Article

An algorithm for calculation of degree distribution and detection of network type: with application in food webs

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Abstract
In present study a Java algorithm to calculate degree distribution and detect network type was presented. Some indices, e.g., aggregation index, coefficient of variation, skewness, etc., were first suggested for detecting network type. Network types of some food webs reported in Interaction Web Database were determined using the algorithm. The results showed that the degree of most food webs was power law or exponentially distributed and they were complex networks. Different from classical distribution patterns (bionomial distribution, Poisson distribution, and power law distribution, etc.), both network type and network complexity can be calculated and compared using the indices above. We suggest that they should be used in the network analysis. In addition, we defined E, $E=s^2-\bar{u}$, where $\bar{u}$ and s^2 is mean and variance of degree respectively, as the entropy of network. A more complex network has the larger entropy. If $E \leq 0$, the network is a random network and, it is a complex network if $E>0$.

Keywords network; food web; type; degree distribution; aggregation indices; entropy; algorithm; Java.

1 Introduction

The food web is a set of species connected by trophic relations. It is an ecological network made of interactive species. Biodiversity, ecosystem structure and function, etc., can be represented by food webs. There are two kinds of food webs, i.e., the one with autotrophic species as base species and the one with scavenger animals as base species (Gonenc et al., 2007). The complexity and trophic levels of food web determine the stability, resilience and robustness of the community. An ecosystem resists the extinction of species if its food web is complex enough. The species loss in food web would at some extent detriment the stability of ecosystem.

Food webs have long been the center of ecological studies. They began with text and table expression and then linear and spatial expression. As the emerging of large numbers of algorithms and software, the studies of network structure are now becoming the focus of food webs. These algorithms and software have been used to explore the ecosystem stability and robustness. For example, they are used to study degree distribution, connectance and network size (Dunne et al., 2002). Odum (1983) pointed out that the community stability could be measured by energy path in the food web. MacArthur (1955) thought that stability may be increased by the increase of links in the food web. Pimm et al. (1991) have discussed effects of different models of food webs on ecosystem structure, stability and robustness. It was found that the mechanism of evolution and population size will affect food web topology (Rossberg et al., 2005). In addition, habitat destruction and climate change are likely to cause the extinction of key species. Once key species extinct, the robustness of food web will be profoundly affected (Allesina et al., 2009).

The networks, including food webs, met in last decade become more and more complex. There are usually large numbers of vertices and links in a complex network (Ibrahim et al., 2011; Goemann et al., 2011; Kuang and Zhang, 2011; Martínez-Antonio, 2011; Paris and Bazzoni, 2011; Rodriguez and Infante, 2011; Tacutu et al., 2011). It is hard to analyze such networks by using classical methods or algorithms. Graph theory, optimization, statistics, and stochastic processes, etc., are becoming the scientific basis and effective tools for studying complex networks (Ferrarini, 2011; Zhang, 2011a, b; Zhang, 2012). Degree distribution and network type is one of the research focuses based on those tools and methods. In this aspect some ecological networks have been proved to be scale-free networks (Zhang, 2011a).

The present study aimed to present a Java algorithm to calculate degree distribution and detect network type. Some indices were first suggested by us for detecting network type. Network types of food webs reported in Interaction Web Database were determined using the algorithm.

2 Materials and Methods

2.1 Methods

Suppose that the portion of nodes with k-degree is p_k, the degree will thus be a random variable and its distribution is degree distribution. It has found that in the random network, degree distribution is binomial distribution, and its limit model is Poisson distribution. In a random network, the majority of vertices have the same degree with the average. In the complex network, degree distribution is a power law distribution, and the network is called a scale-free network (Barabasi and Albert, 1999; Barabasi, 2009). A property of the scale-free network is that the structure and the evolution of network are inseparable. Scale-free networks constantly change because of the arrival of nodes and links (Barabasi and Albert, 1999).

In present algorithm, in addition to power law distribution, binomial distribution, Poisson distribution, and exponential distribution (Zhang, 2012), some other indices and methods were also used to detect network type:

(1) Skewness. This index is used to measure the degree of skewness of a degree distribution relative to the symmetric distribution, for example, the normal distribution (S=0) (Sokal and Rohlf, 1995):

$$S=v\sum(d_i-\bar{u})^2/[(v-1)(v-2)s^3].$$

where $\bar{u}$, s^2: mean and variance of degree; v: number of nodes; d_i: degree of node i, i=1,2,…,v. The smaller the skewness is, the more complex the network is.

