Supplementary Materials

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Supplementary S1: Information sources

We gathered information about species that inhabit freshwater and cropland ecosystems potentially adjacent to each other. We focused on birds, fish, amphibians, aquatic and terrestrial invertebrates, macrophytes, diatoms and crop species. In each case, we searched for the presence of species or groups (functional or taxonomic) within MTEs and their direct ecological interactions, which were mostly of the consumer-resource interaction type, including predator-prey and parasitoid-host. To define trophic interactions, we searched for published information on the diet of identified species or functional groups. Below we provide specific details for freshwater and crop ecosystems, as well as for shared components.

Freshwater ecosystem

Published information for building the community network of the freshwater ecosystem was obtained mainly from the work of Palma et al. (2013), who described communities inhabiting Mediterranean basins of central Chile. Additional information about the presence of fish was taken from the review made by Vila and Habit (2015), while their diet was defined according to Gillespie (2001) and the expert knowledge of local ichthyologists (E. Habit, personal communication). Aquatic bird species inhabiting Chilean MTEs were defined following Jaramillo et al. (2003), Victoriano et al. (2006), Chester (2010), Peña-Villalobos et al. (2012) and the expert knowledge of local ornithologists (M. Sallaberry, personal communication). On the other hand, the potential diet of birds was obtained mainly from del Hoyo et al. (2018), and additional sources (Yorio and Bertellotti 2002, Bertellotti et al. 2003). Trophic and non-trophic interactions between diatoms, macrophytes and aquatic invertebrates were taken from Feio et al. (2017), using the assumptions presented by them for middle reaches and large lowland rivers.

Cropland ecosystem

For building the community network for the cropland ecosystem we began reviewing crop species cultivated in Chilean MTEs. Then, our search was focused on pest and pollinator species associated with those crops. We also searched for invertebrate natural enemies of the pests found. Finally, we collected information on bird species that are regular visitors of cropland areas within Chilean MTEs, a place where birds possibly interact with animals and crops. In most cases, we did not find enough information from the Clarivate WoS and Scholar Google searches. The only exception was for the search related to natural enemies.

Crop species were defined according to ODEPA (2018), while information about pests was gathered from González (1989), Prado (1991) and Luppichini et al. (2013). For pollinator species, we mainly used data from Valdés (2002), Smith-Ramírez and Yáñez (2010), and FAO (2017). In the case of invertebrate natural enemies of pests, we gathered information mainly from the studies of Prado (1991) and Rojas (2005). This was complemented with expert knowledge (B. Lavandero, personal communication), along with research papers and other data sources (for a complete reference list, see the section “References: Pests and

their natural enemies"). Presence of bird species on croplands was defined following Jaramillo et al. (2003), Chester (2010), Celis-Diez et al. (2011), Muñoz-Sáez et al. (2017), and supplemented with expert knowledge (M. Sallaberry, personal communication), and AvesdeChile (2018). Diet of each bird species was obtained from del Hoyo et al. (2018).

Linking freshwater and cropland ecosystems

The groups defined as a link between communities of freshwater and cropland ecosystems must accomplish the following requirements: (i) the biological group must be listed as an amphibious predator, (ii) the biological group must be described as an inhabitant of both freshwater and terrestrial systems, and (iii) the biological group must predate on freshwater and cropland groups.

According to the definition of Sabo and Hoekman (2015), amphibious predators are species of birds, mammals, reptiles, amphibians, and carnivore flying insects that cross aquatic-terrestrial boundaries, predating in both systems simultaneously. These amphibious predators may act as links between ecosystems, permitting the transmission of perturbations across ecosystems. Among the FUs present in our metanetwork, only birds, amphibians, and odonates can be classified as amphibious predators.

For odonates and amphibians, we assumed that both inhabit freshwater and terrestrial systems since it is known that they spend at least part of their life cycle in those ecosystems. The presence of odonates in Chilean MTEs was assumed according to data reported by Palma et al. (2013). For amphibians, we included species that inhabit Mediterranean Chile, according to Ortiz and Díaz-Páez (2006), Rabanal and Nuñez (2009), and information given by local experts (M. Sallaberry and R. Solis, personal communication). On the other hand, for birds, we considered only the species that were listed simultaneously as aquatic birds and cropland birds, according to Jaramillo et al. (2003), Victoriano et al. (2006), Chester (2010), Peña-Villalobos et al. (2012), Muñoz-Sáez et al. (2017) and the expert knowledge of local ornithologists (M. Sallaberry, personal communication). We classified this group of birds as a FU named Birds (FCI).

The diets of birds (FCI), odonates, and amphibians show that these groups predate on both freshwater and cropland FUs. Bird species' diets were obtained from del Hoyo et al. (2018), while the diet of odonates was obtained from Pritchard (1964), McCormick and Polis (1982), Soares et al. (2003) and Simaika and Samways (2008). On the other hand, diets of anurans were obtained from Lafferty and Page (1997), Lobos et al. (1999), Lobos and Jaksic (2005), and Vidal and Labra (2008).

