Supplementary Information (SI) for Environmental Science: Advances.

Quantitative sources of nitrate in typical plain river network areas by a combined PMF and MixSIAR approach

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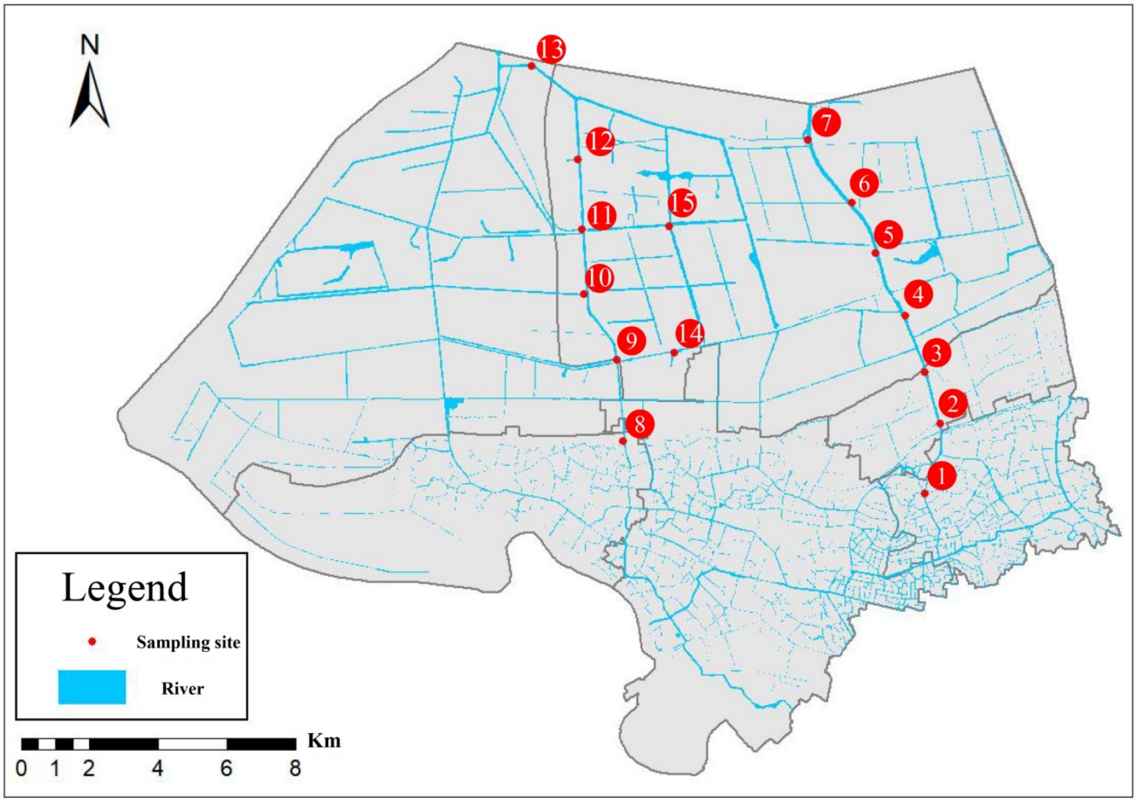

Fig.S1 The stable isotope sampling distribution of river network in Yubei Plain.

