

Measurements of spatial population synchrony: influence of time series transformations

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Highlighted student research:

This paper represents an outstanding contribution to the field of spatial population synchrony. Using empirical and simulated datasets, we highlighted the influence of time series transformation (TSTs) on several measures classically used in synchrony studies to

identify the determinants of spatial population synchrony (i.e. large scale climatic factors such as climate or local factors such as dispersion of individuals between localities). Our results highlight how TSTs influence both synchrony measurements and the conclusions regarding the determinants of population synchrony. Based on these results, we provide guidelines about how time series should be handled in synchrony studies. These guidelines are expected to improve our general understanding of the drivers influencing spatial population synchrony.

Author contributions:

MC and GG formulated the idea, MC, GG and JBF developed the methodology, MC conducted the analyses and wrote the manuscript, GG and PL supervised the work.

Electronic Supplemental Material

Appendix S1: Specifications of the four types of time series and description of the model used

No transformation: raw data

Because the sampling area differed at the different sites, we expressed the abundance of fish as density of fish per 100m² according to the following equation:

$$N_t = \frac{X_t}{S_t} * 100 \quad (1)$$

where N_t is the number of individuals per 100m² at time t , X_t is the number of individuals sampled at time t , and S_t is the sampling area at time t .

TST I: detrending

To detrend the raw data we used a linear model with a negative binomial distribution and a log link function. We chose a negative binomial distribution, because it has been shown to perform well for small samples of over-dispersed count data (Welsh et al. 2000), especially for freshwater fish (Vaudor et al. 2011). We thus fitted the following model independently to each time series:

$$\log(E(X_t)) = \alpha + \beta \text{year}_t + \log(S_t) + \varepsilon_t \quad (2)$$

where E denotes the expectation, year_t is the year of sampling at time t and ε_t is the remaining variance not accounted for by the covariates. The model therefore comprised one offset term ($\log(S_t)$), and three estimated parameters (the overdispersion parameter, the intercept α and the slope β associated to the predictive variable year_t). The parameter α represents the number

of fish caught per unit surface at $t=0$, while the parameter β is the long-term trend coefficient. For subsequent analyses, we used the residuals of this model.

TST II: prewhitening

Since the relationship between $\log(N_{t+1}-N_t)$ and N_t was linear for most of the time series, we used the stock-recruitment Ricker model with a log link function and a negative binomial distribution (i.e. accounting for overdispersion in the data) to eliminate temporal autocorrelation due to intrinsic population dynamic. We thus fitted the following model to each time series separately:

$$\log(E(X_{t+1})) = \log\left(S_{t+1} \frac{X_t}{S_t}\right) + \rho + \eta \frac{X_t}{S_t} + \varepsilon_t \quad (3)$$

where X_{t+1} is the number of fish caught at time $t+1$, and S_{t+1} is the sampling area at time $t+1$. The model therefore comprised one offset term ($\log\left(S_{t+1} \frac{X_t}{S_t}\right)$), and three estimated parameters (the overdispersion parameter, the intercept ρ and the slope η associated to the predictive variable $\frac{X_t}{S_t}$). The parameter ρ corresponds to the intrinsic population growth rate, while the parameter η is the density-dependent coefficient. A significant negative slope indicated negative density-dependence, as caused for example by competition for resource. On the log-scale, this model is a linear, first order, autoregressive (AR(1)) model.

Because the model described by Eq. 3 incorporates only local recruitment, it predicts that X_{t+1} is necessarily null, when $X_t=0$. Yet, our data included some cases in which we observed transitions from $X_t=0$ to $X_{t+1}>0$. Such transitions can be explained in two different ways. First the true population size at time t could in fact have been greater than zero (i.e. false zero due to measurement error), and so $X_{t+1}>0$ could be explained by local recruitment. Second, the local population could really have been extinct (i.e. true zero), and so $X_{t+1}>0$

would be explained by recolonization from neighboring populations. Here, we have assumed that the first situation is unlikely, because of the previously documented efficiency of electrofishing (Zalewski and Cowx 1990, but see discussion). For series containing transitions from $X_t=0$ to $X_{t+1}>0$ we analyzed these transitions using the following model:

$$\log (E(X_{t+1})) = \gamma + \log (S_{t+1}) \quad (4)$$

where γ is the intercept of the model and quantifies the average number of migrant fish caught per unit surface at time $t+1$ while $\log(S_{t+1})$ is an offset term.

In practice, any time series that did not contain at least eight non-null values of X_t or that contained multiple zeros were discarded (because multiple transitions from $X_t=0$ to $X_{t+1}=0$ cannot be handled by the recolonization model described by Eq. 4). The remaining series were used to fit the local recruitment model (i.e. Eq. 3), after cases where $X_t=0$ had been removed (the value of X_{t+1} in Eq.3 is therefore conditional on $X_t>0$). For these series, transitions from $X_t=0$ to $X_{t+1}>0$ were modeled using the recolonization model described by Eq. 4 (the value of X_{t+1} in Eq.4 is therefore conditional on $X_t=0$). To ensure good parameter estimation, this model was adjusted only to time series containing at least three transitions from $X_t=0$ to $X_{t+1}>0$. Time series that contained one or two transitions like these (i.e. 113 time series) were discarded.

The combination of Eq. 3 and 4 to model time series that contained transitions from $X_t=0$ to $X_{t+1}>0$ is comparable to hurdle count models in which a truncated count component (e.g. truncated negative binomial distribution) is used to model positive values, and a binomial component (a negative binomial in our case) is used to model the transitions from zeros to positive values (Zeileis et al. 2008). For all series analyzed this way, residuals of both models were combined and used for subsequent analyses. Series that did not contain null

values of X_t , were treated with the recruitment model (Eq. 3). The residuals were then extracted and used for subsequent analyses.

TST III: detrending and prewhitening

To take into account both long-term trends and population dynamics, we used the same approach as for TST II, above, but added the year as a covariate in Eq. 3 and 4.

Homogenization criteria

Because for TSTs II and III, we explained X_{t+1} in terms of X_t and then used the residuals of the model, the resulting time series contained one fewer data point than the raw data or TST I. To have the same series length for all four types of time series, we therefore deleted the first year of all time series in the raw data. TST I was then computed from this raw data. To avoid any bias in comparing TSTs to raw data, any time series for which the algorithm used to transform the time series and estimate the parameters in the models did not converge were discarded. This selection process left us with 3131 time series for the 34 species (Table 1). Depending on the species, the number of time series ranged from nine to 311 (mean: 92; sd: 93).

Appendix S2: Model equations and parameter descriptions

Effects of TSTs on the time series

$$Y_{ij} = \alpha + A_i + (\mu + M_i) * l_{ij} + (\beta + B_i) * d_{ij} + (\gamma + G_i) * t_{ij} + \varepsilon_{ij} \quad (5)$$

Y_{ij} is one of the three dependent variables (i.e. the Spearman cross correlation coefficients calculated between the raw time series for species i at site j , and the time series altered by each TST for the same species and site); α is the intercept of the model and A_i its random coefficient; l_{ij} is the length of the time series for species i at site j , and μ and M_i are its associated fixed and random coefficients, respectively; d_{ij} is the absolute value of the estimated coefficient of density dependence for species i at site j , and β and B_i were its associated fixed and random effects, respectively; t_{ij} is the absolute value of the estimated coefficient of trend for species i at site j , and γ and G_i are its associated fixed and random effects, respectively; ε_{ij} is the random error term associated with species i at site j . A_i , M_i , B_i , G_i and ε_{ij} are all random normal variables with mean 0 and standard deviations σ_A , σ_M , σ_B , σ_G , and σ_ε respectively.

