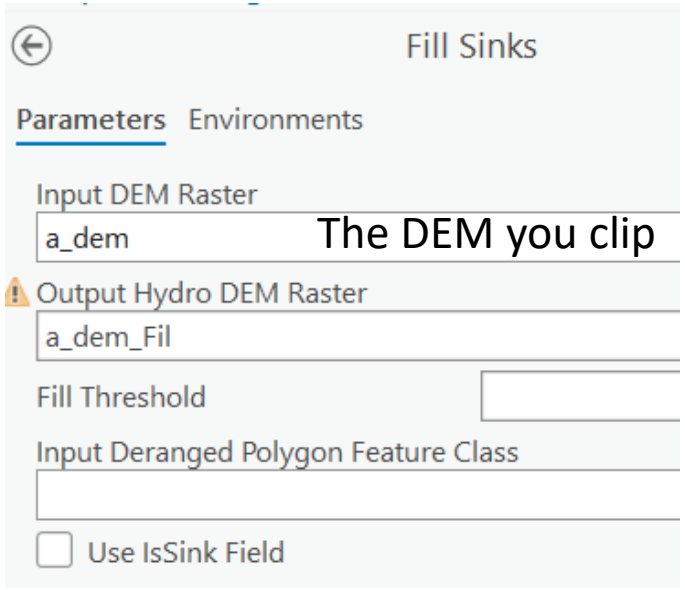


Processes of Drawing Drainage Basins

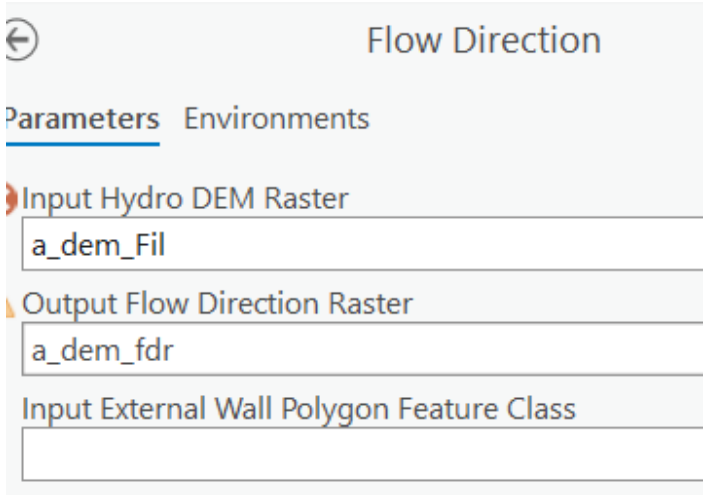
Use ArcGIS pro to draw drainage basins

1. Select and export the tributaries you want.
2. Clip DEM larger than the bounds of all tributaries.
3. Use these functions below to get the drainage basin of each tributary.
4. After these 12 steps you will get the drainage basin of one tributary you choose.
5. Repeat ***3.*** until all of the tributaries are finished.
6. Use “Display XY Data” to convert creature date form csv file to points.
7. Use “Select by location” to separate the creature point by tributaries.
8. Add tributary names into the creature point’s attribute table.
9. Export that attribute table to csv file

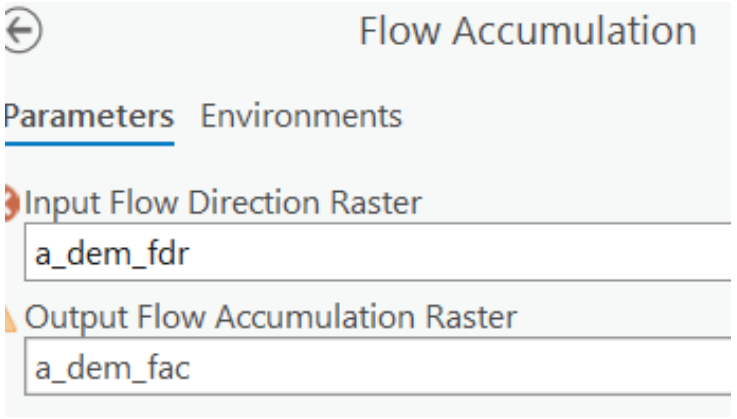
1


Fill Sinks
Parameters
Environments
Input DEM Raster
a_dem
The DEM you clip
Output Hydro DEM Raster
a_dem_Fil
Fill Threshold
Input Deranged Polygon Feature Class
Use IsSink Field

