



UNIVERSITY OF HELSINKI



A photograph of dense, yellowish-green marine plants, likely kelp or seagrass, growing on a rocky substrate. The plants are partially submerged in clear water, with sunlight filtering through the surface.

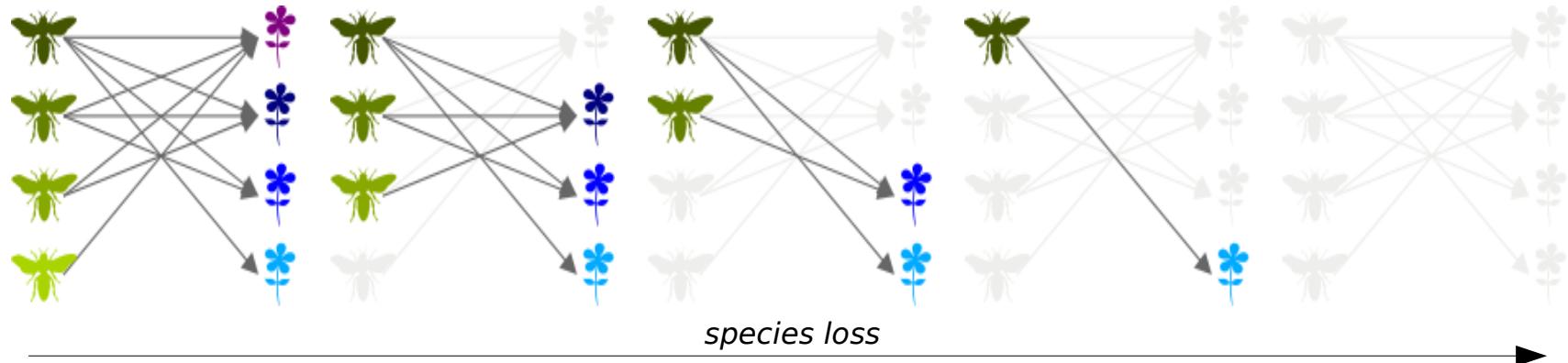
How R species interacting? The use of R in ecological research

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Ecological interactions



- “Backbone of biodiversity” (Jordano, 2016)
- Shape the structure and functioning of ecosystems
- Modulate ecosystem response to disturbance

Marine macrophytes



SEAWEEDS



SEAGRASSES

- Form extensive habitats in coastal waters (“marine forests”)
- Among the most productive ecosystems on the planet
- Source of food and habitat to other species
- Provide key services to humans (CO_2 sequestration)

Macrophyte ecosystems

UPPER TROPHIC LEVELS



MACROPHYTE-ASSOCIATED FAUNA



MARINE MACROPHYTES

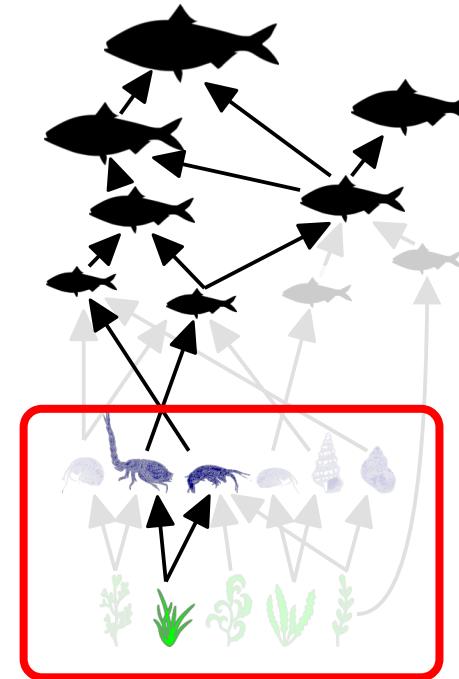
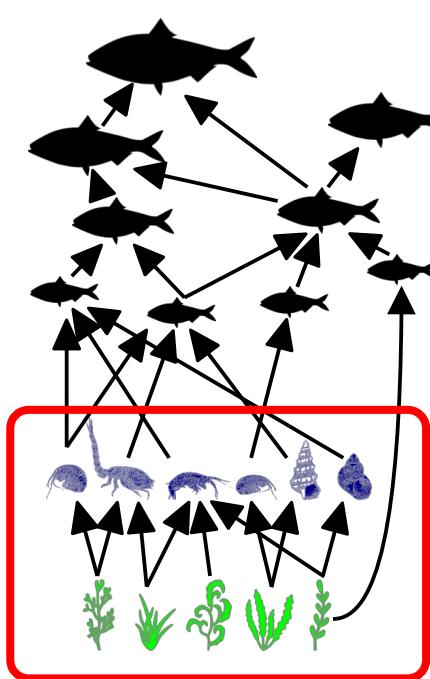
Macrophyte ecosystems