Effects of TSTs on population synchrony

$$Y_{ij} = \alpha + A_i + A_j + \mu * l_{ij} + (\beta + B_i + B_j) * d_{ij} + (\gamma + G_i + G_j) * t_{ij} + \varepsilon_{ij}$$

(6)

Y_{ij} is one of the three dependent variables (i.e. the differences between the CCCs calculated using the raw data and those calculated using each of the TSTs); α is the intercept of the model, and A_i and A_j are the random intercepts associated with time series i and j , respectively; l_{ij} is the common length between the time series i and j and μ is its associated coefficient; d_{ij} is the ordinal variable determining whether density dependence was detected in time series i and j , and β , B_i and B_j are its associated fixed and random coefficients on time

series i and j , respectively; t_{ij} is the ordinal variable determining whether a long-term trend was detected in time series i and j , and γ , G_i , and G_j are the associated fixed and random coefficients for time series i and j , respectively; ε_{ij} is the random error term associated with time series i and j . A_i , A_j , B_i , B_j , G_i , G_j , and ε_{ij} are all random normal variables with mean 0 and standard deviations σ_{A_i} , σ_{A_j} , σ_{B_i} , σ_{B_j} , σ_{G_i} , σ_{G_j} , and σ_ε , respectively.

Appendix S3: Simulated time series

Description of the procedure used to simulate time series

To generate abundance time series, we used the model described by Eq. 3 with the year as a covariate (i.e. the model used for TST III). Time series were simulated according to seven parameters so as to represent the whole processes underlying empirical time series: intrinsic growth rate, strength of density dependence, long-term trend, overdispersion, time series length, mean sampling area and temporal variability of sampling area (the function used to simulate the time series is presented below). For each time series, the value of each parameter was sampled from a normal distribution with mean and standard deviation estimated from empirical time series. Likewise, initial abundances were fixed at random from a normal distribution with mean and variance corresponding to observed abundances.

Parameter combinations for which we were not able to obtain at least 10 time series of at least 8 years of non-null capture or where the model used to transform the time series did not converge were discarded. For each parameter combination, we distinguished four cases within which we considered 100 combinations of parameter values. In the first case, the parameters were fixed for all the time series which nonetheless differed in abundance due to the overdispersion parameter of the negative binomial distribution as well as to time varying sampling area and initial abundances. Thus, differences between the time series were only due to noise in this case. In the second case, all other parameters being equals, time series differed in their strength of density dependence (in addition to the noise) in order to mimic spatial variation in this process (due for example to spatial variation in resource competition or varying levels of carrying capacity at the different sites). The third case was the same as the second one but with differences in the strength of the long-term trend (density-dependent coefficients were equal among time series) to represent spatial variations in environmental

conditions (or spatial variations in population responses to environmental conditions). In the last case, both, the long term trend and the strength of density dependence differed among the time series.

Effects of TSTs on time series and population synchrony levels

For each time series, we used TSTs to remove the long-term trend and/or the temporal autocorrelation due to intrinsic population dynamics. We then used the same procedures as those used for empirical time series (1) to estimate population synchrony levels for the four types of time series (i.e. Spearman cross-correlation coefficients between pairs of time series that had at least eight years of non-null capture in common), (2) to calculate the degree of similarity between raw time series and time series obtained with each TST (i.e. Spearman cross correlation coefficients) and (3) to calculate the degree of dissimilarity between population synchrony levels obtained with raw data and those obtained with TSTs (i.e. difference between CCCs). We then used Wilcoxon tests to find out whether TSTs influenced the degree of similarity between the time series and the degree of dissimilarity in population synchrony levels. We finally used linear models (following the same procedure as the one used for empirical time series) to determine whether the influence of TSTs on time series and population synchrony levels varied depending on time series features (density dependence, long-term trend and time series length). As the results do not qualitatively differ among the four cases considered, we only present the results obtained from all cases taken together.

R function used to simulate the time series

```
library(MASS) # to use the rnegbin function
simul<-function # defining the function to simulate population abundances
(n0=NULL,a=NULL,b=NULL,c=NULL,theta=NULL,tmax=NULL,mu.samp=NULL,sd.samp=NULL){
  data = NULL
  v = c(n0,rep(NA,tmax)) # vector of population size. n0 is the initial size
  samp = abs(round(rnorm(tmax,mu.samp,sd.samp),digits=0)) # vector of sampling area
```

```

for(t in 1:tmax) { # loop to calculate population size according to population dynamic
#parameters
  dates = 1:tmax # temporal scheme
  eta = log(v[t]/samp[t])+log(samp [t+1])+a-b*(v[t]/ samp [t])+c*dates # the modified stock
#recruitment Ricker model
  v[t+1] = rnegbin(1, mu = exp(eta), theta = theta) # calculation of population size at time
#t+1 following a negative binomial distribution with mean equal to exp(eta)
}
data = cbind(samp,v) # data frame containing population size and sampling area at each time
return(data)
}

```

where a is the intrinsic growth rate; b is the density dependent coefficient; c is the long-term trend coefficient; theta is the overdispersion parameter of the negative binomial distribution; tmax is the length of the time series, mu.samp is the mean sampling area and sd.samp its variance. n0 is the initial abundance.

1 **Appendix S4: features of the time series**

Table S1. Percentage of time series with significant long-term trend (estimated with TSTs I and III) and density dependence (estimated with TSTs II and III).

Species name	N	TST I		TST II		TST III	
		Positive trend	Negative trend	Negative DD	Positive trend	Negative trend	Negative DD
<i>Abramis brama</i>	24	4.2	12.5	58.3	8.3	8.3	66.7
<i>Alburnoides bipunctatus</i>	53	43.4	3.8	86.8	24.5	5.7	81.1
<i>Alburnus alburnus</i>	107	18.7	15.0	89.7	12.1	10.3	90.7
<i>Ameiurus melas</i>	17	11.8	11.8	82.4	5.9	17.6	70.6
<i>Anguilla anguilla</i>	205	10.2	25.9	74.6	7.8	14.6	80.5
<i>Barbatula barbatula</i>	245	24.5	14.7	83.7	10.2	12.2	86.5
<i>Barbus barbus</i>	129	19.4	10.9	85.3	16.3	9.3	91.5
<i>Blicca bjoerkna</i>	26	15.4	11.5	88.5	7.7	15.4	96.2
<i>Carassius sp.</i>	12	8.3	16.7	50.0	0.0	16.7	58.3
<i>Chondrostoma nasus</i>	26	23.1	11.5	80.8	30.8	15.4	84.6
<i>Cottus gobio</i>	25	48.0	12.0	56.0	44.0	12.0	84.0
<i>Cottus perifretum</i>	167	31.7	15.0	82.6	16.2	12.0	86.2
<i>Cyprinus carpio</i>	11	0.0	9.1	27.3	0.0	9.1	27.3
<i>Esox lucius</i>	61	13.1	9.8	63.9	4.9	1.6	72.1
<i>Gasterosteus gymnasium</i>	17	29.4	23.5	47.1	17.6	17.6	64.7
<i>Gobio gobio</i>	219	23.3	15.1	81.3	15.1	15.5	86.3
<i>Gobio lozanoi</i>	9	22.2	0.0	77.8	11.1	0.0	100.0
<i>Gobio occitaniae</i>	73	19.2	13.7	75.3	15.1	12.3	82.2
<i>Gymnocephalus cernua</i>	25	20.0	12.0	80.0	12.0	8.0	88.0
<i>Lampetra planeri</i>	67	32.8	10.4	62.7	23.9	4.5	68.7
<i>Lepomis gibbosus</i>	161	13.0	12.4	74.5	9.3	15.5	82.0