(2) Coefficient of variation. In a random network, the majority of nodes have the same degree as the average. The coefficient of variation, H, can be used to describe the type of a network (Zhang, 2007):

$$H=s^2/\bar{u},$$
$$\bar{u}=\sum d_i/v,$$
$$s^2=\sum(d_i-\bar{u})^2/(v-1),$$

where $\bar{u}$, s^2: mean and variance of degree; v: number of nodes; d_i: the degree of node i, i=1,2,...,v. The network is a random network, if $H\leq1$. Calculate $\chi^2=(v-1)H$, and if $\chi_{1-\alpha}^2(v-1)<\chi^2<\chi_{\alpha}^2(v-1)$, the network is a complete random network. It is a complex network, if $H>1$, and to some extent, network complexity increases with H.

Here we define E, $E=s^2-\bar{u}$, as the entropy of network. A more complex network has the larger entropy. If $E\leq0$ the network is a random network and it is a complex network if $E>0$.

(3) Aggregation index. Network type can be determined by using the following aggregation index (Zhang, 2007):

$$H=v*\sum d_i(d_i-1)/[\sum d_i(\sum d_i-1)].$$

The network is a random network, if $H\leq 1$. Calculate $\chi^2=H(\sum d_i-1)+v-\sum d_i$, and if $\chi^2<\chi_\alpha^2(v-1)$, the network is a complete random network. It is a complex network if $H>1$, and network complexity increases with H.