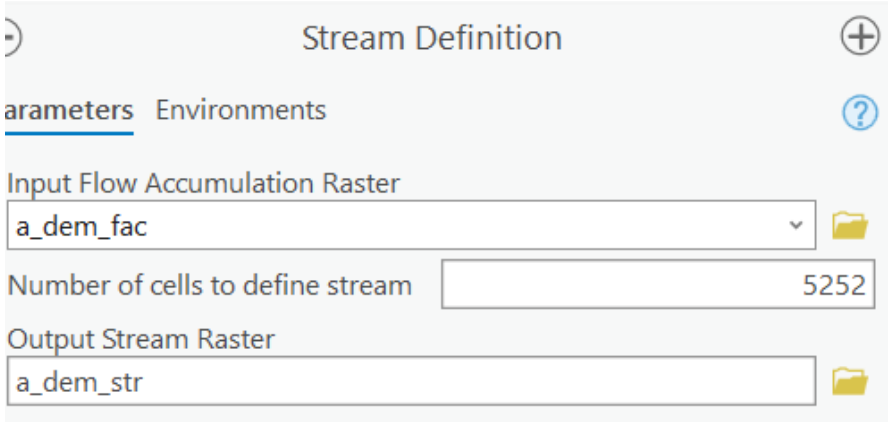
2


Flow Direction
Parameters
Environments
Input Hydro DEM Raster
a_dem_Fil
Output Flow Direction Raster
a_dem_fdr
Input External Wall Polygon Feature Class

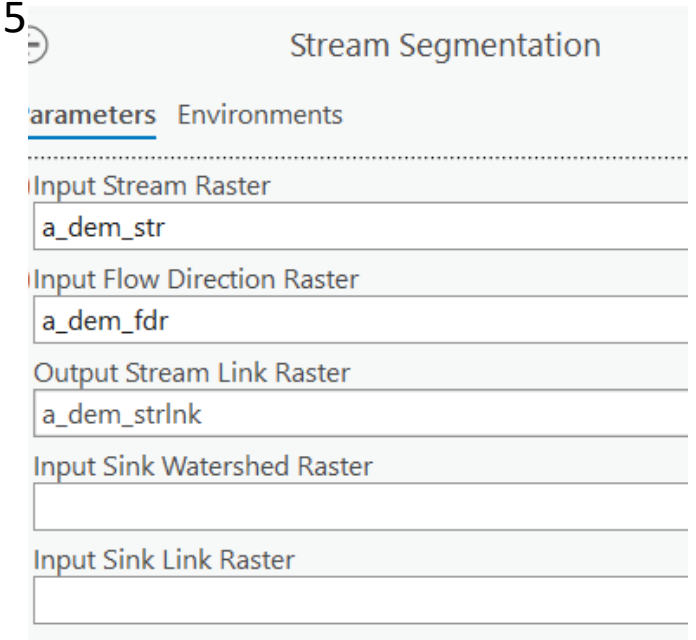
3


Flow Accumulation
Parameters
Environments
Input Flow Direction Raster
a_dem_fdr
Output Flow Accumulation Raster
a_dem_fac

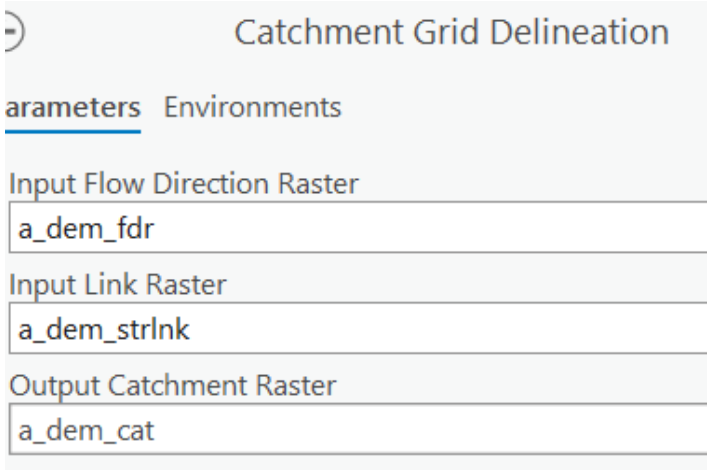
4


Stream Definition
arameters
Environments
Input Flow Accumulation Raster
a_dem_fac
Number of cells to define stream
5252
Output Stream Raster
a_dem_str