<i>Leuciscus burdigalensis</i>	40	10.0	25.0	72.5	2.5	25.0	85.0
<i>Leuciscus leuciscus</i>	60	20.0	8.3	90.0	15.0	13.3	95.0
<i>Perca fluviatilis</i>	83	31.3	7.2	69.9	24.1	10.8	83.1
<i>Phoxinus phoxinus</i>	247	25.1	12.6	87.0	16.6	8.1	91.1
<i>Pungitius laevis</i>	17	11.8	17.6	64.7	11.8	17.6	64.7
<i>Rhodeus amarus</i>	31	38.7	3.2	93.5	16.1	3.2	93.5
<i>Rutilus rutilus</i>	261	16.1	21.5	82.4	10.3	18.8	83.9
<i>Salmo salar</i>	22	13.6	18.2	86.4	0.0	18.2	90.9
<i>Salmo trutta</i>	285	11.2	22.8	83.9	5.6	16.8	89.1
<i>Scardinius erythrophthalmus</i>	27	14.8	18.5	63.0	0.0	18.5	77.8
<i>Squalius cephalus</i>	311	21.2	14.1	80.1	14.8	10.9	88.1
<i>Telestes souffia</i>	25	44.0	12.0	76.0	36.0	4.0	84.0
<i>Tinca tinca</i>	43	9.3	16.3	55.8	9.3	18.6	65.1

N is the number of time series. Positive (Negative) trend is the percentage of time series with significant ($P < 0.05$) positive (negative) long-term trends. Negative DD is the percentage of time series with significant ($P < 0.05$) negative density dependence. For the definition of TSTs, see the text.

```

3 Appendix S5: R code used to transform the time series
4
5 # R code used to perform time series transformation, to estimate synchrony between time
6 #series and to determine whether long-term trend and density dependence are detected in the
7 #time .
8
9 #-----
10 # Generation of a dummy data set
11 # The data frame containing two time series and the necessary information to perform TSTs
12 #-----
13
14 df.TS1 <- NULL
15 df.TS2 <- NULL
16 df <- NULL
17
18 #----- First time series
19 # this is the vector containing the observed population size
20 pop.size.TS1 <- c(50,31,26,17,26,28,90,32,31,30,35,33,53,53,187,88,50,51,54)
21 # this is the vector containing the sampling areas (m^2)
22 samp.area.TS1 <-
23 c(887.84,930.8,930.8,930.8,930.8,906.3,1001.77,758.28,759.7,817.6,1235.1,875.16,989.05,87
24 6.12,807,904.4,825.11,895.5,756)
25 # this is the vector containing the sampling years.
26 samp.year.TS1 <-
27 c(1990,1991,1992,1993,1994,1995,1996,1997,1998,1999,2000,2001,2002,2003,2004,2005,20
28 06,2007,2009)
29
30 #----- Second time series
31 # this is the vector containing the observed population size
32 pop.size.TS2 <- c(8,19,15,14,11,21,12,17,22,21,35,22,31,52,61,47,81,65,72)
33 # this is the vector containing the sampling areas (m^2)
34 samp.area.TS2 <-
35 c(525,307.05,298.2,340.8,369.2,378.48,360.24,372.4,408.88,380,373.16,313.12,320.72,342.7
36 6,334.4,471.45,453.49,465,457.66)
37 # this is the vector containing the sampling years.
38 samp.year.TS2 <-
39 c(1987,1990,1991,1992,1993,1996,1997,1998,1999,2000,2001,2002,2003,2004,2005,2006,20
40 07,2008,2009)
41
42
43 # filling the data frame
44 df <- list()
45 df[[1]] <- data.frame(pop.size.t=pop.size.TS1[-
46 length(pop.size.TS1)],pop.size.t1=pop.size.TS1[-1],samp.area.t=samp.area.TS1[-

```

```

47 length(samp.area.TS1),samp.area.t1=samp.area.TS1[-1],samp.year.t=samp.year.TS1[-
48 length(samp.year.TS1),samp.year.t1=samp.year.TS1[-1])
49 df[[2]] <- data.frame(pop.size.t=pop.size.TS2[-
50 length(pop.size.TS2)],pop.size.t1=pop.size.TS2[-
51 1],samp.area.t=samp.area.TS2[length(samp.area.TS2)],samp.area.t1=samp.area.TS2[-
52 1],samp.year.t=samp.year.TS2[-length(samp.year.TS2)],samp.year.t1=samp.year.TS2[-1])
53
54 # compute densities at time t+1
55 # compute date, assuming there is no gap in the time series
56 for(i in 1:length(df)) {
57   df[[i]]$densities.t1 = with(df[[i]],pop.size.t1/samp.area.t1*100)
58   df[[i]]$date <- 1:nrow(df[[i]])
59 }
60
61 #-----
62 # Transforming the time series
63 #-----
64
65 # Detrending
66 #~~~~~
67
68 # To detrend the raw data we used a linear model with a negative binomial error and a log link
69 #function
70
71 require(MASS)
72
73 df.coef.detrend <- NULL
74 for(i in 1:length(df)) { # loop to apply the model to each time series
75   model <- NULL
76   model <- glm.nb(pop.size.t1 ~ date + offset(log(samp.area.t1)), data = df[[i]])
77   df[[i]]$detrend <- residuals(model) # we extract the residuals (detrended data)
78   df.coef.detrend <- rbind(df.coef.detrend,coef(model)) # stores the estimated coefficients
79 }
80
81 # Prewhitening
82 #~~~~~
83
84 # To eliminate temporal autocorrelation due to intrinsic population dynamic we used the
85 #Ricker model with a log link function and a negative #binomial distribution
86
87 df.coef.prewhit <- NULL
88
89 for(i in 1:length(df)){
90

```

```

91 df[[i]]$prewhitened <- NULL
92 nb.0 <- df[[i]]$pop.size.t == 0 # number of zero counts in the time series (zero in this case)
93 position.0 <- which(df[[i]]$pop.size.t == 0) # position of the zero counts
94 position.pos.counts <- which(df[[i]]$pop.size.t != 0) # position of the positive counts
95
96 #transitions from Nt=0 to Nt1>0
97 if(sum(nb.0)>2) { # if there are at least 3 zero counts in the time series
98   model.0 <- NULL
99   model.0 <- glm.nb(pop.size.t1 ~ offset(log(samp.area.t1)),data=df[[i]][nb.0,])
100   df[[i]][position.0,"prewhitened"] <- residuals(model.0)
101 }
102
103 #transitions Nt>0 to Nt1>0
104 model.pos.counts <- NULL
105 model.pos.counts <- glm.nb(pop.size.t1 ~
106 I(pop.size.t/samp.area.t)+offset(log(samp.area.t1)+log(pop.size.t/samp.area.t1)),data=df[[i]][!
107 nb.0,])
108 df[[i]][position.pos.counts,"prewhitened"] <- residuals(model.pos.counts)
109
110 df.coef.prewhit <- rbind(df.coef.prewhit,coef(model.pos.counts))
111 }
112
113 # Prewhitening and detrending
114 #~~~~~
115
116 # To eliminate temporal autocorrelation due to intrinsic population dynamic and long term
117 #trend we used the Ricker model with a log link function and a negative binomial distribution
118 #with the year as a covariate
119
120 df.coef.prewhit.det <- NULL
121
122 for(i in 1:length(df)){
123
124   df[[i]]$prewhit.det <- NULL
125   nb.0 <- df[[i]]$pop.size.t == 0
126   position.0 <- which(df[[i]]$pop.size.t == 0)
127   position.pos.counts <- which(df[[i]]$pop.size.t != 0)
128
129   #transitions from Nt=0 to Nt1
130   if(sum(nb.0)>2) {
131     model.0 <- NULL
132     model.0 <- glm.nb(pop.size.t1 ~ date + offset(log(samp.area.t1)),data=df[[i]][nb.0,])
133     df[[i]][position.0,"prewhit.det"] <- residuals(model.0)
134   }