HEALTHY



DEGRADED



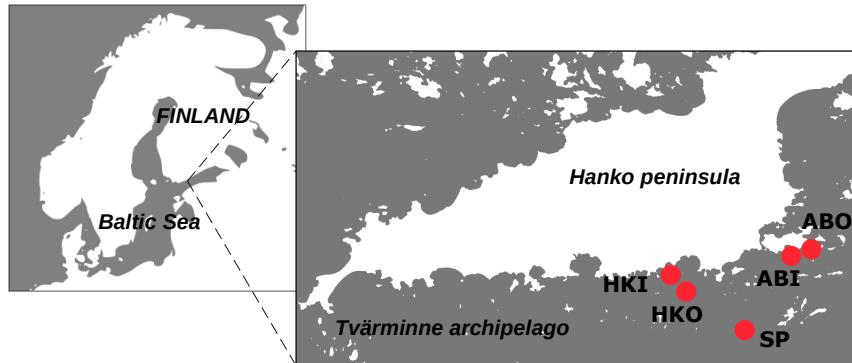
Project objectives

1) Assemble networks mapping macrophyte-animal interactions

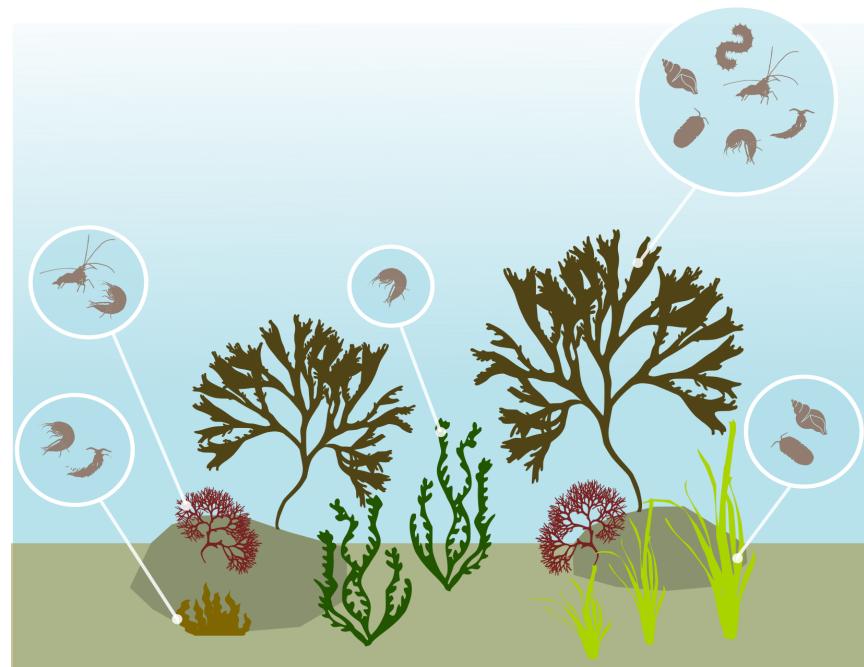
2) Explore network structure

3) Model response to future scenarios of climate change

Fieldwork

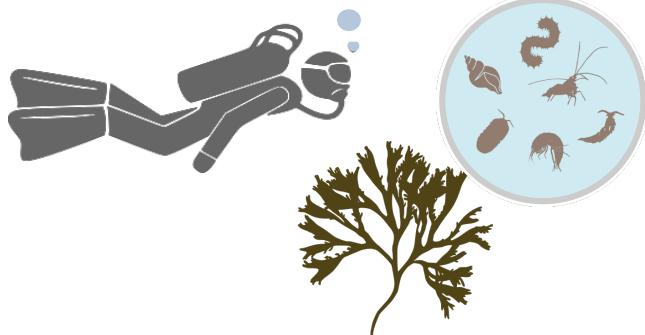


- 5 sites
- 2 seasons (summer, autumn)