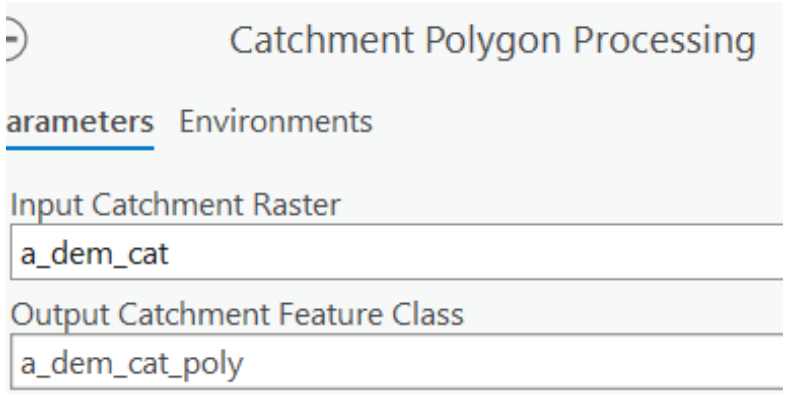
5


Stream Segmentation
arameters
Environments
Input Stream Raster
a_dem_str
Input Flow Direction Raster
a_dem_fdr
Output Stream Link Raster
a_dem_strlnk
Input Sink Watershed Raster
Input Sink Link Raster