```



```

135
136 #transitions Nt>0 to Nt1
137 model.pos.counts <- NULL
138 model.pos.counts <- glm.nb(pop.size.t1 ~ date + I(pop.size.t/samp.area.t) +
139 offset(log(samp.area.t1) + log(pop.size.t/samp.area.t1)),data=df[[i]][!nb.0,])
140 df[[i]][position.pos.counts,"prewhit.det"] <- residuals(model.pos.counts)
141 df.coef.prewhit.det <- rbind(df.coef.prewhit.det,coef(model.pos.counts))
142 }
143
144 #-----
145 # Estimating synchrony between both time series for the raw data and the modified ones
146 #-----
147
148 cor.test(df[[1]][,"densities.t1"],df[[2]][,"densities.t1"],method="spearman")$estimate #0.62
149 cor.test(df[[1]][,"detrend"],df[[2]][,"detrend"],method="spearman")$estimate #0.02
150 cor.test(df[[1]][,"prewhitened"],df[[2]][,"prewhitened"],method="spearman")$estimate #-0.15
151 cor.test(df[[1]][,"prewhit.det"],df[[2]][,"prewhit.det"],method="spearman")$estimate #-0.18
152
153 #-----
154 # Detecting the presence of a long-term trend (Mann-Kendall trend test) in the time series
155 #-----
156
157 require(Kendall)
158
159 # correlations for the first time series
160 with(df[[1]},{
161   print(Kendall(date,densities.t1)) #0.55
162   print(Kendall(date,detrend)) #-0.16
163   print(Kendall(date,prewhitened)) #0.29
164   print(Kendall(date,prewhit.det)) #-0.07
165 })
166 # correlations for the second time series
167 with(df[[2]},{
168   print(Kendall(date,densities.t1)) #0.64
169   print(Kendall(date,detrend)) #0.02
170   print(Kendall(date,prewhitened)) #0.17
171   print(Kendall(date,prewhit.det)) #0.04
172 })
173
174 #-----
175 # Detecting the presence of lag-1 temporal autocorrelation in the time series
176 #-----
177
178 # temporal autocorrelation for the first time series

```

```
179 with(df[[1]],{
180   print(acf(densities.t1,lag.max=1,plot=F)$acf[2]) #0.29
181   print(acf(detrend,lag.max=1,plot=F)$acf[2]) #0.18
182   print(acf(prewhitened,lag.max=1,plot=F)$acf[2]) #-0.10
183   print(acf(prewhit.det,lag.max=1,plot=F)$acf[2]) #-0.13
184 })
185 # temporal autocorrelation for the second time series
186 with(df[[2]],{
187   print(acf(densities.t1,lag.max=1,plot=F)$acf[2]) #0.68
188   print(acf(detrend,lag.max=1,plot=F)$acf[2]) #0.09
189   print(acf(prewhitened,lag.max=1,plot=F)$acf[2]) #-0.38
190   print(acf(prewhit.det,lag.max=1,plot=F)$acf[2]) #-0.26
191 })
192
```

193 **Appendix S6: Influence of TSTs on time series and synchrony measurements in relation**
 194 **with time series features**

Table S2. Coefficients of the linear models performed on the relationship between the characteristics of the time series (independent variables) and the correlations calculated between the raw time series and the modified ones (dependent variables) for both the empirical and the simulated datasets.

Datasets	Dependent variables	Trend	DD	Length
Empirical	raw data/TST I	-27.49	5.9E-3	0.07
	raw data/TST II	6.2E-3	3.7E-3	0.02
	raw data/TST III	-3.44	4.8E-4	-2.4E-3
Simulated	raw data/TST I	-8.5E-2	2.7E-4	-4.7E-3
	raw data/TST II	2.9E-1	3.1E-4	-3.1E-3
	raw data/TST III	-4.6E-1	3.1E-4	-3.0E-3

Significant (P<0.05) results are in bold.

Table S3. Results from mixed-effects model performed on empirical time series for the 34 fish species.

Species name	Raw data/TST I				Raw data/TST II				Raw data/TST III			
	Trend	DD	CL	Conv	Trend	DD	CL	Conv	Trend	DD	CL	Conv
<i>Abramis brama</i>	0.010	0.003	-0.008	FALSE	0.003	0.004	-0.011	FALSE	0.012	-0.005	-0.015	FALSE
<i>Alburnoides bipunctatus</i>	0.003	-0.007	0.016	FALSE	-0.003	-0.006	0.003	TRUE	0.010	-0.004	0.000	TRUE
<i>Alburnus alburnus</i>	0.013	-0.004	-0.001	TRUE	0.002	0.000	-0.003	TRUE	0.008	0.001	-0.004	TRUE
<i>Ameiurus melas</i>	0.026	-0.012	-0.011	TRUE	-0.018	0.011	-0.027	FALSE	0.026	-0.042	-0.040	FALSE
<i>Anguilla anguilla</i>	0.015	-0.001	-0.003	TRUE	0.000	-0.001	-0.003	FALSE	0.009	0.001	-0.005	TRUE
<i>Barbatula barbatula</i>	0.017	-0.005	-0.006	TRUE	0.006	-0.008	-0.005	TRUE	0.017	-0.008	-0.006	FALSE
<i>Barbus barbus</i>	0.018	-0.008	-0.008	TRUE	0.002	-0.005	-0.006	TRUE	0.014	-0.004	-0.009	TRUE
<i>Blicca bjoerkna</i>	0.009	-0.019	-0.011	FALSE	0.015	0.010	-0.011	TRUE	-0.004	0.004	-0.003	FALSE
<i>Carassius sp.</i>	-0.013	0.006	-0.030	FALSE	0.002	0.002	-0.017	FALSE	-0.022	0.015	-0.021	TRUE
<i>Chondrostoma nasus</i>	0.019	0.003	-0.002	TRUE	0.007	0.005	-0.009	FALSE	0.018	0.009	-0.006	FALSE
<i>Cottus gobio</i>	0.030	0.005	-0.019	TRUE	0.018	-0.007	-0.011	TRUE	0.037	0.000	-0.015	TRUE
<i>Cottus perifretum</i>	0.018	-0.006	-0.001	TRUE	0.008	-0.015	-0.004	TRUE	0.016	-0.011	-0.005	FALSE
<i>Cyprinus carpio</i>	-0.001	-0.014	0.008	TRUE	0.010	-0.006	-0.014	TRUE	-0.016	-0.031	-0.009	FALSE
<i>Esox lucius</i>	0.004	-0.012	-0.008	TRUE	0.001	-0.002	-0.006	FALSE	0.003	-0.007	-0.011	TRUE
<i>Gasterosteus gymnurus</i>	0.024	-0.010	-0.024	FALSE	0.007	0.005	-0.003	FALSE	0.032	-0.007	0.014	TRUE
<i>Gobio gobio</i>	0.015	-0.003	-0.007	TRUE	0.000	-0.002	-0.009	TRUE	0.015	-0.004	-0.009	TRUE
<i>Gobio lozanoi</i>	-	-	-	FALSE	-	-	-	FALSE	-	-	-	FALSE
<i>Gobio occitaniae</i>	0.025	-0.009	0.000	FALSE	0.008	-0.005	-0.003	TRUE	0.014	-0.004	-0.001	TRUE
<i>Gymnocephalus cernua</i>	0.006	0.001	-0.010	FALSE	-0.008	-0.005	-0.010	FALSE	0.005	-0.002	-0.014	FALSE
<i>Lampetra planeri</i>	0.018	0.000	-0.002	TRUE	0.004	0.002	-0.012	TRUE	0.015	0.001	-0.009	TRUE
<i>Lepomis gibbosus</i>	0.006	-0.001	-0.007	FALSE	0.004	0.001	-0.010	TRUE	0.013	-0.001	-0.012	FALSE
<i>Leuciscus burdigalensis</i>	0.017	0.000	0.001	TRUE	-0.005	0.001	-0.008	TRUE	0.002	0.006	-0.003	TRUE
<i>Leuciscus leuciscus</i>	0.015	-0.007	-0.009	FALSE	0.005	-0.002	-0.009	FALSE	0.009	0.004	-0.010	TRUE
<i>Perca fluviatilis</i>	0.020	-0.002	-0.010	TRUE	0.001	0.000	-0.008	TRUE	0.016	0.000	-0.012	FALSE
<i>Phoxinus phoxinus</i>	0.018	-0.011	-0.005	FALSE	0.000	-0.008	-0.008	TRUE	0.010	-0.009	-0.009	TRUE
<i>Pungitius laevis</i>	0.010	-0.007	-0.005	FALSE	0.001	0.002	-0.018	FALSE	0.016	0.004	-0.009	TRUE
<i>Rhodeus amarus</i>	0.000	-0.010	0.010	FALSE	0.003	-0.005	-0.011	TRUE	0.000	0.002	-0.007	TRUE
<i>Rutilus rutilus</i>	0.016	-0.003	0.000	TRUE	0.001	-0.002	-0.007	TRUE	0.011	-0.004	-0.008	TRUE
<i>Salmo salar</i>	0.008	-0.003	-0.004	FALSE	-0.003	-0.018	-0.005	TRUE	0.021	0.002	-0.017	TRUE

