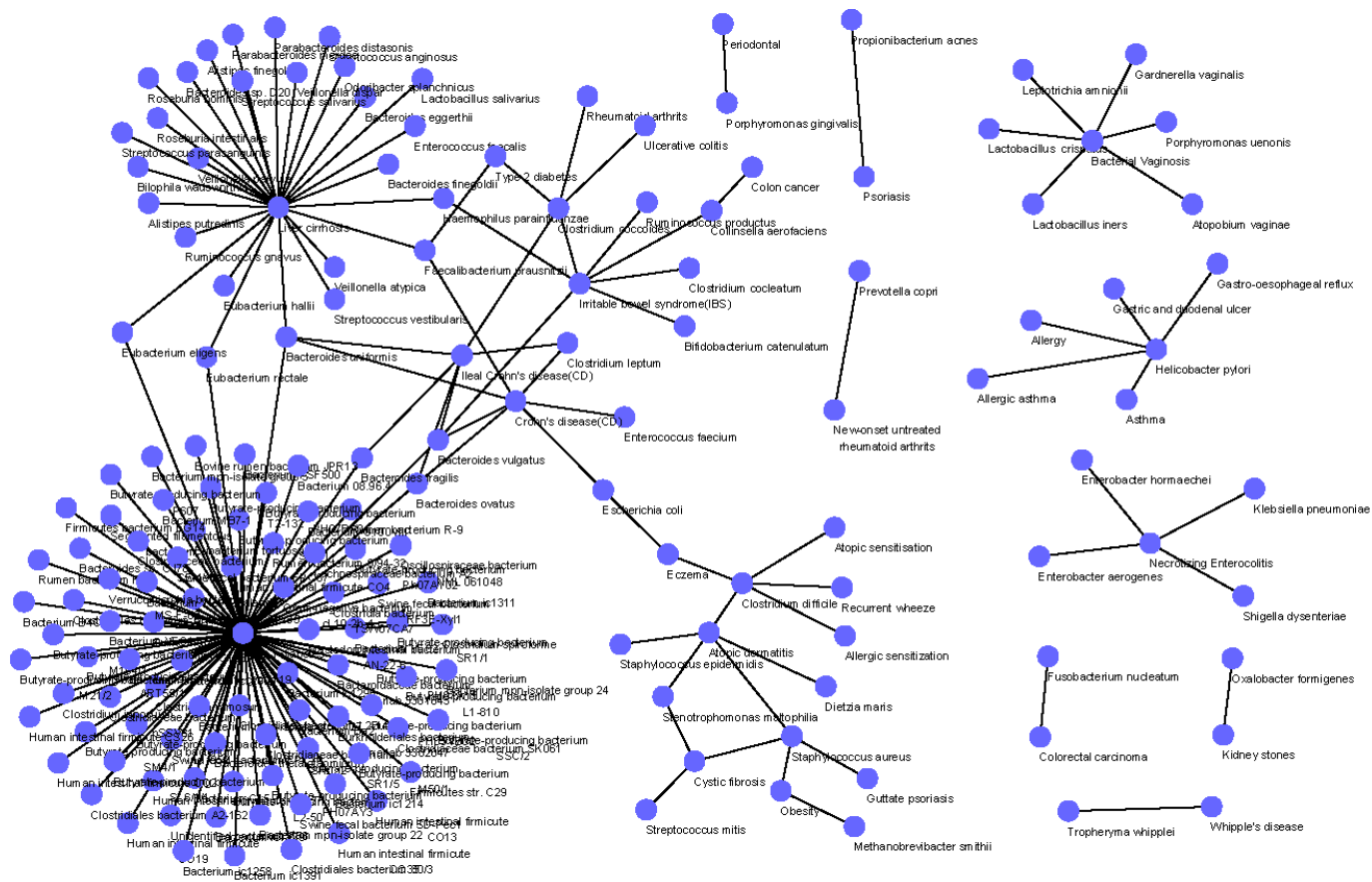


Novel human microbe-disease associations inference based on network consistency projection