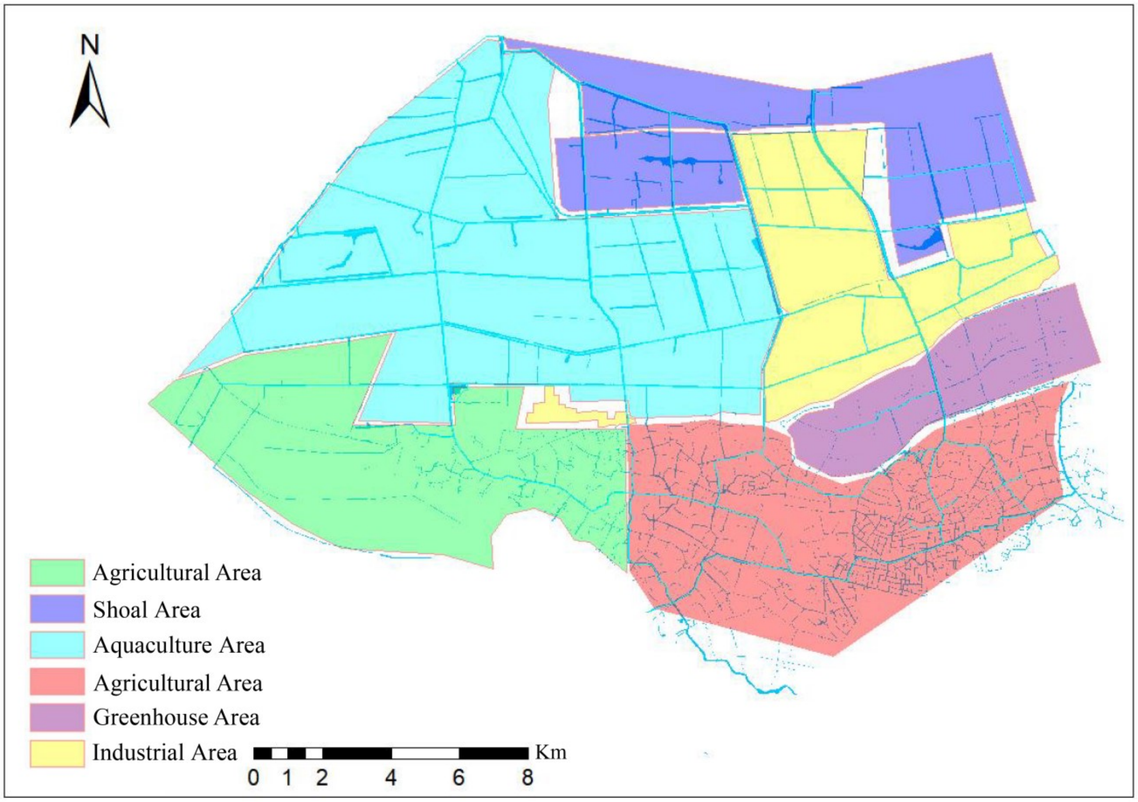

Fig.S2 Distribution of land use types.