<i>Salmo trutta</i>	0.017	-0.002	-0.002	TRUE	0.004	-0.002	-0.005	TRUE	0.013	-0.004	-0.006	TRUE
<i>Scardinius erythrophthalmus</i>	0.008	-0.011	-0.024	FALSE	0.014	0.009	-0.016	FALSE	0.030	-0.014	-0.019	FALSE
<i>Squalius cephalus</i>	0.018	-0.003	-0.003	FALSE	0.002	-0.001	-0.005	TRUE	0.013	0.000	-0.007	TRUE
<i>Telestes souffia</i>	0.002	0.005	-0.018	TRUE	-0.001	-0.001	-0.014	FALSE	0.004	0.008	-0.011	TRUE
<i>Tinca tinca</i>	0.027	-0.013	-0.008	FALSE	-0.001	-0.001	-0.012	FALSE	0.016	-0.002	0.000	FALSE
Simulations	0.011	-0.016	-0.018	TRUE	0.052	0.065	-0.021	TRUE	0.060	0.062	-0.022	TRUE

Dependent variables were the differences between the CCCs estimated with raw data and those estimated with TSTs (for the definition of TSTs, see the text). Each empirical model included three independent variables: (i) the common length (CL) between the time series used to calculate the CCC, and (ii) two ordinal variables determining whether density dependence (DD) and long-term trend (trend) were significantly detected in the two time series. Are also shown the results from the linear models performed on the simulated time series. "Conv" indicates whether the model successfully converged (TRUE) or not (FALSE). For *Gobio Lozanoi* the model could not be fitted because of issues with the Cholesky decomposition matrix. In bold are the significant ($P < 0.05$) results.

Table S4. Species synchrony (i.e. mean of the CCCs computed over all pairs of time series) and species inter-catchments synchrony (i.e. mean of CCCs computed over pairs of time series located in different catchments) estimated for the 34 fish species.

Species name	Overall species synchrony					Overall species inter-catchments synchrony				
	Npairs	Raw data	TST I	TST II	TST III	Npairs	Raw data	TST I	TST II	TST III
<i>Abramis brama</i>	204	-0.005	-0.004	0.006	0.022	161	0.000	0.006	0.034	0.029
<i>Alburnoides bipunctatus</i>	794	0.059	0.011	0.006	-0.011	603	0.036	-0.016	-0.009	-0.035
<i>Alburnus alburnus</i>	2480	0.007	0.008	0.022	0.023	2057	-0.005	-0.005	0.009	0.019
<i>Ameiurus melas</i>	64	0.023	0.019	-0.053	-0.035	28	0.081	0.052	-0.002	0.050
<i>Anguilla anguilla</i>	12173	0.016	0.000	0.006	0.002	10113	0.010	-0.004	0.004	-0.003
<i>Barbatula barbatula</i>	21344	0.052	0.034	0.027	0.026	17939	0.052	0.032	0.024	0.023
<i>Barbus barbus</i>	4813	0.019	0.015	0.004	0.005	4021	0.019	0.012	0.002	-0.002
<i>Blicca bjoerkna</i>	126	0.004	0.016	0.032	0.026	91	0.000	0.006	0.027	0.018
<i>Carassius sp.</i>	46	-0.046	-0.062	-0.002	0.043	35	-0.038	-0.044	0.004	-0.034
<i>Chondrostoma nasus</i>	268	0.004	-0.028	0.001	0.001	198	0.032	-0.032	0.007	-0.008
<i>Cottus gobio</i>	160	0.182	0.032	0.071	0.008	79	0.186	0.060	0.083	0.028
<i>Cottus perifretum</i>	10586	0.029	0.020	0.027	0.023	8417	0.023	0.013	0.023	0.016
<i>Cyprinus carpio</i>	54	0.044	0.034	0.065	0.028	38	0.007	-0.007	0.046	0.082
<i>Esox lucius</i>	1073	0.032	0.036	0.020	0.026	868	0.034	0.048	0.031	0.036
<i>Gasterosteus gymnurus</i>	89	0.160	0.103	0.112	0.036	70	0.154	0.094	0.074	-0.019
<i>Gobio gobio</i>	14353	0.044	0.027	0.031	0.031	11055	0.045	0.030	0.028	0.026
<i>Gobio lozanoi</i>	36	-0.025	-0.014	-0.002	-0.032	36	-	-	-	-
<i>Gobio occitaniae</i>	1848	0.020	0.033	0.036	0.049	837	0.016	0.031	0.027	0.028
<i>Gymnocephalus cernua</i>	214	0.042	0.026	0.038	0.024	179	0.043	0.028	0.054	0.044
<i>Lampetra planeri</i>	2043	0.086	0.050	0.042	0.026	1646	0.068	0.025	0.035	0.014
<i>Lepomis gibbosus</i>	6180	0.017	0.017	0.013	0.012	4929	0.038	0.012	0.024	0.004
<i>Leuciscus burdigalensis</i>	597	0.021	0.027	0.013	0.034	417	0.039	0.026	0.010	0.042
<i>Leuciscus leuciscus</i>	961	0.065	0.056	0.035	0.053	634	0.068	0.063	0.035	0.064
<i>Perca fluviatilis</i>	1720	0.033	0.012	0.017	0.002	1360	0.010	0.007	0.007	0.006
<i>Phoxinus phoxinus</i>	22170	0.042	0.025	0.030	0.023	18415	0.041	0.027	0.028	0.028
<i>Pungitius laevis</i>	105	0.009	0.025	0.013	-0.004	79	0.075	0.058	0.074	0.012
<i>Rhodeus amarus</i>	174	0.048	-0.011	0.027	-0.006	119	0.047	-0.014	0.022	-0.007

<i>Rutilus rutilus</i>	17860	0.002	0.002	0.005	0.006	14920	-0.001	0.000	0.005	0.003
<i>Salmo salar</i>	153	0.108	0.109	0.108	0.085	90	0.150	0.186	0.135	0.132
<i>Salmo trutta</i>	29691	0.036	0.031	0.033	0.027	25672	0.031	0.028	0.030	0.025
<i>Scardinius erythrophthalmus</i>	87	0.004	-0.011	-0.002	-0.018	76	-0.020	-0.031	-0.013	-0.040
<i>Squalius cephalus</i>	27854	0.031	0.018	0.026	0.021	23334	0.028	0.021	0.023	0.020
<i>Telestes souffia</i>	220	0.077	0.064	0.080	0.040	109	0.111	0.089	0.111	0.055
<i>Tinca tinca</i>	445	0.063	0.046	0.063	0.045	371	0.063	0.062	0.070	0.041

Npairs is the number of cross-correlation coefficients for overall and inter-catchments species synchrony. Significant ($P < 0.05$) results are in bold. For the definition of TSTs, see the text.