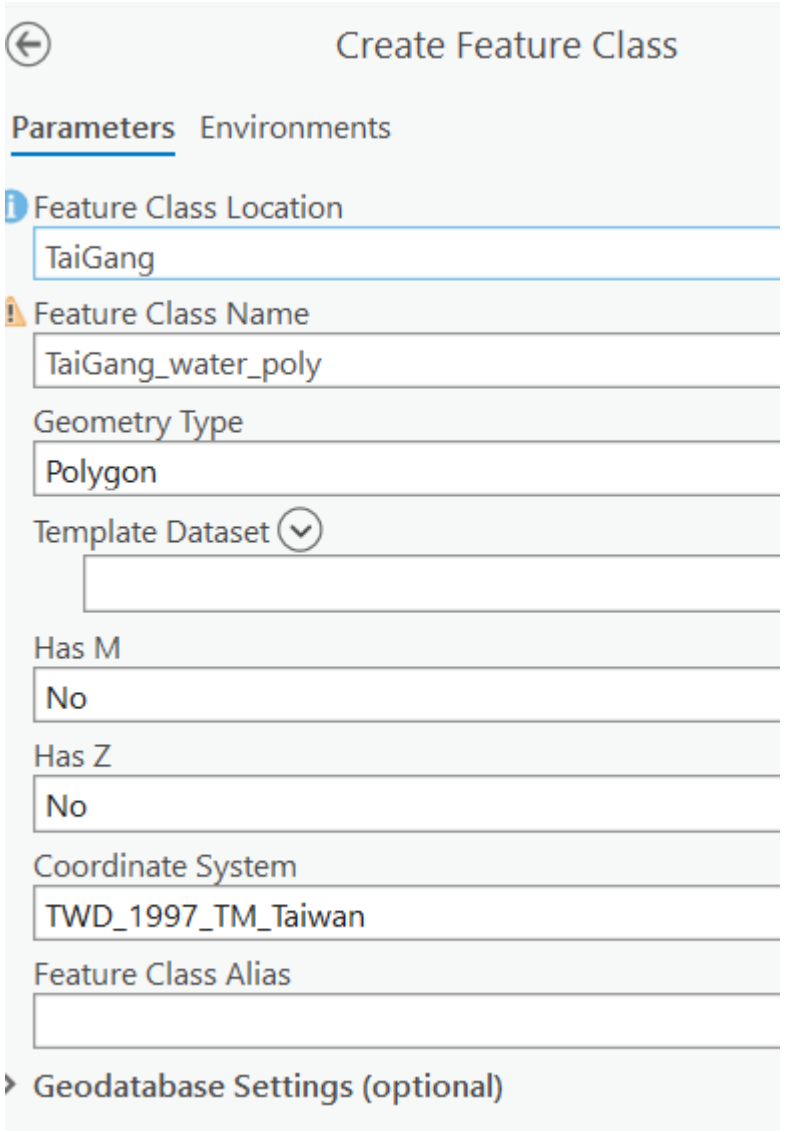
6


Catchment Grid Delineation
arameters
Environments
Input Flow Direction Raster
a_dem_fdr
Input Link Raster
a_dem_strlnk
Output Catchment Raster
a_dem_cat

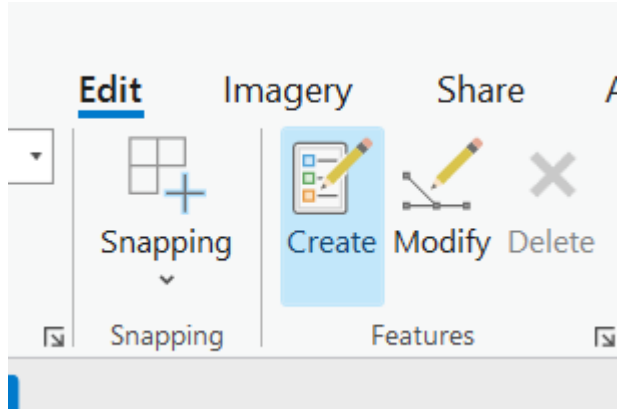
7



8



9



Then draw the

Processes of Doing NMDS

Use Python to processing data (pseudocode)

```
READ RAWDATA
   df_all = pd.read_csv(r'YOUR DATA PATH’)

SEPERATE RIVERS
   df_XXX = df_all[df_all['river'] == "XXX"].reset_index(drop=True)

FIND SPECIES
   species_XXX = df_XXX['scientific'].drop_duplicates().reset_index(drop=True).tolist()

MAKE SPECIES 01 LIST
   list_XXX=[]
   for i in range(len(species_all)):
      if(species_all[i] in species_XXX):
         list_XXX.append(1)
      else:
         list_XXX.append(0)
```

Base on the pseudocode, the output csv file should be like this.

Species name

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	all	Odorrana s	Limnonect	Agathia la	Cyana qua	Lycodon r	Pareas atay	Myophonu	Urocissa c	Actinodura	Delichon c	Trochalopt	Hypsipetes
2	BaoYan	0	0	0	0	0	0	0	0	0	0	0	0
3	CuKeng	1	1	0	0	1	1	0	1	0	0	0	1
4	FanFan	1	0	0	1	1	0	1	0	0	0	0	1
5	FuBuEr	0	0	0	0	0	0	0	0	0	0	0	0
6	MeiLuo	0	0	0	0	0	0	0	0	0	0	0	0
7	MeiYou	0	0	0	0	0	0	1	0	0	1	0	0
8	NanShi	1	1	1	1	1	1	1	1	0	0	0	1
9	QingShui	0	0	1	0	0	0	0	0	0	0	0	0
10	SanGuang	1	0	0	0	1	1	0	0	0	0	0	1
11	SongLuo	1	1	0	0	1	0	0	1	0	0	0	1
12	TaiGang	1	0	0	0	0	0	1	0	1	0	0	1
13	TianGou	0	0	0	0	1	0	1	0	1	1	1	0
14	TuChang	1	0	0	0	1	0	1	1	0	0	0	0