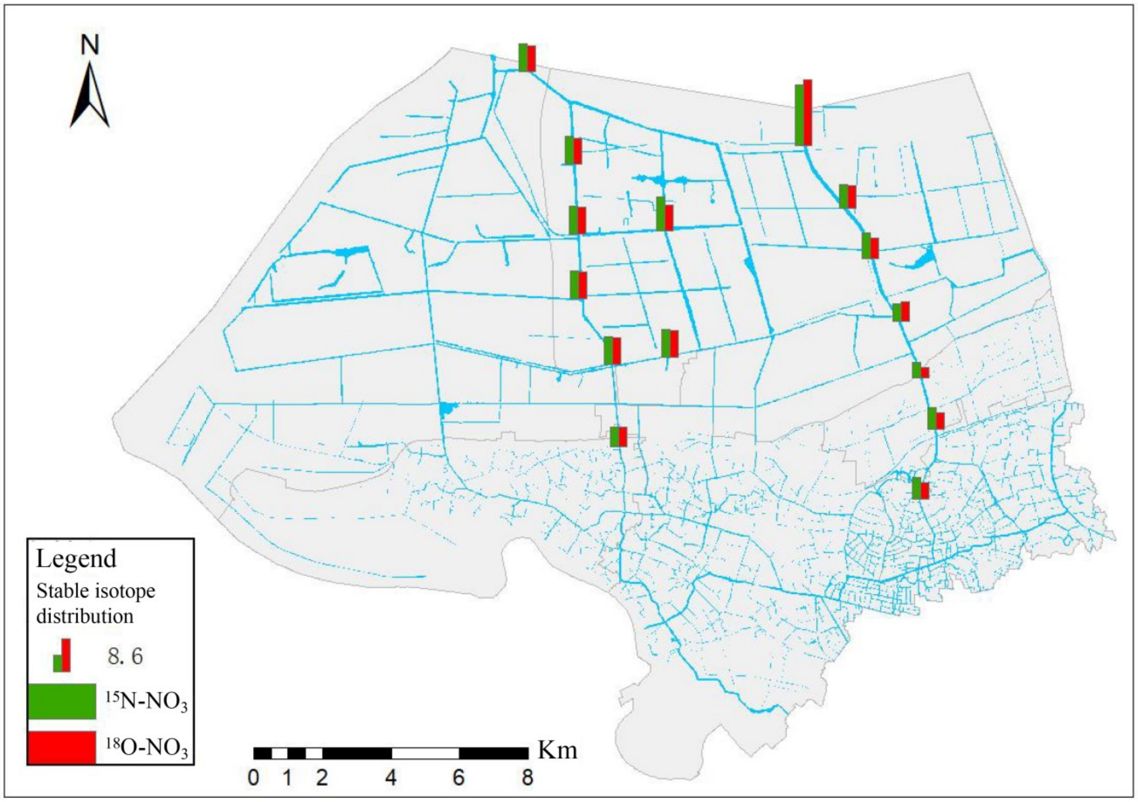

Fig.S3 Distribution of the $\delta^{15}N/\delta^{18}O-NO_3^-$ value.

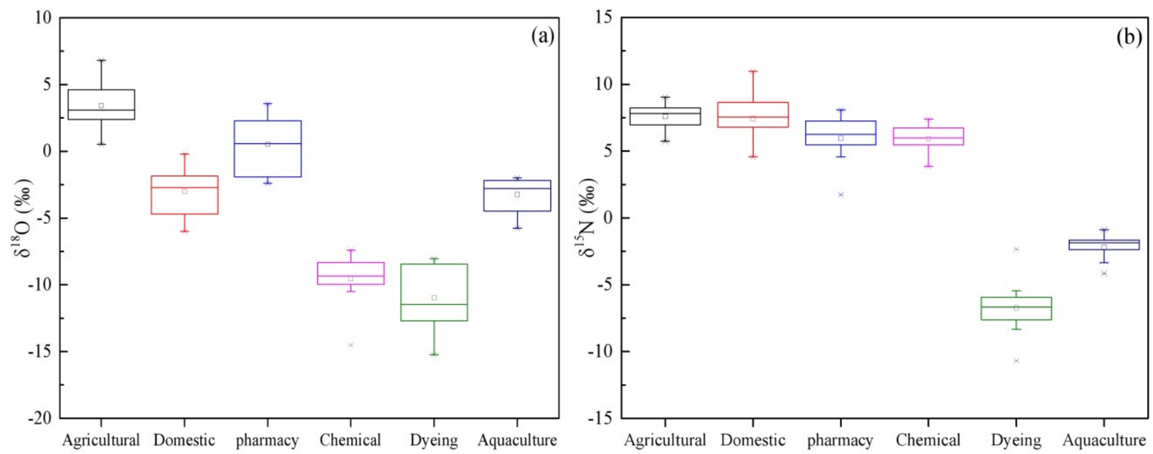

Fig.S4 The $\delta^{15}N/\delta^{18}O-NO_3^-$ value of potential pollution source.