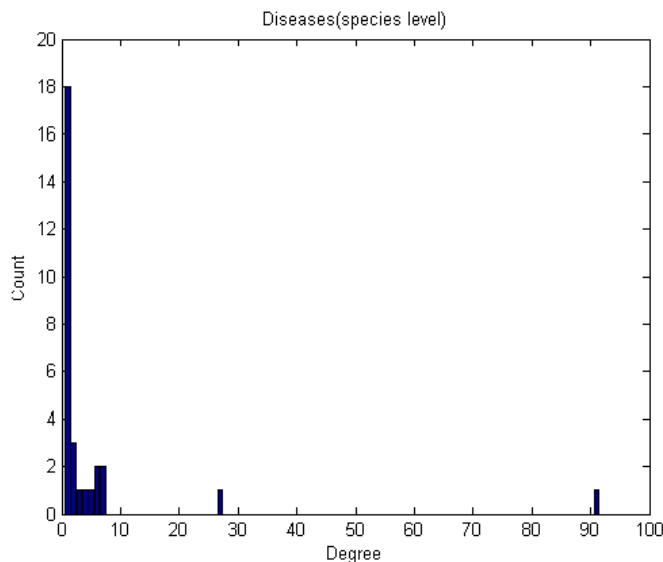
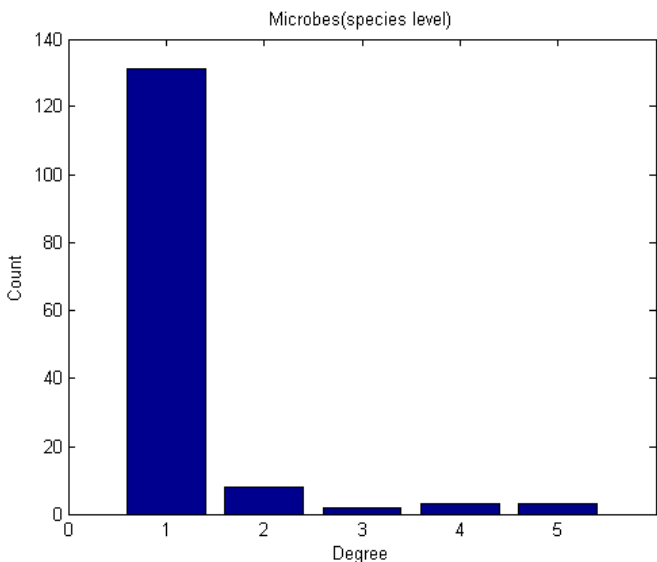
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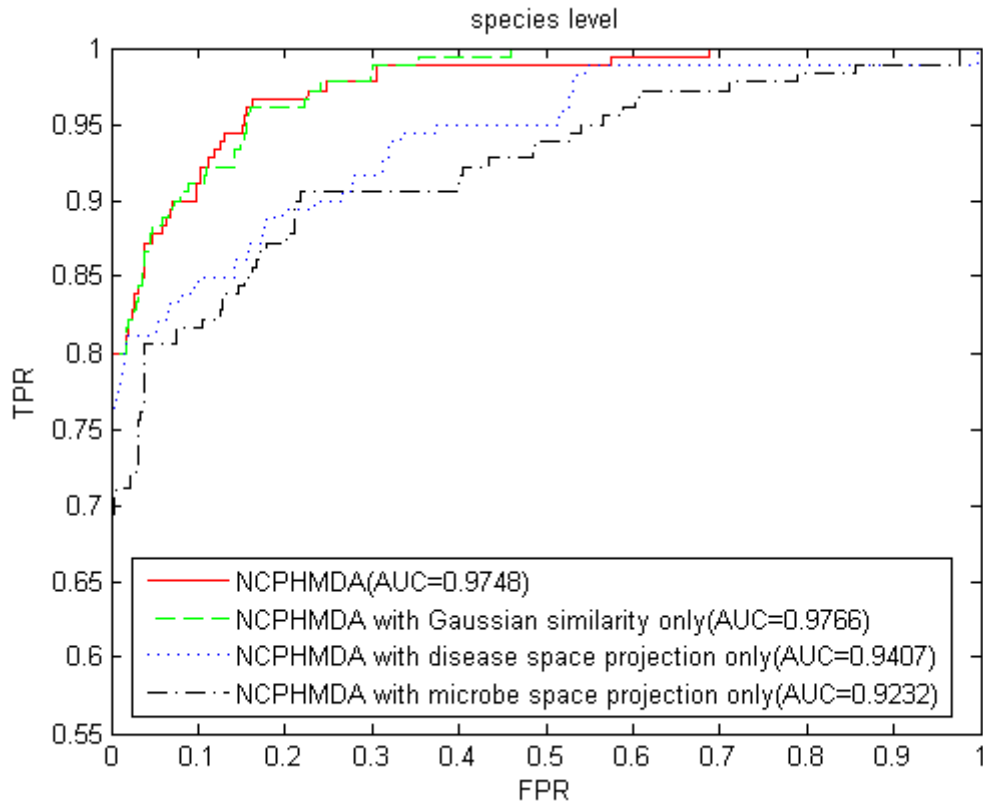
* corresponding author's email: zpzhang@csu.edu.cn



S1. The microbe-disease association network of species level.