For birds (FCI), amphibians (anurans), and odonates, we did not find enough information from the Clarivate WoS and Scholar Google searches; therefore, we gathered data from alternative sources.

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Supplementary S2: Steps of the model construction process

Step 1: Grouping biological entities

Most of the raw information used to build the metanetwork is not species-specific and usually is at the family taxonomic level. On the other hand, we constructed much of our freshwater sub-network based on the work of Palma et al. (2013), who not provided detailed information on the diet of aquatic species (or families). The latter contrasts with the greater knowledge about species' diets for the cropland ecosystem. To solve this problem, we decided to create groups ("Functional Units") using a level of aggregation relatively homogeneous for all the living groups, which at the same time generates a more manageable number of network elements. In the present work we defined a Functional Unit as a group that may be either a functional group, a taxonomic group, a trophic group, or a guild). Biological entities within a FU share a roughly equivalent relational role within the network and thus exhibit a similar function as mass and energy conveyors. In the case of freshwaters, macrophyte families were classified into functional groups, following Ramírez and San Martín (2006), as hydrophyte (truly aquatic plants), helophyte (emergent species), and hydrophyte/helophyte, if a family has members that belong to the two functional groups. Diatom orders were grouped into guilds according to their potential for tolerating nutrient limitation and physical disturbance, following the guild classification of Passy (2007) and Rimet and Bouchez (2012). Specifically, according to the information obtained from the study made by Heine-Fuster et al. (2021), we assigned a guild to each species. When the data was unavailable for a species, we deduced the species' guild from the work of Rimet and Bouchez (2012). We assigned diatom orders to the following ecological guilds: high-profile, motile, planktic, and planktic/high-profile. The last guild is formed by an order that has species belonging to both planktic and high-profile guilds. We excluded the low-profile diatom species from our model since they do not interact with macrophytes and (or) invertebrates in middle reaches and large lowland rivers, according to Feio et al. (2017).

For aquatic invertebrates, we used the functional classification proposed by Palma et al. (2013), aggregating families into the groups of predators, filter-feeders, shredders, grazers, collectors, filter-feeders/collectors/predators, collectors/predators, collectors/shredders, collectors/grazers, and collectors/grazers/predators. Fish were classified into four groups: (i) omnivores, a group including fish families preying on invertebrates and diatoms; (ii) omnivores-FM, which are omnivores that also prey on fish and macrophytes; (iii) carnivores; and (iv) detritivores. Aquatic bird species were assigned to three trophic groups according to their feeding preferences. Aquatic birds that prey on both vertebrates and invertebrates were classified as carnivores. On the other hand, species feeding on a carnivore diet that also consume plants were classified as omnivores. This last group was divided into omnivores-AP and omnivores-TP, that consume aquatic and terrestrial plants, respectively.

For the cropland ecosystem, we grouped most of the biological entities using a taxonomic criterion, which generated a suitable number of elements. Moreover, highly related species

tend to exhibit similar functional traits (Srivastava et al. 2012) and ecological interactions (Bersier and Kehrli 2008, Gómez et al. 2010). Consequently, we classified the families of pests, pollinators and pests' natural enemies at the level of order, with the exception of some groups that will be explained case by case. The groups of pests included were Acariformes (Sarcoptiformes and Trombidiformes), Collembola, Hemiptera, Thysanoptera, Lepidoptera, Diptera, Hymenoptera, Coleoptera, Orthoptera and the class Gastropoda. The last group was included at the level of class due to that in most cases we did not find information about them at the order level. The families Aphididae, Curculionidae, and Noctuidae were classified as independent FUs because they are highly generalist pests. Families of pests' natural enemies were classified into the following groups: Araneae, Acari (Trombidiformes and Mesostigmata), Hemiptera, Thysanoptera, Orthoptera, Mantodea, Neuroptera, Coleoptera, Diptera, Hymenoptera and Strepsiptera. Finally, we grouped pollinator families into Coleoptera, Diptera, Hemiptera, Hymenoptera, and Lepidoptera. The tribes Apini and Bombini were classified as independent FUs because they are highly generalist pollinators. A special group was created for representing the families that play the role of both pests' natural enemies and pollinators (PNE/P). This group includes the dipteran families Tachinidae and Syrphidae. According to their feeding habits, cropland birds were classified into: carnivores, a group of birds that preys both on vertebrates and invertebrates; omnivores-C, a group that consumes animal and vegetal, including crop plants; and omnivores-I, a group that mainly consumes invertebrates and non-crop plants. Crop species were grouped into annuals, orchards, and vegetables. In general, annual crops do not require zoopollination, excepting bean, raps and sunflower, which productions receive a low-to-moderate positive impact from pollinators (Klein et al. 2007, FAO 2017). For this reason, annual crops were separated into two groups depending on whether crop species are pollinated by animals or not. On the other hand, orchards were sub-grouped into deciduous and perennial. Each FU described above was represented as a node (vertex) of our network model.