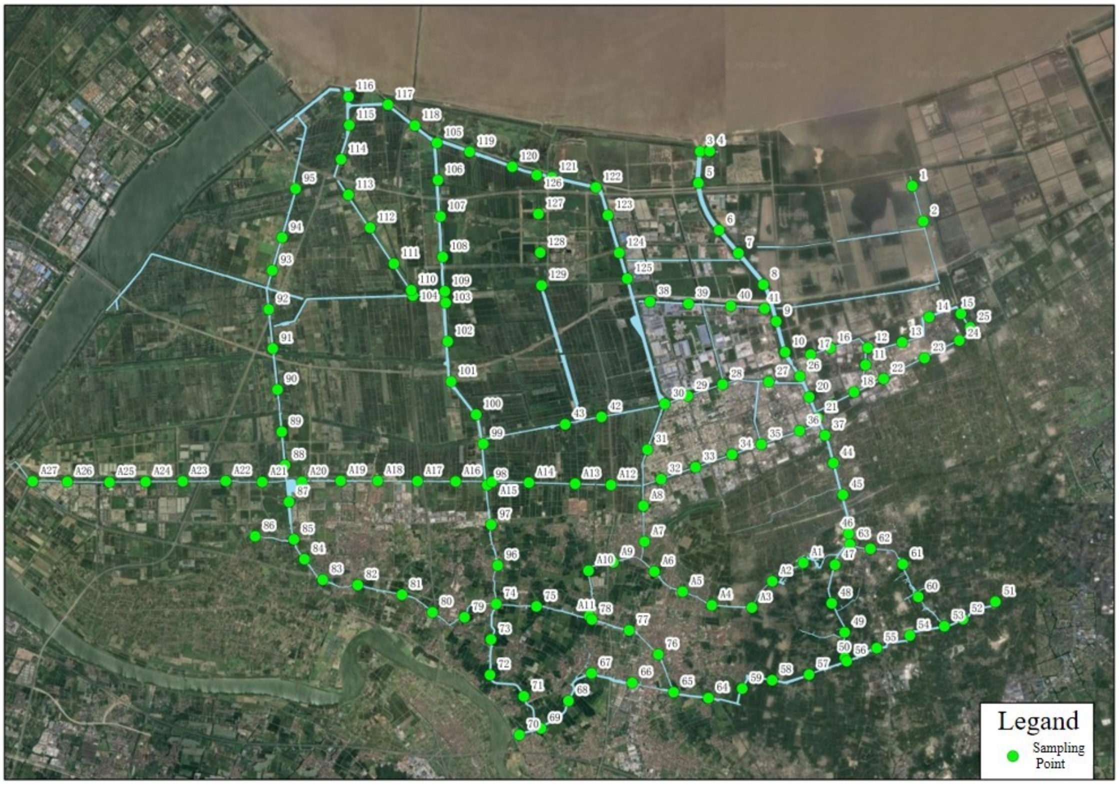

Fig.S5 The water sampling points of river network in Yubei Plain.