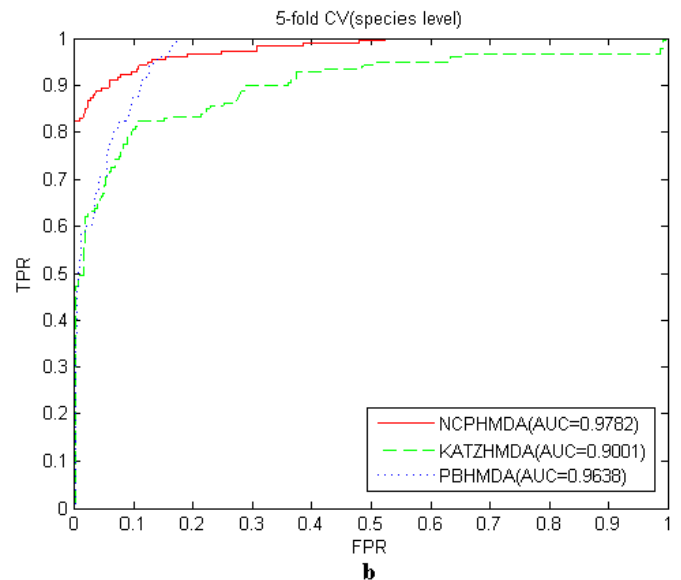
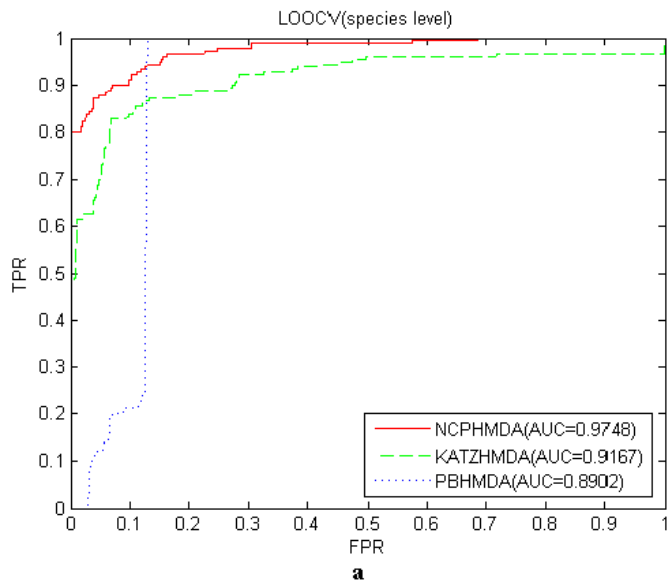


S2. Degree distribution for microbes and diseases in the microbe-disease association network of species level. (a) Degree distribution of microbes. (b) Degree distribution of diseases.



S3. The ROC curves and AUC values of NCPHMDA based on LOOCV in different situations (species level).

- (a) NCPHMDA with all information, (b) NCPHMDA with Gaussian interaction profile kernel similarity only, (c) NCPHMDA with disease space projection only, (d) NCPHMDA with microbe space projection only.



S4. The ROC curves and AUC values of NCPHMDA, KATZHMDA and PBHMDA based on LOOCV and 5-fold CV (species level).

- (a) The ROC curves and AUC values of NCPHMDA, KATZHMDA and PBHMDA based on LOOCV, (b) The ROC curves and AUC values of NCPHMDA, KATZHMDA and PBHMDA based on 5-fold CV.

S5. The code for NCPHMDA.

```
load microbesimilarity.mat
load diseasesimilarity.mat
load diseasesymptomsimilarity.mat
load diseasemicrobeinteraction.mat
```

```
[nd,nm]=size(diseasemicrobeinteraction);
```

```
for i=1:nd
    for j=1:nd
        if(diseasesymptomsimilarity(i,j))
            kd(i,j) = diseasesymptomsimilarity(i,j);
        else
            kd(i,j) = diseasesimilarity(i,j);
        end
    end
end
```

```
km=microbesimilarity;
```

```
nep_d = zeros(nd,nm)+10^-30;
nep_m = zeros(nd,nm)+10^-30;
nep =zeros(nd,nm);
```

```
for i=1:nd
    nep_m(i,:) = (diseasemicrobeinteraction(i,:)*km)/norm(diseasemicrobeinteraction(i,:));
end
```

```
for j=1:nm
    nep_d(:,j) = (kd*diseasemicrobeinteraction(:,j))/norm(diseasemicrobeinteraction(:,j));
end
```

```
for i=1:nd
    for j=1:nm
        nep(i,j) = (nep_d(i,j) + nep_m(i,j))/(norm(kd(i,:))+norm(km(:,j)));
    end
end
```

```
result=nep';
```