Step 2: Establishing links among Functional Units

Once FUs (network nodes) were formed, we proceeded to establish the links among them. First, for each pair of potentially adjacent nodes j and i, we constructed a biadjacency matrix B_{ij}, whose rows and columns represent the groups of biological entities composing the node j and i, respectively. The cells of B_{ij} were filled with ones if the corresponding biological entities exhibit an ecological interaction and with zeros otherwise. To simplify the analysis, we excluded all the matrices B_{ii} and B_{ji}, finally giving a total of $(n^2 - n)/2$ biadjacency matrices for n FUs. Then, for establishing a between-node interaction, we calculated the connectance of each bipartite adjacency matrix as the ratio of number of recorded filled cells in B_{ij} over the total number of cells in B_{ij}. We defined that a link exists between nodes i and j if the connectance value of B_{ij} is equal to or greater than 0.2. This procedure allows us to discard all the links with scarce supporting evidence for an interaction. Finally, the nodes with no interactions with any other node were eliminated from the network. This process results in an undirected graph with FUs as nodes and ecological interactions as links.

Step 3: Macrostructure of the network model

Using the undirected graph previously made, we constructed a signed directed graph, transforming each undirected link into a signed directed arc. The signed digraph used for describing our study system can be represented as a community matrix M. Each element m_{ij} of M represents the direct ecological effect of node j on node i, with a value of 0 (no interaction), 1 (positive effect) or -1 (negative effect). All nodes were assumed to have self-damping and thus all $m_{ii} < 0$.

The system was organized in four levels of resolution. At the lowest level 1, each node (FU) represents a group of biological entities that may be either a functional group, a taxonomic group, a trophic group, or a guild (Fig. 1, nodes from 1 to 63). At level 2, FUs (nodes) that share general functional features are grouped into "aggregates" (Fig. 1, groups from A to K). The freshwater ecosystem's aggregates are aquatic birds, fish, aquatic invertebrates, diatoms, and macrophytes (Fig. 1, groups from A to E). Cropland ecosystem aggregates are cropland birds, pests' natural enemies (invertebrates), pests, pollinators, and crops (Fig. 1, groups from G to K). We also included an aggregate containing species that function as a link between freshwater and cropland ecosystems (Fig. 1, group F). At level 3, aggregates are grouped into two community networks, one belonging to the freshwater ecosystem and the other to the cropland ecosystem (Fig. 1). Also, at this level, we included a community module containing the ecosystems-linking aggregate. This group comprises birds, amphibians, and odonates that act as predators in both ecosystems. We expect these mobile species, exerting amphibious predation, will be the most relevant groups in transmitting effects within the freshwater-cropland metanetwork since they mediate indirect interactions between adjacent networks (Power 1984, Knight et al. 2005, Frost et al. 2016).

At the highest level 4, the ecosystems-linking module and the community networks belonging to each ecosystem are grouped into a metanetwork representing the fundamental structure of the system (Fig. 1).

Additionally, for conducting some analyses, we defined three different scales of influence for each FU: i) the intra-aggregate scale is defined for assessing the influence of a FU on other FUs belonging to the same aggregate, ii) the intra-ecosystem scale is defined for assessing the influence of a FU on other FUs belonging to different aggregates within the same ecosystem (i.e., freshwater or cropland). and iii) the inter-ecosystem scale is defined for assessing the influence of a FU on other FUs belonging to a different ecosystem. Nodes belonging to the ecosystem-linking aggregate were not considered for defining these categories.