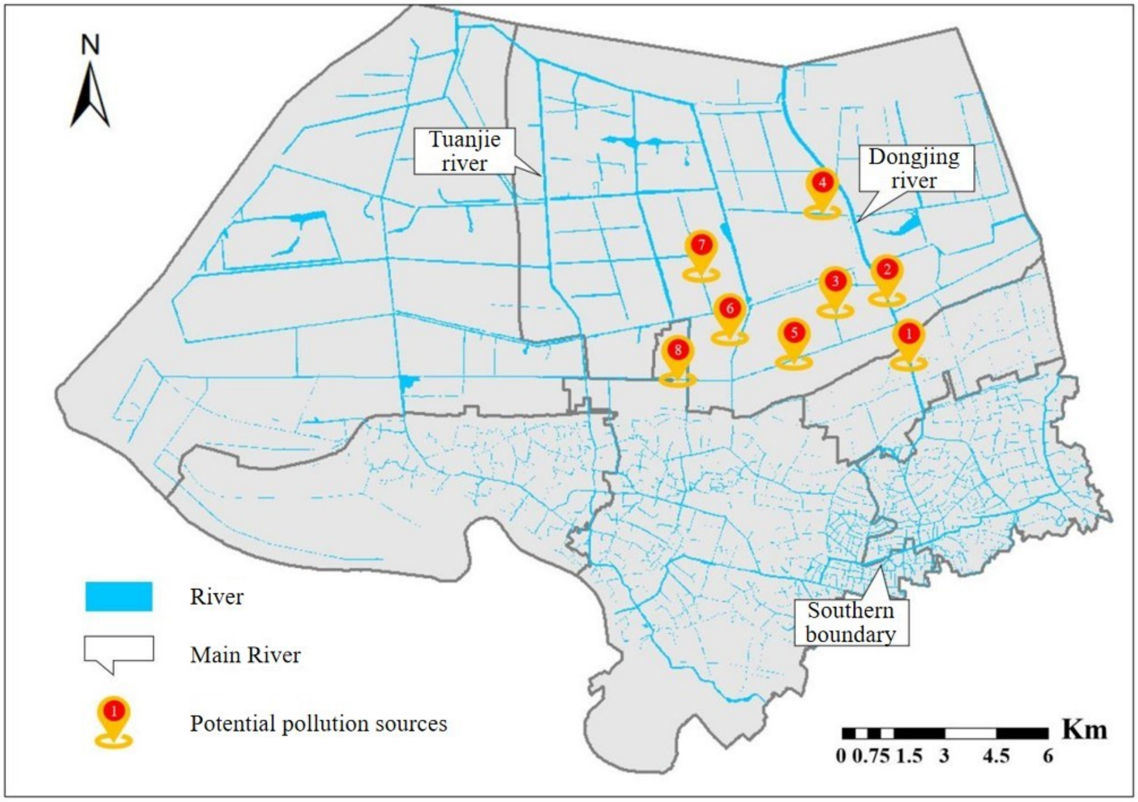

Fig.S6 Map of suspected discharge outlets in potential pollution areas.

Fig.S7 Schematic diagram of the suspected discharge outlet site.

Table.S1 The concentration of stable isotope in Yubei Plain River Network (‰).

FID	$^{15}N-NO_3$	$^{18}O-NO_3$	^{18}O
1	5.99	3.29	-4.92
2	9.08	6.91	-4.74
3	6.62	5.23	-4.89
4	3.98	5.65	-5.06
5	5.57	4.35	-4.93
6	5.02	5.04	-4.90
7	5.66	4.29	-4.77
8	7.77	6.93	-4.45
9	6.23	5.76	-4.61
10	7.24	6.85	-4.94
11	7.32	6.94	-5.17
12	7.37	6.99	-5.82
13	7.43	7.05	-5.57
14	7.48	7.13	-6.01
15	7.52	7.18	-4.55

Table.S2 The concentration of TP, TN, NH4+ and CODMn in Yubei Plain River Network (mg/L).

Sampling	**TN**	**NH_4^+**	**TP**	**COD_{Mn}**
A1	2.50	0.37	0.11	4.5
A2	2.44	0.487	0.17	4.8
A3	2.34	0.946	0.34	6.3
A4	2.62	0.555	0.55	6.2
A5	2.49	0.621	0.45	6.2
A6	3.28	1.064	0.56	8.1
A7	2.55	0.575	0.25	6.6
A8	2.55	0.666	0.27	7.1
A9	2.49	1.083	0.27	6.0
A10	2.00	0.454	0.21	7.0
A11	2.18	0.544	0.19	6.2
A12	2.26	0.809	0.66	9.7
A13	3.04	0.866	0.58	11.1
A14	2.52	0.754	0.35	9.3
A15	3.46	0.626	0.55	8.5
A16	3.88	0.709	0.65	8.7
A17	4.05	0.666	0.54	8.8
A18	3.60	0.525	0.46	8.4
A19	3.76	0.509	0.44	7.8
A20	3.92	0.573	0.45	7.3
A21	2.67	0.435	0.18	4.6
A22	3.18	0.559	0.25	4.9
A23	3.31	0.640	0.26	5.2
A24	3.03	0.387	0.19	4.0
A25	2.53	0.350	0.16	3.5
A26	2.73	0.330	0.15	3.5
A27	2.93	0.311	0.16	3.1
#1	1.63	0.443	0.06	8.5
#2	2.70	0.479	0.06	8.8
#3	3.03	0.427	0.19	8.5
#4	2.90	0.613	0.32	9.4
#5	2.59	0.586	0.24	8.2
#6	2.45	0.510	0.21	8.8
#7	1.47	0.399	0.14	7.5