The following code is the Java algorithm, netType, to calculate degree distribution and detect network type:

```
/*v: number of vertice; d[1-v][1-v]: adjacency matrix to reflect the feature of edges, e.g., dij=dji=0 means no edge between vertice i and j; dij=-dji, and |dij|=1, means there is an edge between vertice i and j; dij=dji=2, means there are parallel edges between vertice i and j; dii=3 means there is a self-loop for vertex i; dii=4 means isolated vertex; dii=5 means isolated vertex i with self-loop. */
public class netType {
public static void main(String[] args){
int i,j,v,n;
if (args.length!=1)
System.out.println("You must input the name of table in the database. For example, you may type the following in the command window: java netType nettype, where nettype is the name of table. Graph is stored in the table using two arrays listing and was transformed to adjacency matrix by method adjMatTwoArr.");
String tablename=args[0];
readDatabase readdata=new readDatabase("dataBase",tablename, 3);
n=readdata.m;
int a[]=new int[n+1];
int b[]=new int[n+1];
int c[]=new int[n+1];
int d[][]=new int[n+1][n+1];
for(i=1;i<=n;i++) {
a[i]=(Integer.valueOf(readdata.data[i][1])).intValue();
b[i]=(Integer.valueOf(readdata.data[i][2])).intValue();
c[i]=(Integer.valueOf(readdata.data[i][3])).intValue(); }
adjMatTwoArr adj=new adjMatTwoArr();
adj.dataTrans(a,b,c);
v=adj.v;
for(i=1;i<=v;i++)
for(j=1;j<=v;j++) d[i][j]=adj.d[i][j];
netType(v,d); }
public static void netType(int v, int d[][]) {
int i,j,k,l,m,rr,ty,r;
double it,pp,ss,qq,k1,k2,chi,mean,var,hr,h,skew;
int deg[]=new int[v+1];
int p[]=new int[v+1];
double fr[]=new double[v+1];
double pr[]=new double[v+1];
for(i=1;i<=v;i++) {
deg[i]=0;
for(j=1;j<=v;j++) {
if (Math.abs(d[i][j])==1) deg[i]++;
if ((d[i][j]==2) | (d[i][j]==3) | (d[i][j]==5)) deg[i]+=2; } }
for(i=1;i<=v;i++) p[i]=i;
for(i=1;i<=v-1;i++) {
k=i;
for(j=i;j<=v-1;j++) if (deg[j+1]>deg[k]) k=j+1;
l=p[i];
p[i]=p[k];
p[k]=l;
m=deg[i];
deg[i]=deg[k];
deg[k]=m; }
pp=qq=0;
System.out.println("Ranks          Vertice          Degrees\n");
for(i=1;i<=v;i++) {
System.out.println(i+"     "+p[i]+"     "+deg[i]);
pp+=deg[i];
```

```
qq+=deg[i]*(deg[i]-1); }
System.out.println();
rr=10;
it=(deg[1]-deg[v])/(double)rr;
for(i=1;i<=10;i++) {
fr[i]=0;
for(j=1;j<=v;j++)
if ((deg[j]>=(deg[v]+(i-1)*it)) & (deg[j]<(deg[v]+i*it))) fr[i]++; }
System.out.println("Frequency distribution of degrees:");
for(i=1;i<=10;i++)
System.out.print(deg[v]+it/2.0+(i-1)*it+"    ");
System.out.println();
for(i=1;i<=10;i++)
System.out.print(fr[i]/v+"    ");
System.out.println("\n");
mean=pp/v;
ss=0;
for(i=1;i<=v;i++)
ss+=Math.pow(deg[i]-mean,2);
var=ss/(v-1);
skew=v/((v-2)*Math.sqrt(var));
System.out.println("Skewness of degree distribution: "+skew+"\n");
h=v*qq/(pp*(pp-1));
System.out.println("Aggregation index of the network: "+h);
if (h<=1) System.out.println("It is a random network.\n");
if (h>1) System.out.println("It is a complex network.\n");
h=var/mean;
System.out.println("Variation coefficient H of the network: "+h);
System.out.println("Entropy E of the network: "+(var-mean));
if (h<=1) System.out.println("It is a random network.\n");
if (h>1) System.out.println("It is a complex network.\n");
ty=1;        //Binomial distri., pr= Crn pr qn-r, r=0,1,2,…, n;
ss=0;
for(i=0;i<=rr-1;i++) ss+=i*fr[i+1];
pp=ss/(v*(rr-1));
qq=1-pp;
pr[0]=Math.pow(qq,rr-1);
for(i=1;i<=rr-1;i++) pr[i]=(rr-i)*pp*pr[i-1]/(i*qq);
chi=xsquare(v, rr, pr, fr);
System.out.println("Binomial distribution Chi-square="+chi);
System.out.println("Binomial p="+pp);
k1=20.09;
coincidence(ty, k1, chi);
ty=2;
//Poisson distri., pr = e-λλr/r! , r=0,1,2,…
pr[0]=Math.exp(-mean);
for(r=1;r<=rr-1;r++) pr[r]=mean/r*pr[r-1];
chi=xsquare(v, rr, pr, fr);
System.out.println("Poisson distribution chi-square="+chi);
System.out.println("Poisson lamda="+mean);
k1=20.09;
coincidence(ty, k1, chi);
ty=3;      //Exponential distri., F(x) =1-e-λx, x≥0
chi=0;
for(i=1;i<=10;i++) {
k1=deg[v]+it/2.0+(i-1)*it;
k2=deg[v]+it/2.0+i*it;
pp=v*(Math.exp(-k1/mean)-Math.exp(-k2/mean));
chi+=Math.pow(fr[i]-pp,2)/pp; }
System.out.println("Exponential distribution lamda="+1.0/mean);
k1=20.09;
coincidence(ty, k1, chi);
powerDistr(v, deg); }
public static double xsquare(int v, int rr, double p[], double h[]) {
double hk,ss=0;
for(int i=0;i<=rr-1;i++) {
hk=p[i]*v;
if (p[i]==0) hk=h[i+1];
ss+=Math.pow(p[i]*v-h[i+1],2)/hk;}
return ss;
```

```
}
public static void coincidence(int ty, double k1, double ss) {
if (ss<=k1)
if (ss>=0) {
if (ty==1) System.out.println("Degrees are binomially distributed.\n");
if (ty==2) System.out.println("Degrees are Poisson distributed.\n");
if (ty==3) System.out.println("Degrees are exponentially distributed.\n");
if ((ty==1) | (ty==2)) System.out.println("It is a random network"); }
if ((ss>k1) & ((ty==1) | (ty==2))) System.out.println("It is likely not a random network\n");
if ((ss>k1) & (ty==3)) System.out.println("It is not an exponential network\n");
}
public static void powerDistr(int v, int x[]) {
//Power law distri., f(x)=x-α, x≥xmin
int i,j,k,n,r,xmin;
double xmax,a,alpha,dd,maa;
int xminn[]=new int[v+1];
int xmins[]=new int[v+1];
double z[]=new double[v+1];
double zz[]=new double[v+1];
double cx[]=new double[v+1];
double cf[]=new double[v+1];
double dat[]=new double[10000];
k=1;
xminn[1]=x[1];
for(i=1;i<=v;i++) {
n=0;
for(j=1;j<=k;j++)
if (x[i]!=xminn[j]) n++;
if (n==k) {
k++;
xminn[k]=x[i]; } }
for(i=1;i<=k-1;i++) xmins[i]=xminn[i];
for(i=1;i<=v-1;i++) {
k=i;
for(j=i;j<=v-1;j++)
if (x[j+1]>x[k]) k=j+1;
r=x[i];
x[i]=x[k];
x[k]=r; }
for(i=1;i<=v;i++) z[i]=x[v-i+1];
for(r=1;r<=v;r++) {
xmin=xmins[r];
n=0;
for(i=1;i<=v;i++)
if (z[i]>=xmin) {
n++;
zz[n]=z[i]; }
maa=0;
for(i=1;i<=n;i++) maa+=Math.log(zz[i]/xmin);
a=n/maa;
for(i=0;i<=n-1;i++) cx[i+1]=i*1.0/n;
for(i=1;i<=n;i++) cf[i]=1-Math.pow(xmin/zz[i],a);
dat[r]=0;
for(i=1;i<=n;i++) {
cf[i]=Math.abs(cf[i]-cx[i]);
if (cf[i]>dat[r]) dat[r]=cf[i]; } }
dd=1e+100;
for(i=1;i<=v;i++)
if (dat[i]<dd) dd=dat[i];
for(i=1;i<=v;i++)
if (dat[i]<=dd) {
k=i;
break; }
xmin=xmins[k];
n=0;
for(i=1;i<=v;i++)
if (x[i]>=xmin) {
n++;
zz[n]=x[i]; }
maa=0;
```

```
for(i=1;i<=n;i++) maa+=Math.log(zz[i]/xmin);
alpha=1+n/maa;
alpha=(n-1)*alpha/n+1.0/n;
System.out.println("Power law distribution KS D value="+dd);
if (dd<(1.63/Math.sqrt(n))) System.out.println("Degrees are power law distributed, it is a scale-free complex network");
System.out.println("Power law alpha="+alpha);
System.out.println("Power law xmin="+xmin); }
}
```