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R Code

Code 1: Stability and press perturbation analysis

```
#Community Matrix
M #read.table()

M=as.matrix(M) #M must be a matrix

iter=1500 #Iteration number
s.e=-4   #Self-effect
f.max=2 #Maximum value for the uniform distribution
f.min=0.5 #Minimum value for the uniform distribution
d=dim(M) #Matrix dimension
dime=d[1]

A=matrix(0,dime,dime) #Empty matrix 1

AA=matrix(0,iter,(dime*dime)) #Empty matrix 2

stab=matrix(0,iter,1) #Empty matrix 3

one.zero=matrix(0,iter,1) #Empty matrix 4

#Adding random values and self-effect (fixed)

 for (h in 1:iter){
  for (j in 1:dime){for (k in 1:dime){

    A[j,k]=round(runif(1,f.min,f.max),1)*M[j,k]

  }
  }

  for (i in 1:dime){
    A[i,i]=c(s.e)

  }

  AA[h,1:(dime*dime)]=as.vector(A)

 }
```

```
#Stability

 for (m in 1:iter){
  eig=eigen(matrix(c(AA[m,]),dime,dime,byrow = T))
  e=eig$values
  sum.e=sum(sign(Re(e)))
  sum.e
  stab[m]=sum.e
  one.zero[m]=if (sum.e==-dime) 1 else 0
 }

#Stable fraction
frac=sum(one.zero)/iter
frac

#Prediction (Press perturbation analysis)
P=matrix(0,(iter),(dime*dime))

for (w in 1:iter){

 P[w,1:(dime*dime)]=as.vector(t(solve(-(matrix(c(AA[w,]),dime,dime,byrow = F)))))

}

Mean_node=matrix(0,1,dime*dime,byrow=T)# Empty matrix for mean values

#Mean net effects values considering standard deviation
for (e in 1:(dime*dime)){

 if.pos= if (mean(P[,e])>0) (mean(P[,e])-sd(P[,e])) else (0)
 if.neg= if (mean(P[,e])<0) (mean(P[,e])+sd(P[,e])) else (0)

 is.zero.if.pos= if (if.pos<=0) 0 else(mean(P[,e]))
 is.zero.if.neg= if (if.neg>=0) 0 else(mean(P[,e]))

 Trunc.val=if (mean(P[,e])>0) (is.zero.if.pos) else (is.zero.if.neg)

 Mean_node[,e]= Trunc.val
}


#Final matrix with mean net effects values
Matrix_Mean=matrix(c(Mean_node),dime,dime,byrow=T)
```