#8	2.89	0.540	0.18	8.8
#9	2.41	0.283	0.11	6.6
#10	2.59	0.342	0.12	7.2
#11	3.67	0.308	0.33	9.5
#12	3.73	0.284	0.48	10.9
#13	3.43	0.377	0.67	8.8
#14	2.71	0.313	0.49	9.1
#15	2.38	0.337	0.32	7.5
#16	3.85	0.456	0.27	9.4
#17	3.05	0.382	0.20	9.5
#18	2.95	0.842	0.22	5.0
#19	2.58	0.748	0.21	5.5
#20	3.01	0.678	0.21	5.4
#21	2.79	0.699	0.22	5.5
#22	2.62	0.559	0.21	5.3
#23	2.91	0.655	0.22	5.5
#24	4.29	0.559	0.48	4.7
#25	3.27	0.400	0.18	5.0
#26	2.70	0.949	0.20	5.7
#27	2.88	1.37	0.27	6.5
#28	3.67	1.92	0.21	7.0
#29	2.54	0.414	0.22	6.5
#30	2.90	0.903	0.61	5.3
#31	3.32	0.163	0.20	6.5
#32	2.76	0.735	0.23	6.4
#33	2.41	1.24	0.27	5.0
#34	2.79	1.00	0.26	7.3
#35	3.31	0.941	0.34	7.1
#36	2.50	0.139	0.17	4.8
#37	2.90	0.132	0.14	4.6
#38	1.93	1.08	0.17	5.0
#39	1.12	1.05	0.12	5.2
#40	1.46	1.05	0.16	7.2
#41	1.99	1.39	0.17	7.6
#42	1.95	1.34	0.34	7.4
#43	1.96	1.00	0.48	7.4
#44	2.50	0.802	0.27	7.6
#45	3.13	0.143	0.19	6.6
#46	3.13	0.172	0.15	6.1
#47	2.35	0.159	0.12	4.3

#48	2.45	0.129	0.11	4.4
#49	2.52	0.158	0.11	4.6
#50	2.87	0.126	0.14	4.5
#51	1.54	0.302	0.07	4.2
#52	7.16	0.306	0.09	4.1
#53	2.85	0.531	0.12	4.4
#54	2.67	0.686	0.14	4.2
#55	2.48	0.367	0.11	4.0
#56	3.26	0.134	0.11	4.2
#57	2.71	0.398	0.14	4.1
#58	2.94	0.629	0.15	4.0
#59	2.98	0.523	0.15	4.0
#60	3.19	0.363	0.07	4.1
#61	3.20	0.168	0.13	4.4
#62	1.99	0.246	0.13	4.7
#63	2.39	0.291	0.12	4.2
#64	2.46	0.389	0.11	4.1
#65	2.35	0.099	0.11	3.9
#66	2.41	0.071	0.09	3.8
#67	2.54	0.249	0.10	3.8
#68	2.60	0.080	0.09	3.6
#69	2.80	0.077	0.10	3.5
#70	2.33	0.246	0.08	3.7
#71	2.46	0.209	0.15	4.0
#72	1.92	0.134	0.15	4.5
#73	2.20	0.430	0.17	4.8
#74	2.94	0.222	0.18	4.9
#75	2.59	1.74	0.32	6.7
#76	2.60	0.295	0.10	4.4
#77	2.36	0.329	0.15	3.8
#78	2.43	0.275	0.15	5.2
#79	2.37	0.335	0.10	3.9
#80	2.24	0.396	0.12	4.0
#81	2.28	0.438	0.13	3.9
#82	2.09	0.603	0.19	4.4
#83	2.23	0.643	0.31	5.2
#84	2.73	0.493	0.20	5.7
#85	1.96	0.744	0.28	5.8
#86	2.41	0.435	0.41	6.4
#87	3.05	0.799	0.51	7.4