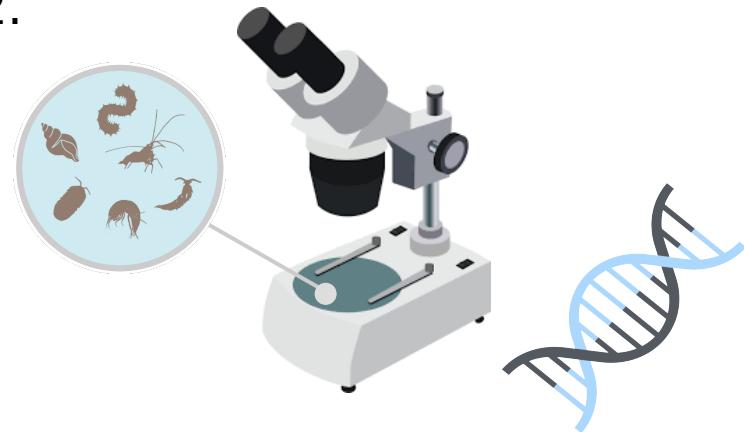


1) Assembling the networks

1.



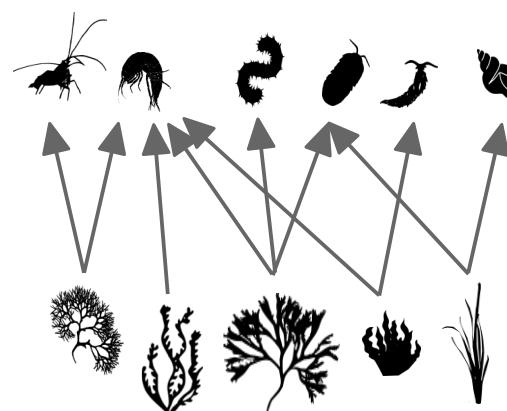
2.



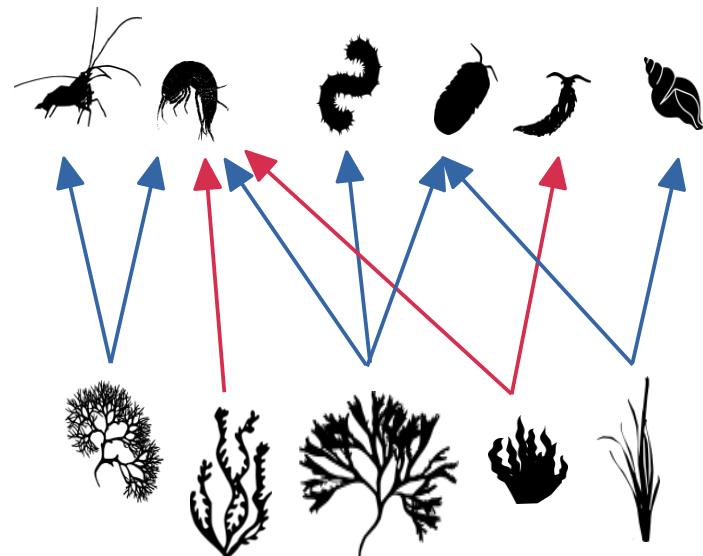
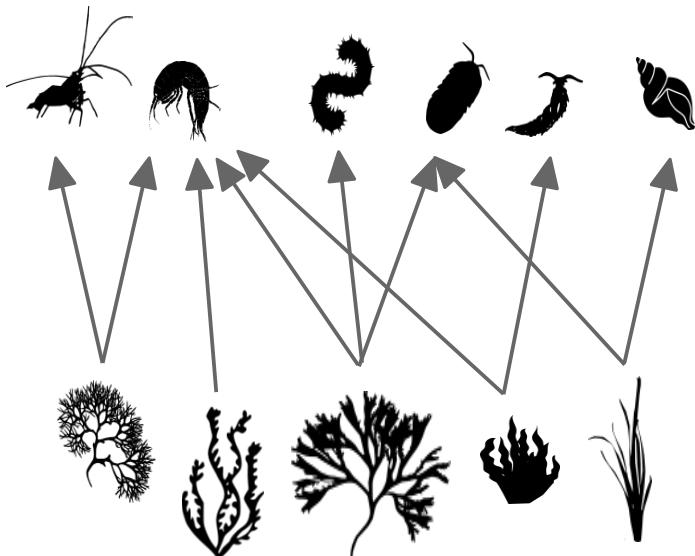
3.