Code 2: Importance of each network node for the transmission of effects (z-scores calculation considering real number values)

```
#Cropland: rows and columns from 1 to 36
#Aquatic: rows and columns from 37 to 60
#Amphibian: row and column 61
#Bird (link): row and column 62
#Odonata: row and column 63

###############
#Control Matrix

#Community Matrix (control)
CM #read.table()

CM=as.matrix(CM) #CM must be a matrix

iter=1500 #Iteration number
s.e=-4   #Self-effect
f.max=2 # Maximum value for the uniform distribution
f.min=0.5 #Minimum value for the uniform distribution
d=dim(CM) #Matrix dimension
dime=d[1]

A_C=matrix(0,dime,dime) #Empty matrix 1

AA_C=matrix(0,iter,(dime*dime)) #Empty matrix 2

#Adding random values and self-effect (fixed)

for (h in 1:iter){
  for (j in 1:dime){for (k in 1:dime){

    A_C[j,k]=round(runif(1,f.min,f.max),1)*CM[j,k]

  }
  }

  for (i in 1:dime){
    A_C[i,i]=c(s.e)

  }
```

```
  AA_C[h,1:(dime*dime)]=as.vector(A_C)

}

#Prediction (Press perturbation analysis)
P=matrix(0,(iter),(dime*dime))

for (w in 1:iter){

  P[w,1:(dime*dime)]=as.vector(t(solve(-(matrix(c(AA_C[w,]),dime,dime,byrow = F)))))

}

Mean_node=matrix(0,1,dime*dime,byrow=T)# Empty matrix for mean values

#Mean net effects values considering standard deviation
for (e in 1:(dime*dime)){

  if.pos= if (mean(P[,e])>0) (mean(P[,e])-sd(P[,e])) else (0)
  if.neg= if (mean(P[,e])<0) (mean(P[,e])+sd(P[,e])) else (0)

  is.zero.if.pos= if (if.pos<=0) 0 else(mean(P[,e]))
  is.zero.if.neg= if (if.neg>=0) 0 else(mean(P[,e]))

  Trunc.val=if (mean(P[,e])>0) (is.zero.if.pos) else (is.zero.if.neg)

  Mean_node[,e]= Trunc.val
}

#Control mean matrix
M_control_Mean_node=matrix(c(Mean_node),dime,dime,byrow = T)

#### Mean of the quadrants (control)
MCAC=M_control_Mean_node[1:36,37:60]
MACC=M_control_Mean_node[37:60,1:36]

mean_aquat_crop_control=mean(MCAC)
mean_crop_aquat_control=mean(MACC)

mean_aquat_crop_control
mean_crop_aquat_control
```

```
##############################################################################
#####
#Treatment matrices (node removal)

#Empty matrix. Rows will contain the average matrices after the prediction, without the
node of interest
matrix_mean_nodes=matrix(0,63,(62*62))

#Empty matrix to put the matrices CM after extracting the node of interest
matrix_minus_nodes=matrix(0,63,(62*62))

#Iteration to extract the node of interest from the CM matrix and order the matrices as
vectors
for (z in (1:63)){
  matrix_minus_nodes[z,]=as.vector(CM[-z,-z])
}

#Iteration to obtain the average predictions from the matrices without the node of
interest
for (v in (1:63)) {

  MT=matrix(matrix_minus_nodes[v,],62,62)# Treatment matrix

  iter=1500 #Iteration number
  s.e=-4   #Self-effect
  f.max=2 # Maximum value for the uniform distribution
  f.min=0.5 #Minimum value for the uniform distribution
  d=dim(MT) #Matrix dimension
  dime=d[1]

  A=matrix(0,dime,dime) #Empty matrix 1

  AA=matrix(0,iter,(dime*dime)) #Empty matrix 2

  #Adding random values and self-effect (fixed)
  for (h in 1:iter){
    for (j in 1:dime){for (k in 1:dime){

      A[j,k]=round(runif(1,f.min,f.max),1)*MT[j,k]
    }
    }

    for (i in 1:dime){
      A[i,i]=c(s.e)
```

```
  }

  AA[h,1:(dime*dime)]=as.vector(A)

 }

 #Prediction (Press perturbation analysis)
 P=matrix(0,(iter),(dime*dime))

 for (w in 1:iter){

  P[w,1:(dime*dime)]=as.vector(t(solve(-(matrix(c(AA[w,]),dime,dime,byrow = F)))))

 }

 mean_node=matrix(0,1,62*62,byrow=T)# Empty matrix for mean value

 #Mean net effects values considering standard deviation
 for (e in 1:(62*62)){

  if.pos= if (mean(P[,e])>0) (mean(P[,e])-sd(P[,e])) else (0)
  if.neg= if (mean(P[,e])<0) (mean(P[,e])+sd(P[,e])) else (0)

  is.zero.if.pos= if (if.pos<=0) 0 else(mean(P[,e]))
  is.zero.if.neg= if (if.neg>=0) 0 else(mean(P[,e]))

  Trunc.val=if (mean(P[,e])>0) (is.zero.if.pos) else (is.zero.if.neg)

  mean_node[,e]= Trunc.val
 }

 matrix_mean_nodes[v,]=mean_node

}

#Names of the variables (nodes)
names=c("Bird_C_Carni","Bird_C_Omni_C","Bird_C_Omni_I","Acari_Bcontrol",
      "Araneae_BControl","Coleoptera_BControl","Diptera_Bcontrol",
      "Diptera_BControl_Pollinator","Hemiptera_BControl","Hymenoptera_BControl",
      "Mantodea_BControl","Neuroptera_BControl","Orthoptera_BControl",
      "Thysanoptera_BControl","Acariformes_Pest","Aphididae_Pest",
      "Coleoptera_Pest","Collembola_Pest","Curculionidae_Pest","Diptera_Pest",
      "Gastropoda_Pest","Hemiptera_Pest","Hymenoptera_Pest","Lepidoptera_Pest",
```

```
      "Noctuidae_Pest","Orthoptera_Pest","Thysanoptera_Pest","Apini_Pollinator",
      "Bombini_Pollinator","Diptera_Pollinator","Hymenoptera_Pollinator",
      "Annual_non-pollinated","Annual_pollinated","Decidious_orchard",
      "Perennial_orchard","Vegetable","Bird_A_Carni","Bird_A_Omni_AI",
      "Bird_A_Omni_ATI","Fish_Carnivore","Fish_Detritivore","Fish_Omnivore_FIDM",
      "Fish_Omnivore_ID","AI_Collector","AI_Collector_Grazer",
      "AI_Collector_Grazer_Predator","AI_Collector_Predator","AI_Collector_Shredder",
"AI_Filter","AI_Filter_Collector_Predator","AI_Grazer","AI_Predator","AI_Shredder",
"Diatom_High_Profile","Diatom_Motile","Diatom_Planktic","Diatom_Planktic_High_Profil
e","Macrophyte_Helophyte","Macrophyte_Hydrophyte","Macrophyte_Hydrophyte_Helop
hyte","Amphibian","Bird_ATL","Odonata")


#Empty vector to put the mean of the quadrant "effect from the freshwater to the
cropland system"
mean_aquat_crop=matrix(0,63,1)

#Empty vector to put the mean of the quadrant "effect from the cropland to the
freshwater system"
mean_crop_aquat=matrix(0,63,1)

#### Mean of the quadrants
#Cropland system
for (l in 1:36){

 MPN36=matrix(c(matrix_mean_nodes[l,]),62,62,byrow = T)
 MPN36_CA=MPN36[1:35,36:59]
 MPN36_AC=MPN36[36:59,1:35]
 mean_aquat_crop[l,]=mean(MPN36_CA)
 mean_crop_aquat[l,]=mean(MPN36_AC)
}

#Freshwater system
for (l in 37:60){

 MPN37=matrix(c(matrix_mean_nodes[l,]),62,62,byrow = T)
 MPN37_CA=MPN37[1:36,37:59]
 MPN37_AC=MPN37[37:59,1:36]
 mean_aquat_crop[l,]=mean(MPN37_CA)
 mean_crop_aquat[l,]=mean(MPN37_AC)
}

#System-linking
for (l in 61:63){
```

```
  MPN61=matrix(c(matrix_mean_nodes[l,]),62,62,byrow = T)
  MPN61_CA=MPN61[1:36,37:60]
  MPN61_AC=MPN61[37:60,1:36]
  mean_aquat_crop[l,]=mean(MPN61_CA)
  mean_crop_aquat[l,]=mean(MPN61_AC)
}

#Estimation of the difference between the value obtained from the control matrix
# and the value obtained from the matrix without the specific node

#Freshwater to cropland
delta_aquat_crop=mean_aquat_crop_control-mean_aquat_crop

#Cropland to freshwater
delta_crop_aquat=mean_crop_aquat_control-mean_crop_aquat

### Z-scores estimation

#Mean of the difference: Freshwater to cropland
mean_delta_aquat_crop=mean(delta_aquat_crop)

#Standard deviation of the difference: Freshwater to cropland
sd_delta_aquat_crop=sd(delta_aquat_crop)

#Z-score of the difference: Freshwater to cropland
zeta_delta_aquat_crop=(delta_aquat_crop-
mean_delta_aquat_crop)/sd_delta_aquat_crop

########

#Mean of the difference: Cropland to freshwater
mean_delta_crop_aquat=mean(delta_crop_aquat)

#Standard deviation of the difference: Cropland to freshwater
sd_delta_crop_aquat=sd(delta_crop_aquat)

#Z-score of the difference: Cropland to freshwater
zeta_delta_crop_aquat=(delta_crop_aquat-
mean_delta_crop_aquat)/sd_delta_crop_aquat

######
# Freshwater to cropland
zdac=data.frame(names,zeta_delta_aquat_crop)
```

```
# Cropland to freshwater
zdca=data.frame(names,zeta_delta_crop_aquat)
```