Table S5. Scale of synchrony and synchrony at short distances estimated for the 34 fish species.

Species name	Npairs	Scale of synchrony (kms)				Synchrony at short distances			
		Raw data	TST I	TST II	TST III	Raw data	TST I	TST II	TST III
<i>Abramis brama</i>	204	-(-;-)	-(-;-)	-(-;-)	-(-;-)	-0.03(-0.1;0.05)	-0.04(-0.1;0.05)	-0.07(-0.2;0.05)	-0.04(-0.1;0.06)
<i>Alburnoides bipunctatus</i>	794	209(-;-)	308(196;418)	193(121;288)	270(94.1;708)	0.09(-0.03;0.2)	0.08(0.03;0.1)	0.1(0.03;0.2)	0.07(0.002;0.1)
<i>Alburnus alburnus</i>	2480	271(147;632)	169(-;-)	540(-;-)	371(-;-)	0.07(0.01;0.1)	0.04(-0.02;0.09)	0.03(-0.02;0.08)	0.002(-0.03;0.03)
<i>Ameiurus melas</i>	64	-(-;-)	-(-;-)	-(-;-)	-(-;-)	-0.05(-0.4;0.3)	-0.03(-0.2;0.1)	-0.04(-0.2;0.1)	-0.03(-0.2;0.1)
<i>Anguilla anguilla</i>	12173	265(166;417)	454(-;-)	403(-;-)	413(73.8;784)	0.04(0.01;0.06)	0.02(-0.008;0.04)	0.01(-0.003;0.02)	0.01(7e-04;0.03)
<i>Barbatula barbatula</i>	21344	217(190;251)	255(204;446)	263(195;480)	376(168;472)	0.1(0.08;0.1)	0.1(0.07;0.1)	0.1(0.07;0.1)	0.08(0.05;0.1)
<i>Barbus barbus</i>	4813	296(-;-)	366(230;501)	280(203;398)	284(208;397)	0.05(-0.03;0.1)	0.03(0.01;0.05)	0.07(0.03;0.1)	0.07(0.04;0.1)
<i>Blicca bjoerkna</i>	126	-(-;-)	-(-;-)	279(-;-)	346(-;-)	-0.07(-0.3;0.1)	-0.01(-0.2;0.2)	0.08(-0.02;0.2)	0.03(-0.09;0.2)
<i>Carassius sp.</i>	46	326(-;-)	-(-;-)	202(-;-)	221(139;344)	0.004(-0.2;0.2)	-0.02(-0.2;0.2)	0.1(-0.08;0.3)	0.3(0.1;0.5)
<i>Chondrostoma nasus</i>	268	155(-;-)	84.5(-;-)	185(-;-)	-(-;-)	0.06(-0.07;0.2)	0.009(-0.1;0.1)	0.06(-0.05;0.2)	-0.003(-0.1;0.09)
<i>Cottus gobio</i>	160	-(-;-)	-(-;-)	259(-;-)	-(-;-)	-0.1(-0.3;0.09)	-0.03(-0.2;0.1)	0.008(-0.08;0.1)	-0.002(-0.1;0.1)
<i>Cottus perifretum</i>	10586	310(274;347)	349(279;406)	310(264;357)	310(266;355)	0.06(0.05;0.08)	0.04(0.02;0.07)	0.04(0.03;0.06)	0.05(0.03;0.06)
<i>Cyprinus carpio</i>	54	270(-;-)	270(-;-)	270(-;-)	-(-;-)	0.02(-0.1;0.2)	0.001(-0.1;0.1)	0.002(-0.1;0.1)	-0.01(-0.1;0.1)
<i>Esox lucius</i>	1073	-(-;-)	-(-;-)	-(-;-)	-(-;-)	-0.004(-0.04;0.04)	-0.02(-0.07;0.03)	-0.03(-0.08;0.02)	-0.003(-0.04;0.04)
<i>Gasterosteus gymnurus</i>	89	393(-;-)	119(-;-)	339(-;-)	80.8(-;-)	0.07(-0.09;0.2)	0.1(-0.2;0.4)	0.09(-0.04;0.2)	0.2(-0.1;0.4)
<i>Gobio gobio</i>	14353	338(275;401)	387(255;477)	338(298;378)	385(324;437)	0.04(0.02;0.05)	0.02(0.003;0.04)	0.05(0.04;0.06)	0.03(0.01;0.05)
<i>Gobio lozanoi</i>	36	25.1(-;-)	26.9(18.9;34)	26.5(17.3;34.3)	27.9(-;-)	0.3(-0.09;0.8)	0.5(0.05;0.9)	0.4(0.006;0.7)	0.4(-0.05;0.8)
<i>Gobio occitaniae</i>	1848	80.8(56.9;253)	216(79.8;258)	200(64.8;238)	172(133;217)	0.1(0.03;0.3)	0.09(0.01;0.2)	0.1(0.02;0.2)	0.1(0.05;0.1)
<i>Gymnocephalus cernua</i>	214	-(-;-)	390(-;-)	390(-;-)	-(-;-)	-0.02(-0.1;0.06)	0.02(-0.06;0.1)	0.004(-0.08;0.08)	-0.009(-0.1;0.09)
<i>Lampetra planeri</i>	2043	102(13.3;836)	114(-;-)	109(-;-)	78.4(51.4;121)	0.07(4e-04;0.1)	0.06(-0.006;0.1)	0.06(-0.008;0.1)	0.1(0.04;0.2)
<i>Lepomis gibbosus</i>	6180	91.1(68.1;130)	108(-;-)	85.8(33.5;145)	105(-;-)	0.1(0.06;0.2)	0.04(-0.01;0.09)	0.07(0.005;0.1)	0.04(-0.02;0.09)
<i>Leuciscus burdigalensis</i>	597	-(-;-)	-(-;-)	89.2(-;-)	-(-;-)	-0.02(-0.07;0.04)	-0.02(-0.07;0.04)	0.003(-0.06;0.07)	-0.02(-0.07;0.03)
<i>Leuciscus leuciscus</i>	961	221(50.9;395)	221(-;-)	221(115;328)	221(55;389)	0.04(0.003;0.08)	0.03(-0.005;0.07)	0.05(0.02;0.09)	0.04(0.004;0.08)
<i>Perca fluviatilis</i>	1720	217(-;-)	327(-;-)	-(-;-)	-(-;-)	0.03(-0.02;0.08)	0.01(-0.02;0.04)	-0.01(-0.04;0.02)	-0.008(-0.04;0.03)
<i>Phoxinus phoxinus</i>	22170	200(179;218)	208(166;240)	210(187;229)	224(157;256)	0.1(0.06;0.1)	0.09(0.06;0.1)	0.09(0.05;0.1)	0.09(0.05;0.1)
<i>Pungitius laevis</i>	105	46.3(30.1;67.3)	62(31.4;272)	50.3(-;-)	44.3(25.6;64.9)	0.3(0.07;0.6)	0.3(0.02;0.5)	0.3(-0.01;0.5)	0.3(0.04;0.6)