#88	3.41	0.334	0.29	5.6
#89	3.87	0.392	0.29	4.6
#90	3.03	0.846	0.34	5.5
#91	3.30	1.00	0.50	6.3
#92	2.93	1.73	0.81	9.2
#93	3.69	1.98	1.33	10.4
#94	3.81	1.10	0.65	9.4
#95	3.35	0.739	0.54	8.7
#96	2.86	0.028	0.25	4.0
#97	3.02	0.024	0.21	4.2
#98	2.92	0.025	0.20	4.2
#99	2.64	0.033	0.18	4.3
#100	3.29	0.040	0.17	4.6
#101	3.05	0.041	0.26	5.0
#102	3.76	0.045	0.41	5.7
#103	3.79	0.048	0.43	6.3
#104	2.75	0.026	0.32	6.5
#105	2.53	0.029	0.26	6.6
#106	2.79	0.058	0.28	6.8
#107	2.75	0.018	0.33	6.2
#108	2.74	0.021	0.32	6.5
#109	2.83	0.038	0.35	6.1
#110	2.65	0.060	0.30	6.0
#111	2.83	0.105	0.32	6.3
#112	3.07	0.028	0.31	7.1
#113	3.17	0.041	0.37	7.3
#114	3.57	0.019	0.42	7.7
#115	3.16	0.077	0.38	6.5
#116	2.64	0.056	0.30	6.8
#117	2.80	0.025	0.31	7.1
#118	2.72	0.031	0.29	6.8
#119	2.58	0.079	0.24	5.7
#120	2.20	0.031	0.21	5.1
#121	1.17	0.074	0.23	7.1
#122	2.17	0.078	0.24	6.8
#123	2.02	0.080	0.21	8.1
#124	2.33	0.074	0.25	8.9
#125	3.10	0.104	0.22	10.3
#126	2.11	0.084	0.26	8.4
#127	3.30	0.055	0.28	9.6

#128	4.91	0.075	0.34	9.8
#129	3.38	0.084	0.42	11.9

Table.S3 The land use types in the YuBei Plain river network.

No	Region	Land use types	Area(km^2)
1	Hangzhou Bay Industrial Park	Industrial	37.45
2	Lihai Industrial Park	Industrial	1.41
3	Aquaculture Area	Aquaculture	103.93
4	Farmland and Village Area	Aquaculture; Domestic	58.06
5	Mixed Agricultural Area	Aquaculture; Domestic	66.78
6	Greenhouse Cultivation Area	Aquaculture; Domestic	23.0
7	Residential Area	Domestic	12.62
8	Coastal Wetland Area	Wetland	37.04