2.2 Data source

Interaction Web Database (National Center for Ecological Analysis and Synthesis, 2011; http://www.nceas.ucsb.edu/interactionweb/) was chosen as the data source of the present study. Interaction Web Database contains seven food webs, namely Anemone-Fish, Host-Parasite, Plant-Ant, Plant-Herbivore, Plant-Pollinator, Plant- Seed disperser, and Predator-Prey sub-webs. For each web, the species with corresponding inetrspecific relationship but not all species in the ecosystem or community, were included. Each of seven food webs was used to calculate degree distribution and detect network type.

For Anemone-Fish web, we used the data of Fautin and Allen (1997) and Ollerton et al. (2007), as indicated in Table 3. The data for other webs were chosen as follows:

Host-Parasite webs: we used the data for Canadian freshwater fish and their parasites (Arthur et al., 1976), which were from the investigation to seven water systems. Moreover, the data from Cold Lake (Leong et al., 1981; 10 hosts and 40 parasites) and Parsnip River (Arai et al.,1983; 17 hosts and 53 parasites) were also used.

Plant-Ant web: the data of Bluthgen (2004) from tropical rain forests, Australia, were used. There ware 51 plants and 41 ants in this web.

Plant-Pollinator webs: we used a set of data collected from KwaZulu-Natal, South Africa (Ollerton et al., 2003; 9 plants and 56 pollinators), and the data from Canada (Small, 1976; 13 plants and 34 pollinators)

Plant-Herbivore web: the data from Texas, USA (Joern,1979; 54 plants and 24 herbivores) were used.

Predator-Prey webs: four sets of data (Berwick, Catlins, Coweeta and Venlaw) were used. The major species included algae, fish, arthropods and amphibians.

Plant-Seed disperser webs: two sets of data were used. One from a forest in Papua New Guinea (Beehler, 1983; 31 plants and 9 birds), and one from a tropical forest in Panama (Poulin et al., 1999; 13 plants and 11 birds).

A typical raw data in Interaction Web Database is indicated in Table 1.

Table 1 An example of the data of Interaction Web Database.

Species	Unidentified detritus	Terrestrial invertebrates	Plant material	*Achnanthes lanceolata*
Unidentified detritus	0	0	0	0
Terrestrial invertebrates	0	0	1	0
Plant material	0	1	0	0
Achnanthes lanceolata	0	0	0	0

General information In this paper, the authors examined the feeding patterns of grasshoppers from two arid grassland communities in Trans-Pecos, Texas. The studies took place from May until November in 1974 and 1975.

Date type The authors recorded the identities of insect and plant species and their interactions. Data are presented as a binary interaction matrix, in which cells with a "1" indicate an interaction between a pair of species, and a "0" indicates no interaction.