<i>Rhodeus amarus</i>	174	116(-;-)	113(-;-)	286(-;-)	118(-;-)	0.1(-0.2;0.4)	0.09(-0.2;0.4)	0.01(-0.1;0.1)	0.05(-0.1;0.2)
<i>Rutilus rutilus</i>	17860	262(188;390)	304(-;-)	371(92.4;649)	352(-;-)	0.03(0.01;0.05)	0.01(-0.003;0.03)	0.01(9e-04;0.02)	0.008(-0.004;0.02)
<i>Salmo salar</i>	153	199(-;-)	172(-;-)	166(-;-)	149(-;-)	0.02(-0.2;0.2)	0.1(-0.03;0.2)	0.08(-0.07;0.2)	0.09(-0.03;0.2)
<i>Salmo trutta</i>	29691	335(288;402)	349(312;395)	374(286;478)	364(307;429)	0.1(0.1;0.2)	0.1(0.1;0.2)	0.1(0.1;0.2)	0.1(0.1;0.1)
<i>Scardinius erythrophthalmus</i>	87	413(-;-)	413(-;-)	413(-;-)	-(-;-)	0.1(-0.03;0.3)	0.01(-0.1;0.2)	0.07(-0.08;0.2)	-0.01(-0.2;0.2)
<i>Squalius cephalus</i>	27854	245(210;280)	276(210;361)	280(222;317)	311(123;355)	0.08(0.05;0.1)	0.03(0.01;0.05)	0.08(0.05;0.1)	0.05(0.02;0.09)
<i>Telestes souffia</i>	220	59.7(-;-)	-(-;-)	183(-;-)	183(-;-)	0.1(-0.1;0.4)	-0.03(-0.1;0.04)	0.01(-0.06;0.08)	0.01(-0.06;0.08)
<i>Tinca tinca</i>	445	117(-;-)	382(-;-)	-(-;-)	123(-;-)	0.007(-0.2;0.2)	0.001(-0.07;0.07)	-0.01(-0.1;0.08)	0.07(-0.09;0.2)

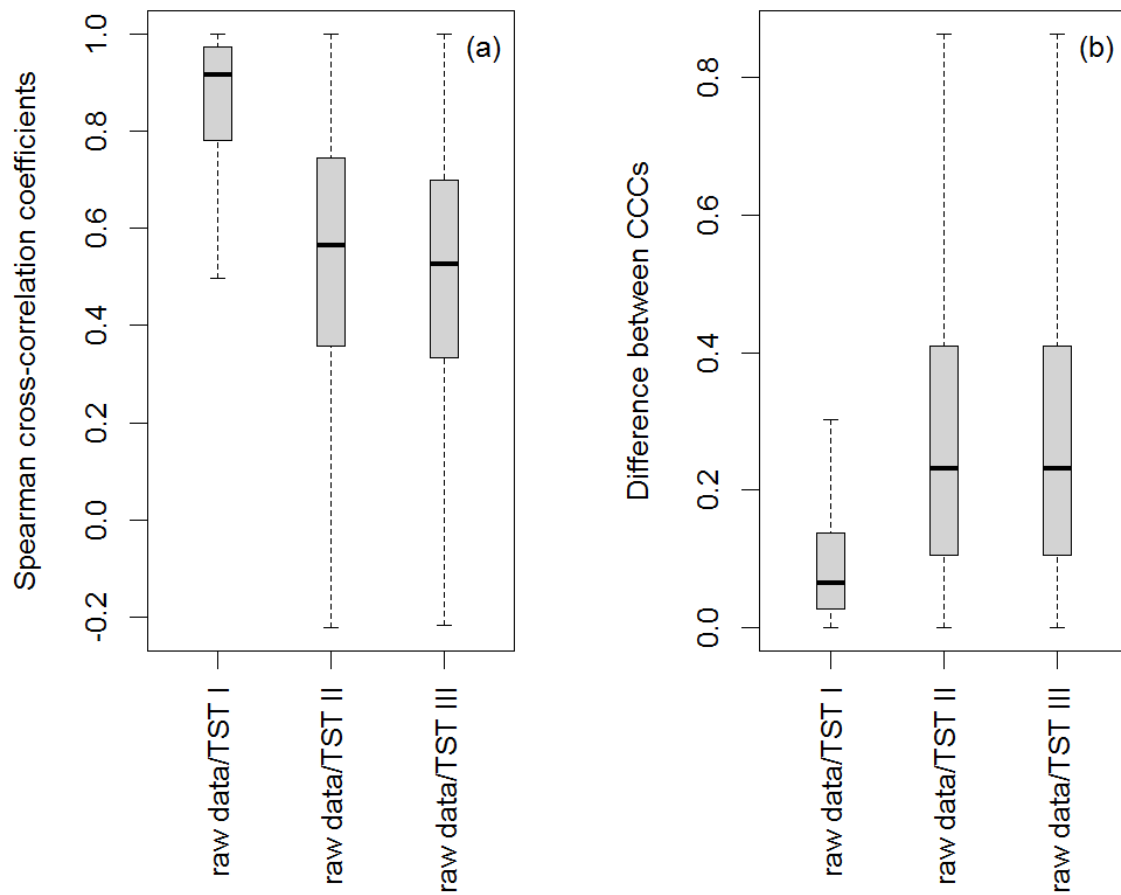
Npairs is the number of cross-correlation coefficients; scale of synchrony (kms) is the estimated distance above which the level of synchrony is no longer different from 0 (for some species this value was not relevant as the level of synchrony was negative at short distances); synchrony at short distances is the overall level of synchrony for sites close to each others. 95% confidence intervals are presented within brackets (for the scale of synchrony it was not possible to estimate confidence intervals when the upper or lower bounds of the relationship between population synchrony and the Euclidean distance did not cross the line $y=0$). For the definition of TSTs, see the text.

Table S6. Influence of the Euclidean distance between populations and temperature synchrony on the level of synchrony between populations for the 34 fish species.