4.



1) Assembling the networks



- Trophic interactions
- Non-trophic interactions

1) Assembling the networks

Dataset: invertebrate abundance on macrophytes



Invertebrate species

date	sample_n	Amphibalanus_improvisus	Ampullaceana_baltica	Anelidae_sp.	Bivalvia_sp	Cerastoderma_glaucum	Chironomid_larva_pupa	Cordylophora_caspia	Cyanophthalma_obscura	Dytiscidae_sp.	Electra_crustulenta	Gammarus_sp.	Hediste_diversicolor	Hydrobiidae/Tateidae_sp.	Idotea_baltica
Oct_2021	SP_01	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Oct_2021	SP_02	0	1	0	0	0	1	0	0	0	0	0	0	0	0
Oct_2021	SP_03	0	2	0	0	0	0	0	0	2	0	0	0	5	0
Oct_2021	SP_04	0	3	0	0	0	0	0	0	0	0	5	0	6	1
Oct_2021	SP_05	0	0	0	0	0	2	0	0	0	0	6	0	13	0
Oct_2021	SP_06	1	4	0	0	0	4	0	0	0	0	1	1	0	2
Oct_2021	SP_07	1	1	0	0	0	2	0	0	0	0	0	1	2	0
Oct_2021	SP_08	0	11	0	0	0	1	0	0	0	1	0	2	0	21
Oct_2021	SP_09	0	6	0	0	0	0	0	0	0	0	1	7	0	1
Oct_2021	SP_10	0	7	0	0	0	2	0	0	0	0	1	0	0	28
Oct_2021	SP_11	0	2	0	0	0	0	0	0	0	0	0	0	0	0
Oct_2021	SP_12	3	3	0	0	0	0	0	0	0	0	0	0	0	1
Oct_2021	SP_13	0	9	0	0	0	0	0	0	0	1	0	3	0	3
Oct_2021	SP_14	2	1	0	0	0	0	0	1	0	0	0	2	0	1
Oct_2021	SP_15	23	8	0	0	0	0	0	0	0	0	1	1	0	0
Oct_2021	SP_16	0	9	0	0	0	1	0	0	0	0	0	3	0	15
Oct_2021	SP_17	0	7	0	0	0	0	0	0	0	0	0	0	0	30
Oct_2021	SP_18	0	6	0	0	0	0	0	0	0	0	0	1	0	27
Oct_2021	SP_19	0	17	0	0	1	0	0	0	0	0	0	10	0	76
Oct_2021	SP_20	0	14	0	0	0	0	0	0	0	0	0	6	0	65
Oct_2021	SP_21	0	8	0	0	0	0	0	0	0	0	0	0	0	1
Oct_2021	SP_22	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Oct_2021	SP_23	0	10	0	0	0	0	0	0	0	0	0	2	0	0
Oct_2021	SP_24	0	6	0	0	0	0	0	0	0	0	0	0	0	0
Oct_2021	SP_25	0	2	0	0	0	0	0	0	0	0	0	0	0	1
Oct_2021	SP_26	2	17	0	0	0	0	0	0	0	0	1	2	0	3
Oct_2021	SP_27	27	55	0	0	1	0	0	0	0	0	1	6	0	9
Oct_2021	SP_28	137	60	0	0	0	0	0	0	0	0	1	39	0	0
Oct_2021	SP_29	45	68	0	0	0	0	0	0	0	0	1	1	0	2
Oct_2021	SP_30	16	18	0	0	0	0	0	0	0	0	1	7	0	1
Oct_2021	HKI_01	0	0	0	0	0	0	0	0	0	0	0	2	0	0
Oct_2021	HKI_02	0	0	0	0	0	0	0	0	0	0	0	0	5	0
Oct_2021	HKI_03	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oct_2021	HKI_04	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Oct_2021	HKI_05	0	0	0	0	0	0	0	0	0	0	0	5	0	0
Oct_2021	HKI_06	0	0	0	0	0	0	0	0	0	0	0	15	0	0
Oct_2021	HKI_07	0	0	0	0	0	0	0	0	0	0	0	3	0	11
Oct_2021	HKI_08	0	0	0	0	0	0	0	0	1	0	0	4	0	5
Oct_2021	HKI_09	0	0	0	0	0	0	1	0	0	0	0	3	0	10
Oct_2021	HKI_10	0	0	0	0	0	0	1	0	0	0	0	16	0	0
Oct_2021	HKI_11	0	0	0	0	0	0	1	0	0	0	0	4	0	7
Oct_2021	HKI_12	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Oct_2021	HKI_13	0	0	0	0	0	0	1	0	0	0	0	2	0	4
Oct_2021	HKI_14	0	0	0	0	0	0	0	0	0	0	0	6	0	3
Oct_2021	HKI_15	0	0	0	0	0	0	0	0	0	0	0	0	0	2
Oct_2021	HKI_16	0	1	0	0	0	0	0	0	0	0	0	2	0	1
Oct_2021	HKI_17	0	0	0	0	0	0	4	0	0	0	0	3	0	3
Oct_2021	HKI_18	0	0	0	0	0	0	0	0	0	0	0	1	0	0
Oct_2021	HKI_19	0	0	0	0	0	0	1	0	0	0	1	17	0	0
Oct_2021	HKI_20	0	0	0	0	0	0	0	0	0	0	0	2	0	4
Oct_2021	HKI_21	0	0	0	0	0	0	0	0	0	0	0	6	0	0
Oct_2021	HKI_22	0	1	0	0	0	1	0	0	0	0	0	1	10	7