Code 3: Importance of each network node for the transmission of effects (z-scores calculation considering absolute values)

```
#Cropland: rows and columns from 1 to 36
#Aquatic: rows and columns from 37 to 60
#Amphibian: row and column 61
#Bird (link): row and column 62
#Odonata: row and column 63

###############
#Control Matrix

#Community Matrix (control)
CM #read.table()

CM=as.matrix(CM) #CM must be a matrix

iter=1500 #Iteration number
s.e=-4   #Self-effect
f.max=2 # Maximum value for the uniform distribution
f.min=0.5 #Minimum value for the uniform distribution
d=dim(CM) #Matrix dimension
dime=d[1]

A_C=matrix(0,dime,dime) #Empty matrix 1

AA_C=matrix(0,iter,(dime*dime)) #Empty matrix 2

#Adding random values and self-effect (fixed)

for (h in 1:iter){
 for (j in 1:dime){for (k in 1:dime){

   A_C[j,k]=round(runif(1,f.min,f.max),1)*CM[j,k]

 }
 }

 for (i in 1:dime){
```

```
   A_C[i,i]=c(s.e)

  }

  AA_C[h,1:(dime*dime)]=as.vector(A_C)

}

#Prediction (Press perturbation analysis)
P=matrix(0,(iter),(dime*dime))

for (w in 1:iter){

  P[w,1:(dime*dime)]=as.vector(t(solve(-(matrix(c(AA_C[w,]),dime,dime,byrow = F)))))

}

Mean_node=matrix(0,1,dime*dime,byrow=T)# Empty matrix for mean values

#Mean net effects values considering standard deviation
for (e in 1:(dime*dime)){

  if.pos= if (mean(P[,e])>0) (mean(P[,e])-sd(P[,e])) else (0)
  if.neg= if (mean(P[,e])<0) (mean(P[,e])+sd(P[,e])) else (0)

  is.zero.if.pos= if (if.pos<=0) 0 else(mean(P[,e]))
  is.zero.if.neg= if (if.neg>=0) 0 else(mean(P[,e]))

  Trunc.val=if (mean(P[,e])>0) (is.zero.if.pos) else (is.zero.if.neg)

  Mean_node[,e]= Trunc.val
}

#Control mean matrix
M_control_Mean_node=matrix(c(Mean_node),dime,dime,byrow = T)

#### Mean of the quadrants (control)
MCAC=M_control_Mean_node[1:36,37:60]
MACC=M_control_Mean_node[37:60,1:36]

mean_aquat_crop_control= mean(abs(MCAC))
mean_crop_aquat_control= mean(abs(MACC))

mean_aquat_crop_control
```

```
mean_crop_aquat_control

##########################################################################
#####
#Treatment matrices (node removal)

#Empty matrix. Rows will contain the average matrices after the prediction, without the
node of interest
matrix_mean_nodes_abs=matrix(0,63,(62*62))

#Empty matrix to put the matrices CM after extracting the node of interest
matrix_minus_nodes=matrix(0,63,(62*62))

#Iteration to extract the node of interest from the CM matrix and order the matrices as
vectors
for (z in (1:63)){
 matrix_minus_nodes[z,]=as.vector(CM[-z,-z])
}

#Iteration to obtain the average predictions from the matrices without the node of
interest
for (v in (1:63)) {

 MT=matrix(matrix_minus_nodes[v,],62,62)# Treatment matrix

 iter=1500 #Iteration number
 s.e=-4   #Self-effect
 f.max=2 # Maximum value for the uniform distribution
 f.min=0.5 #Minimum value for the uniform distribution
 d=dim(MT) #Matrix dimension
 dime=d[1]

 A=matrix(0,dime,dime) #Empty matrix 1

 AA=matrix(0,iter,(dime*dime)) #Empty matrix 2

 #Adding random values and self-effect (fixed)
 for (h in 1:iter){
  for (j in 1:dime){for (k in 1:dime){

    A[j,k]=round(runif(1,f.min,f.max),1)*MT[j,k]
  }
  }
```

```
  for (i in 1:dime){
    A[i,i]=c(s.e)

  }

  AA[h,1:(dime*dime)]=as.vector(A)

}

#Prediction (Press perturbation analysis)
P=matrix(0,(iter),(dime*dime))

for (w in 1:iter){

  P[w,1:(dime*dime)]=as.vector(t(solve(-(matrix(c(AA[w,]),dime,dime,byrow = F)))))

}

mean_node=matrix(0,1,62*62,byrow=T)# Empty matrix for mean value

#Mean net effects values considering standard deviation
for (e in 1:(62*62)){

  if.pos= if (mean(P[,e])>0) (mean(P[,e])-sd(P[,e])) else (0)
  if.neg= if (mean(P[,e])<0) (mean(P[,e])+sd(P[,e])) else (0)

  is.zero.if.pos= if (if.pos<=0) 0 else(mean(P[,e]))