In Table 1, the values 1 and 0 represent having or not having interspecific trophic relationship. The values neither 1 nor 0 represent frequencies and these values were transformed to 1 in present study. Table 1 should be transformed to the format needed by the Java algorithm above, as indicated in Table 2.

Table 2 The data transformed from Table 1.

ID of Taxon 1	ID of Taxon 2	Value
1	2	1
1	3	1
2	3	1
2	4	1
3	4	1

3 Results

The data of Anemone-Fish web is indicated in Table 3.

Table 3 Species and ID of Anemone-Fish web.

Genera	Species	ID	Genera	Species	ID
Amphiprion spp.	Akallopisos	1	Amphiprion spp.	percula	19
Amphiprion spp.	Akindynos	2	Amphiprion spp.	perideraion	20
Amphiprion spp.	Allardi	3	Amphiprion spp.	polymnus	21
Amphiprion spp.	Bicinctus	4	Amphiprion spp.	rubrocinctus	22
Amphiprion spp.	chrysogaster	5	Amphiprion spp.	sandaracinos	23
Amphiprion spp.	chrysopterus	6	Amphiprion spp.	sebae	24
Amphiprion spp.	clarkii	7	Amphiprion spp.	tricinctus	25
Amphiprion spp.	ephippium	8	Premnas	biaculeatus	26
Amphiprion spp.	frenatus	9	Heteractis	crispa	27
Amphiprion spp.	fuscocaudatus	10	Entacmaea	quadricolor	28
Amphiprion spp.	latezonatus	11	Heteractis	magnifica	29
Amphiprion spp.	latifasciatus	12	Stichodactyla	mertensii	30
Amphiprion spp.	leucokranos	13	Heteractis	aurora	31
Amphiprion spp.	mccullochi	14	Stichodactyla	gigantea	32
Amphiprion spp.	melanopus	15	Stichodactyla	haddoni	33
Amphiprion spp.	nigripes	16	Macrodactyla	doreensis	34
Amphiprion spp.	ocellaris	17	Heteractus	malu	35
Amphiprion spp.	omanensis	18	Cryptodendrum	adhaesivum	36

Table 3 is transformed to the data type needed by the Java algorithm, as indicated in Table 4.

Table 4 A data type of Anemone-Fish web.

ID of taxon 1	ID of taxon 2	Value	ID of taxon 1	ID of taxon 2	Value
1	27	1	7	32	1
1	28	1	7	34	1
1	29	1	8	28	1
1	30	1	8	30	1
1	31	1	8	31	1
1	32	1	9	27	1
1	33	1	9	28	1
1	34	1	9	29	1
1	35	1	9	32	1
1	36	1	10	29	1
2	27	1	10	30	1
2	28	1	10	32	1
2	29	1	11	27	1
2	30	1	11	29	1
2	31	1	11	32	1
2	32	1	12	27	1
2	33	1	12	29	1
3	27	1	12	30	1
3	28	1	13	27	1
3	29	1	13	33	1
3	30	1	13	34	1
3	31	1	14	27	1
3	33	1	14	28	1
3	34	1	14	33	1
4	29	1	15	28	1
4	30	1	15	32	1
4	31	1	16	27	1
4	33	1	16	30	1
5	27	1	17	29	1
5	28	1	17	30	1
5	29	1	18	27	1
5	30	1	18	28	1
5	31	1	19	28	1
5	32	1	20	30	1
6	27	1	21	27	1
6	28	1	22	30	1
6	30	1	23	28	1
6	31	1	24	29	1
7	27	1	25	33	1
7	29	1	26	28	1

Some results running the Java algorithm for Anemone-Fish web are as follows:

Skewness of degree distribution: 0.2739383901373063
Aggregation index of the network: 1.519811320754717
It is a complex network.
Variation coefficient H of the network: 3.361428571428571
It is a complex network.
Binomial distribution Chi-square=84779.33198479559
Binomial p=0.2222222222222222
It is likely not a random network
Poisson distribution chi-square=462.75941519476396
Poisson lamda=4.444444444444445
It is likely not a random network

Exponential distribution lamda=0.22499999999999998
Degrees are exponentially distributed.
Power law distribution KS D value=0.0
Degrees are power law distributed, it is a scale-free complex network
Power law alpha=NaN
Power law xmin=14

It is obvious that the food web is a complex network.
The results for all food webs are listed in Table 5 and 6.

Table 5 Summary of results for calculation of degree distribution and network type.