MixSIAR model

```
# source$data_type: raw
# source$by_factor: NA
# random effects: 0
# fixed effects: 0
# nested factors:
# factors:
# continuous effects: 0
# error structure: Process only (MixSIR, for N = 1)
# source$conc_dep: FALSE

var rho[n.sources,n.iso,n.iso], src_cov[n.sources,n.iso,n.iso],
src_var[n.sources,n.iso,n.iso], src_Sigma[n.sources,n.iso,n.iso], Sigma.ind[N,n.iso,n.iso],
mix.cov[N,n.iso,n.iso];

model{
  # fit source data (big for loop over sources)
  for(src in 1:n.sources){
    # uninformative priors on source means (src_mu vector)
    for(iso in 1:n.iso){
      src_mu[src,iso] ~ dnorm(0,.001);
    }

    # uninformative priors on source variances (src_tau matrix)
    for(i in 2:n.iso){
      for(j in 1:(i-1)){
        src_tau[src,i,j] <- 0;
        src_tau[src,j,i] <- 0;
      }
    }
    for(i in 1:n.iso){
      src_tau[src,i,i] ~ dgamma(.001,.001);
    }

    # uninformative priors on source correlations (rho matrix)
    for(i in 2:n.iso){
      for(j in 1:(i-1)){
        rho[src,i,j] ~ dunif(-1,1);
        rho[src,j,i] <- rho[src,i,j];
      }
```

```
      }
      for(i in 1:n.iso){
        rho[src,i,i] <- 1;
      }

      # Construct source precision matrix (src_Sigma)
      src_var[src,,] <- inverse(src_tau[src,,]);
      src_cov[src,,] <- src_var[src,,] %*% rho[src,,] %*% src_var[src,,];
      src_Sigma[src,,] <- inverse(src_cov[src,,]);

      # each source data point is distributed normally according to the source means and
precisions
      for(r in 1:n.rep[src]){
        SOURCE_array[src,,r] ~ dmnorm(src_mu[src,],src_Sigma[src,,]);
      }
   } # end source data fitting loop

      # draw p.global (global proportion means) from an uninformative Dirichlet,
      # then ilr.global is the ILR-transform of p.global
      p.global[1:n.sources] ~ ddirch(alpha[1:n.sources]);
      for(src in 1:(n.sources-1)){
        gmean[src] <- prod(p.global[1:src])^(1/src);
        ilr.global[src] <- sqrt(src/(src+1))*log(gmean[src]/p.global[src+1]); # page 296,
Egozcue 2003
      }

     # DON'T generate individual deviates from the global/region/pack mean (but keep
same model structure)
     for(i in 1:N) {
         for(src in 1:(n.sources-1)) {
             ilr.ind[i,src] <- 0;
             ilr.tot[i,src] <- ilr.global[src] + ilr.ind[i,src]; # add all effects together for each
individual (in ilr-space)
         }
     }

     # Inverse ILR math (equation 24, page 294, Egozcue 2003)
     for(i in 1:N){
         for(j in 1:(n.sources-1)){
            cross[i,,j] <- (e[,j]^ilr.tot[i,j])/sum(e[,j]^ilr.tot[i,j]);
         }
```

```
        for(src in 1:n.sources){
          tmp.p[i,src] <- prod(cross[i,src,]);
        }
        for(src in 1:n.sources){
          p.ind[i,src] <- tmp.p[i,src]/sum(tmp.p[i,]);
        }
    }

    for(src in 1:n.sources) {
        for(i in 1:N){
            # these are weights for variances
            p2[i,src] <- p.ind[i,src]*p.ind[i,src];
        }
    }


    # for each isotope and population, calculate the predicted mixtures
    for(iso in 1:n.iso) {
        for(i in 1:N) {

            mix.mu[iso,i] <- inprod(src_mu[,iso],p.ind[i,]) +
inprod(frac_mu[,iso],p.ind[i,]);
        }
    }


  # calculate mix variance and likelihood
  for(i in 1:N){
     for(iso in 1:n.iso){

        process.var[iso,i] <- inprod(1/src_tau[,iso,iso],p2[i,]) +
inprod(frac_sig2[,iso],p2[i,]);
        mix.prcsn[iso,i] <- 1/process.var[iso,i];
        X_iso[i,iso] ~ dnorm(mix.mu[iso,i], mix.prcsn[iso,i]);
        loglik_mat[i,iso] <- logdensity.norm(X_iso[i,iso], mix.mu[iso,i], mix.prcsn[iso,i]);
     }
     loglik[i] <- sum(loglik_mat[i,])
  }
}   # end model
```