  is.zero.if.neg= if (if.neg>=0) 0 else(mean(P[,e]))

  Trunc.val=if (mean(P[,e])>0) (is.zero.if.pos) else (is.zero.if.neg)

  mean_node[,e]= Trunc.val
}

matrix_mean_nodes_abs[v,]=mean_node

}

#Names of the variables (nodes)
names=c("Bird_C_Carni","Bird_C_Omni_C","Bird_C_Omni_I","Acari_Bcontrol",
      "Araneae_BControl","Coleoptera_BControl","Diptera_Bcontrol",
      "Diptera_BControl_Pollinator","Hemiptera_BControl","Hymenoptera_BControl",
      "Mantodea_BControl","Neuroptera_BControl","Orthoptera_BControl",
      "Thysanoptera_BControl","Acariformes_Pest","Aphididae_Pest",
```

```
      "Coleoptera_Pest","Collembola_Pest","Curculionidae_Pest","Diptera_Pest",
      "Gastropoda_Pest","Hemiptera_Pest","Hymenoptera_Pest","Lepidoptera_Pest",
      "Noctuidae_Pest","Orthoptera_Pest","Thysanoptera_Pest","Apini_Pollinator",
      "Bombini_Pollinator","Diptera_Pollinator","Hymenoptera_Pollinator",
      "Annual_non-pollinated","Annual_pollinated","Decidious_orchard",
      "Perennial_orchard","Vegetable","Bird_A_Carni","Bird_A_Omni_AI",
      "Bird_A_Omni_ATI","Fish_Carnivore","Fish_Detritivore","Fish_Omnivore_FIDM",
      "Fish_Omnivore_ID","AI_Collector","AI_Collector_Grazer",
      "AI_Collector_Grazer_Predator","AI_Collector_Predator","AI_Collector_Shredder",
      "AI_Filter","AI_Filter_Collector_Predator","AI_Grazer","AI_Predator","AI_Shredder",
"Diatom_High_Profile","Diatom_Motile","Diatom_Planktic","Diatom_Planktic_High_Profil
e","Macrophyte_Helophyte","Macrophyte_Hydrophyte","Macrophyte_Hydrophyte_Helop
hyte","Amphibian","Bird_ATL","Odonata")


#Empty vector to put the mean of the quadrant "effect from the freshwater to the
cropland system"
mean_aquat_crop=matrix(0,63,1)

#Empty vector to put the mean of the quadrant "effect from the cropland to the
freshwater system"
mean_crop_aquat=matrix(0,63,1)

#### Mean of the quadrants
#Cropland system
for (l in 1:36){

  MPN36=matrix(c(matrix_mean_nodes_abs[l,]),62,62,byrow = T)
  MPN36_CA=MPN36[1:35,36:59]
  MPN36_AC=MPN36[36:59,1:35]
  mean_aquat_crop[l,]=mean(abs(MPN36_CA))
  mean_crop_aquat[l,]=mean(abs(MPN36_AC))
}

#Freshwater system
for (l in 37:60){

  MPN37=matrix(c(matrix_mean_nodes_abs[l,]),62,62,byrow = T)
  MPN37_CA=MPN37[1:36,37:59]
  MPN37_AC=MPN37[37:59,1:36]
  mean_aquat_crop[l,]=mean(abs(MPN37_CA))
  mean_crop_aquat[l,]=mean(abs(MPN37_AC))
}
```

```
#System-linking
for (l in 61:63){

  MPN61=matrix(c(matrix_mean_nodes_abs[l,]),62,62,byrow = T)
  MPN61_CA=MPN61[1:36,37:60]
  MPN61_AC=MPN61[37:60,1:36]
  mean_aquat_crop[l,]=mean(abs(MPN61_CA))
  mean_crop_aquat[l,]=mean(abs(MPN61_AC))
}

#Estimation of the difference between the value obtained from the control matrix
# and the value obtained from the matrix without the specific node

#Freshwater to cropland
delta_aquat_crop=mean_aquat_crop_control-mean_aquat_crop

#Cropland to freshwater
delta_crop_aquat=mean_crop_aquat_control-mean_crop_aquat

### Z-scores estimation

#Mean of the difference: Freshwater to cropland
mean_delta_aquat_crop=mean(delta_aquat_crop)

#Standard deviation of the difference: Freshwater to cropland
sd_delta_aquat_crop=sd(delta_aquat_crop)

#Z-score of the difference: Freshwater to cropland
zeta_delta_aquat_crop=(delta_aquat_crop-
mean_delta_aquat_crop)/sd_delta_aquat_crop

########

#Mean of the difference: Cropland to freshwater
mean_delta_crop_aquat=mean(delta_crop_aquat)

#Standard deviation of the difference: Cropland to freshwater
sd_delta_crop_aquat=sd(delta_crop_aquat)

#Z-score of the difference: Cropland to freshwater
zeta_delta_crop_aquat=(delta_crop_aquat-
mean_delta_crop_aquat)/sd_delta_crop_aquat

######
```

```
# Freshwater to cropland
zdac=data.frame(names,zeta_delta_aquat_crop)

# Cropland to freshwater
zdca=data.frame(names,zeta_delta_crop_aquat)
```