Tributary name

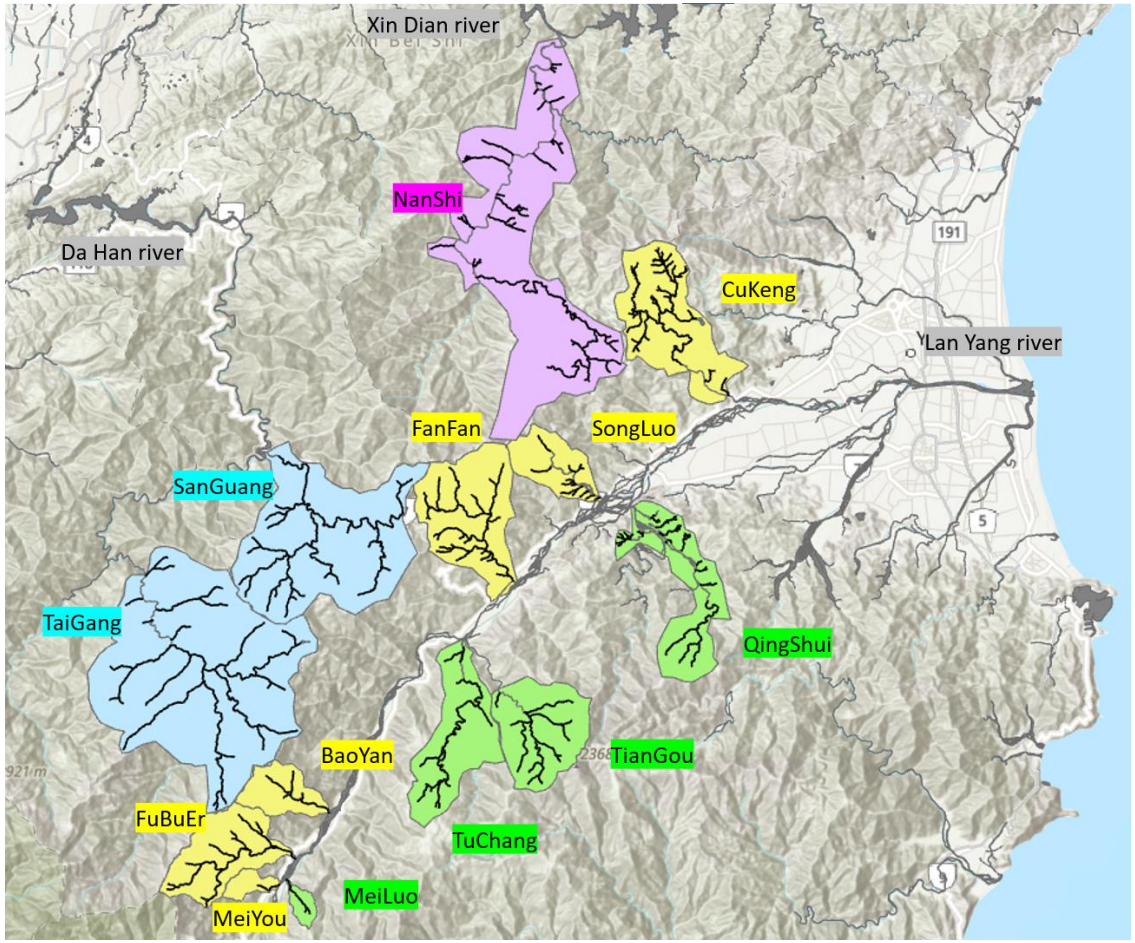
If there exist the species in the tributary, put 1.
If not, put 0.

Refer to the map to make group file.

L: left tributary

R: right tributary

O: others



	A	B
1	Sample	Group
2	BaoYan	L
3	CuKeng	L
4	FanFan	L
5	FuBuEr	L
6	MeiLuo	R
7	MeiYou	L
8	NanShi	O
9	QingShui	R
10	SanGuang	O
11	SongLuo	L
12	TaiGang	O
13	TianGou	R
14	TuChang	R
15		

Run these code with the organized csv file in RStudio, then You will get the NMDS result.

```
library(ggplot2)
library(vegan)
library(ggforce)

# read data
data_LAN <- read.csv("data1106.csv", header = T, row.names = 1)
dfGroup <- read.csv("group.csv", header = T, row.names = 1)

# do NMDS
dfNmds<-metaMDS(data_LAN,distance="bray",k = 2, trymax = 100)

# form the data
data = data.frame(dfNmds$points)
data$group = dfGroup$Group

ggplot(data,aes(x = MDS1, y = MDS2, color = group, group = group, fill = group))+
  geom_point(size=2)+
  theme_classic()+
  stat_ellipse( geom = "polygon", level = 0.95, alpha=0.3)+
  geom_text( aes(label=rownames(data)), vjust=1.5, size=2.5, color = "black")+
  labs( subtitle = paste("stress=",round(dfNmds$stress,3),sep=""))
```