	Anemone-Fish web	Host-Parasite webs			Plant-Ant web	Plant-Pollinator webs	
Data source	Anemone fish	Aishihik Lake	Cold Lake	Parsnip River	Bluthgen, 2004	Ollerton et al,2003	Small, 1976
Skewness of degree distribution	0.2739	0.2524	0.2822	0.2404	0.1626	0.2065	0.2330
Aggregation index of the network	1.5198	1.6913	1.7425	1.6709	1.8597	3.1461	1.3843
Variation coefficient of the network	3.3614	4.0615	3.7425	4.0627	6.3754	7.8742	3.3478
Binomial distribution Chi-square	84779.33	316459.4	1500517	53631.9	346819.3	156.63	536.45
Binomial p	0.2222	0.2099	0.1556	0.1905	0.1715	0.0325	0.2577
Poisson distribution Chi-square	462.759415	538.79	498.22	1661.19	11352.2	1007.7	1197.5
Poisson lamda	4.4444	4.3333	3.6400	4.5143	6.1957	3.1692	6
Exponential distribution lamda	0.2249	0.2308	0.2747	0.2215	0.1614	0.3155	0.1667
Power law distribution KS D value	0	0	0	0	0.1586	0	0
Power law alpha	-	-	-	-	-	-	-
Power law Xmin	14	15	15	17	6	35	18
Type of degree distribution	Exponential, power law	Power law	Power law	Power law	Power law	Power law	Power law
Network type	Complex network	Complex network	Complex network	Complex network	Complex network	Complex network	Complex network

From variation coefficient and aggregation index in Table 5 and 6, we can find that all values are greater than 1 and all webs are thus complex networks. Plant-Pollinator web (Ollerton et al, 2003) is the most complex, seconded by Predator-prey web (Catlins) and Plat-Ant web (Bluthgen, 2004), the complexity of Plant-Seed disperser web (Poulin, 1999) is the lowest. It can be fond that the skewness of Plant-Pollinator web (Ollerton et al, 2003) is the smallest and its degree distribution is the most skewed, which reveals it is the most complex network.

The results show that the degree distribution of most of the food webs is power law and exponential distribution, and all of the food webs are complex networks.

Table 6 Summary of results for calculation of degree distribution and network type.

	P-H web	Plant-Seed disperser webs		Predator-Prey webs			
Data source	Joern, 1979	Veehler 1983	Poulin, 1999	Berwick	Catlins	Coweeta1	Venlaw
Skewness of degree distribution	0.2261	0.1969	0.3612	0.1735	0.2069	0.2313	0.1918
Aggregation index of the network	1.8139	1.6254	1.2334	1.7743	2.0198	1.8211	1.7875
Variation coefficient H of the network	4.6468	4.8003	2.0656	5.7552	5.6528	4.6157	5.3199
Binomial distribution Chi-square	48066.1	1451.8	898.8	256.2	180662.6	382.9	3897.6
Binomial p	0.1182	0.2	0.3333	0.1252	0.1043	0.0958	0.1643
Poisson distribution Chi-square	2167.1	1306.7	64.4	8483.6	945.7	1286.7	2241.8
Poisson lamda	4.4359	5.95	4.4167	6.0759	4.4898	4.3448	5.4203
Exponential distribution lamda	0.2254	0.1681	0.2264	0.1646	0.2227	0.2302	0.1845
Power law distribution KS D value	0	0	0	0	0	0	0
Power law alpha	-	2.9967	-	-	-	-	-
Power law Xmin	23	6	11	35	27	26	26
Type of degree distribution	Power law	Exponential, power law	Exponential, power law	Exponenti al, power law	Exponential , power law	Power law	Exponential, power law
Network type	Complex network	Complex network	Complex network	Complex network	Complex network	Complex network	Complex network

Note: P-H web means Plant-Herbivore web.

4 Discussion

Different from classical distribution patterns (bionomial distri., Poisson distri., and power law distri., etc.), both network type and network complexity can be calculated and compared using the indices above, i.e., aggregation index, coefficient of variation, skewness, etc. We suggest they should be used in the network analysis.

Other indices to detect aggregation strength can also be used in network analysis. For example, the Lloyd index:

$$L=1+(s^2-\bar{u})/\bar{u}^2,$$

where $\bar{u}$, s^2: mean and variance of network degree. The network is a random network, if $L\leq1$. It is a complex network, if $L>1$, and network complexity increases with L. It is obvious that at certain extent the entropy E, defined above, is equivalent to L.

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