Supplementary figures and tables

Figure S1. Map showing the different land uses within the study area.
Figure S2. Map showing the agricultural land and the water bodies within the study area
Figure S3. Heat map for the estimated Net Effect Matrix.
Figure S4: Signed directed graph of the ecological interactions metanetwork composed of the freshwater community, systems-linking module, and the cropland community (higher resolution version of Figure 1).
Figure S5: Signed directed graph showing the direct interactions between the aggregates.
Table S1. List of macrophytes, diatoms, aquatic invertebrates, fish, and birds found in the Chilean Mediterranean freshwater ecosystem.
Table S2. List of crops, pollinators, pests, pests' natural enemies, and birds found in the Chilean Mediterranean cropland ecosystem.
Table S3. List of birds, amphibians, and insects found in the ecosystem-linking aggregate within a freshwater-cropland metanetwork from Mediterranean Chile.
Table S4. Interactions between macrophytes and diatoms.
Table S5. Interactions between aquatic invertebrates and their resources.
Table S6. Interactions between fish and their prey.
Table S7. Interactions between freshwater inhabitant birds and their prey.
Table S8. Interactions between crops and pollinators.
Table S9. Interactions between crops and pests.
Table S10. Interactions between invertebrate natural enemies and pests.
Table S11. Interactions between cropland inhabitant birds and their prey.
Table S12. Interactions between ecosystem-linking birds and their prey.
Table S13. Interactions between ecosystem-linking amphibians and their prey.
Table S14. Interactions between ecosystem-linking odonatans and their prey.
Table S15. Community matrix for the freshwater-cropland metanetwork from Mediterranean Chile.
Table S16. Diet overlap values estimated for the Functional Units of the freshwater network, the cropland network and the entire metanetwork.
Table S17. Relevance of Functional Units at intra-aggregate, inter-ecosystem, and inter-ecosystem scales.
Table S18. Spearman's rank correlation coefficient for relationship between standard centrality measures and node importance measures estimated in this study.
Table S19. Kendall's rank correlation coefficient for relationship between standard centrality measures and node importance measures estimated in this study.
Table S20. List of introduced species for each aggregate of the freshwater-cropland metanetwork.
Table S21. Number of introduced species and the importance of each aggregate in the transmission of effects between ecosystems.
Table S22. Countries and regions with MTEs considered in our analysis.