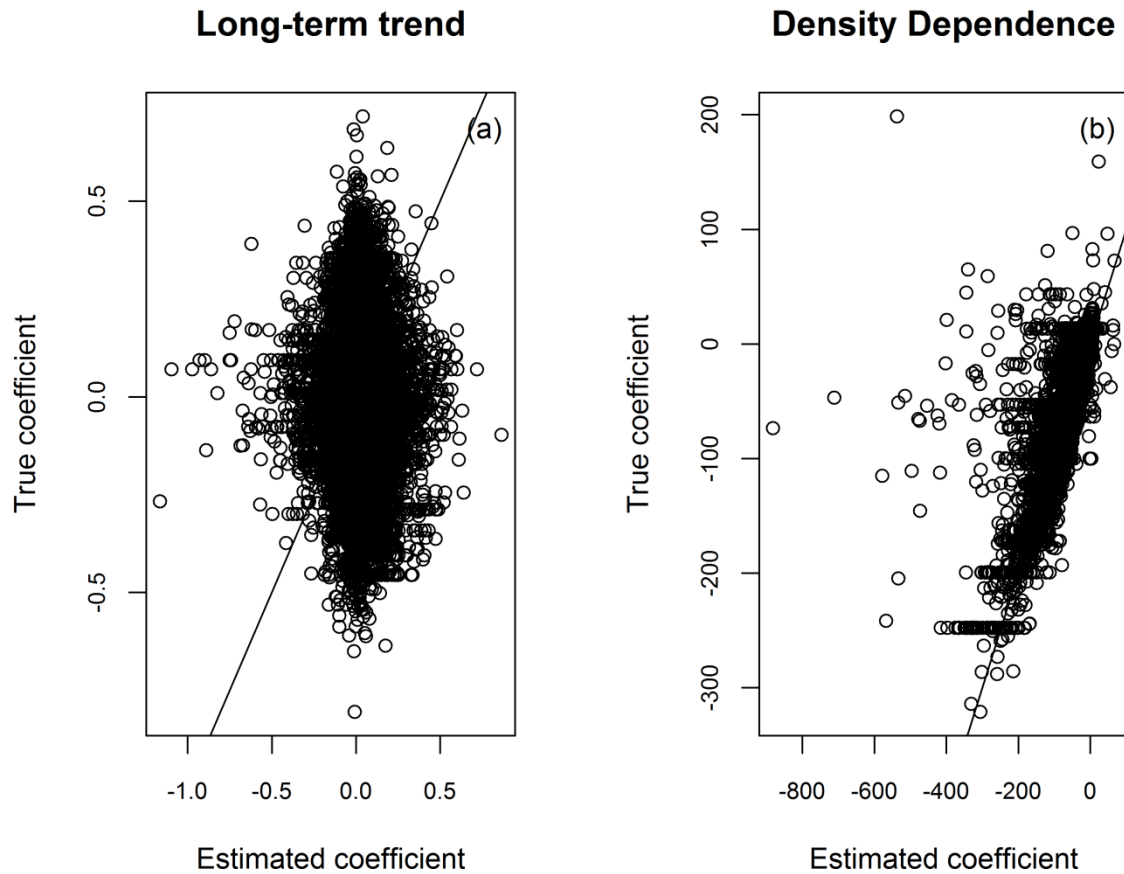
Species name	Npairs	Euclidean distance				Temperature synchrony			
		Raw data	TST I	TST II	TST III	Raw data	TST I	TST II	TST III
<i>Abramis brama</i>	204	0.064	0.065	-0.028	0.016	-0.041	-0.0349	0.019	-0.052
<i>Alburnoides bipunctatus</i>	794	-0.018	-0.120	-0.037	-0.080	0.023	0.0997	0.033	0.078
<i>Alburnus alburnus</i>	2480	-0.072	-0.025	-0.030	-0.001	0.009	-0.0113	-0.029	-0.032
<i>Ameiurus melas</i>	64	0.022	0.039	0.056	0.046	-0.209	-0.2475	0.017	0.065
<i>Anguilla anguilla</i>	12173	-0.008	-0.021	-0.012	-0.020	-0.016	0.0166	-0.003	0.009
<i>Barbatula barbatula</i>	21344	-0.045	-0.050	-0.049	-0.039	0.011	0.0052	0.006	-0.001
<i>Barbus barbus</i>	4813	-0.098	-0.057	-0.071	-0.071	0.038	0.0217	0.016	0.030
<i>Blicca bjoerkna</i>	126	-0.055	-0.086	-0.193	-0.167	0.041	-0.0136	0.071	0.029
<i>Carassius sp.</i>	46	-0.012	0.042	-0.130	-0.386	-0.183	-0.0328	-0.150	-0.050
<i>Chondrostoma nasus</i>	268	-0.048	-0.013	-0.074	-0.012	0.048	0.0074	0.003	-0.024
<i>Cottus gobio</i>	160	0.105	0.000	-0.015	0.005	0.099	0.1242	0.154	0.112
<i>Cottus perifretum</i>	10586	-0.086	-0.075	-0.067	-0.070	0.067	0.0404	0.034	0.042
<i>Cyprinus carpio</i>	54	-0.015	0.021	0.023	0.066	-0.022	-0.1097	-0.132	-0.057
<i>Esox lucius</i>	1073	0.006	0.020	0.036	0.010	0.069	0.0369	0.028	0.042
<i>Gasterosteus gymnurus</i>	89	-0.197	-0.140	-0.189	-0.092	0.122	-0.0697	0.060	0.038
<i>Gobio gobio</i>	14353	-0.048	-0.042	-0.074	-0.070	0.050	0.0544	0.058	0.061
<i>Gobio lozanoi</i>	36	0.062	-0.057	-0.093	-0.118	-0.041	0.0253	-0.123	-0.097
<i>Gobio occitaniae</i>	1848	-0.081	-0.099	-0.074	-0.123	0.094	0.1553	0.116	0.141
<i>Gymnocephalus cernua</i>	214	0.022	-0.076	-0.032	-0.058	0.013	0.0178	0.023	0.054
<i>Lampetra planeri</i>	2043	0.004	0.010	-0.017	-0.010	0.090	0.0729	0.068	0.049
<i>Lepomis gibbosus</i>	6180	0.002	0.014	0.011	0.008	0.023	0.0058	0.000	0.002
<i>Leuciscus burdigalensis</i>	597	0.028	0.030	0.021	0.037	-0.020	-0.0911	-0.031	-0.124
<i>Leuciscus leuciscus</i>	961	-0.082	-0.065	-0.101	-0.081	0.047	0.0194	0.024	0.009
<i>Perca fluviatilis</i>	1720	-0.003	-0.012	0.022	0.020	-0.026	-0.0170	-0.032	-0.052
<i>Phoxinus phoxinus</i>	22170	-0.008	-0.018	-0.018	-0.018	-0.007	0.0094	-0.005	0.003
<i>Pungitius laevis</i>	105	0.095	0.013	0.092	0.092	-0.108	-0.1265	-0.041	-0.137
<i>Rhodeus amarus</i>	174	-0.006	0.091	-0.027	0.040	-0.119	-0.1375	-0.067	-0.079
<i>Rutilus rutilus</i>	17860	-0.022	-0.012	-0.018	-0.010	0.011	0.0056	0.010	0.011
<i>Salmo salar</i>	153	-0.101	-0.146	-0.086	-0.084	-0.011	0.0733	-0.034	-0.024

<i>Salmo trutta</i>	29691	-0.116	-0.130	-0.107	-0.104	0.065	0.0749	0.061	0.070
<i>Scardinius erythrophthalmus</i>	87	-0.228	-0.027	-0.100	0.032	0.378	0.0605	0.010	0.095
<i>Squalius cephalus</i>	27854	-0.036	-0.021	-0.037	-0.024	0.016	0.0011	0.031	0.007
<i>Telestes souffia</i>	220	0.050	0.083	-0.027	-0.038	0.010	-0.0129	0.112	0.063
<i>Tinca tinca</i>	445	-0.061	-0.011	-0.034	-0.003	0.094	-0.0017	0.035	0.018

Npairs is the number of cross-correlation coefficients. Results represent correlation coefficients computed between two dissimilarity matrices (Mantel tests). Significant ($P < 0.05$) correlations are in bold. For the definition of TSTs, see the text.



198
 199 **Fig. S1** (a) Correlations between the raw time series and the time series obtained with each of
 200 the TSTs and (b) differences between the CCCs calculated using the raw data and those
 201 calculated using the TSTs (n=20118). For the definition of TSTs, see the text
 202



203
204 **Fig. S2** Relationship between the true and the estimated coefficients of (a) long-term trend
205 (n=20118) and (b) density dependence (n=20083). The black line represents a perfect
206 correlation between the true and the estimated coefficients. For the definition of TSTs, see the
207 text
208

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