Macrophyte species



1) Assembling the networks

```
64 #####Network assembly
65 #The idea is to assemble a network for each season, site and depth with weighted links.
66 #As we have multiple replicates for the same species, when a link is shared the weight will be the average of replicates' weights
67 #Potentially add the presence of epiphytic algae as a link attribute so to visualize it with a different color
68 #Evaluate presence of shared links between sites.
69
70
71 seasons<-unique(AllData$date)
72 sites<-c("SP","HKI","HKO","ABI","ABO")
73
74 #For every site create matrix with epifauna in rows and macrophytes in columns.
75 #Add in every cell average link weight (among replicates) for every epifauna-macrophyte pair:
76 #if association is not recorded in every replicate when calculating mean weight 0s are also accounted for (so it should be fine)
77
78 AllMacro<-unique(AllData$species)
79 AllInv<-colnames(AllData)[5:34]
80
81 n_m<-length(AllMacro)
82 n_i<-length(AllInv)
83
84 #common network layout
85 #all invertebrate and macrophyte species in the same position to visualize differences in network structure
86
87 lay_x0<-seq(5,n_i-5,length=length(AllMacro)) #to space out macrophyte nodes
88 macro_xy<-list()
89 for (i in 1:n_m){
90   macro_xy[[AllMacro[i]]]<-c(lay_x0[i],0)
91 }
92
93 lay_x1<-1:n_i
94 inv_xy<-list()
95 for (i in 1:n_i){
96   inv_xy[[AllInv[i]]]<-c(lay_x1[i],1)
97 }
98
99 #function to make specific layout for each network
100 make_lay<-function(g){
101   vn<-length(V(g))
102   lay<-c() #specific layout for each network
103   for (i in 1:vn){
104     if (V(g)$type[i]==TRUE){
105       lay<-rbind(lay,macro_xy[[V(g)$name[i]]])
106     }
107     else{
108       lay<-rbind(lay,inv_xy[[V(g)$name[i]]])
109     }
110   }
111   return(lay)
```



Create network layout

1) Assembling the networks

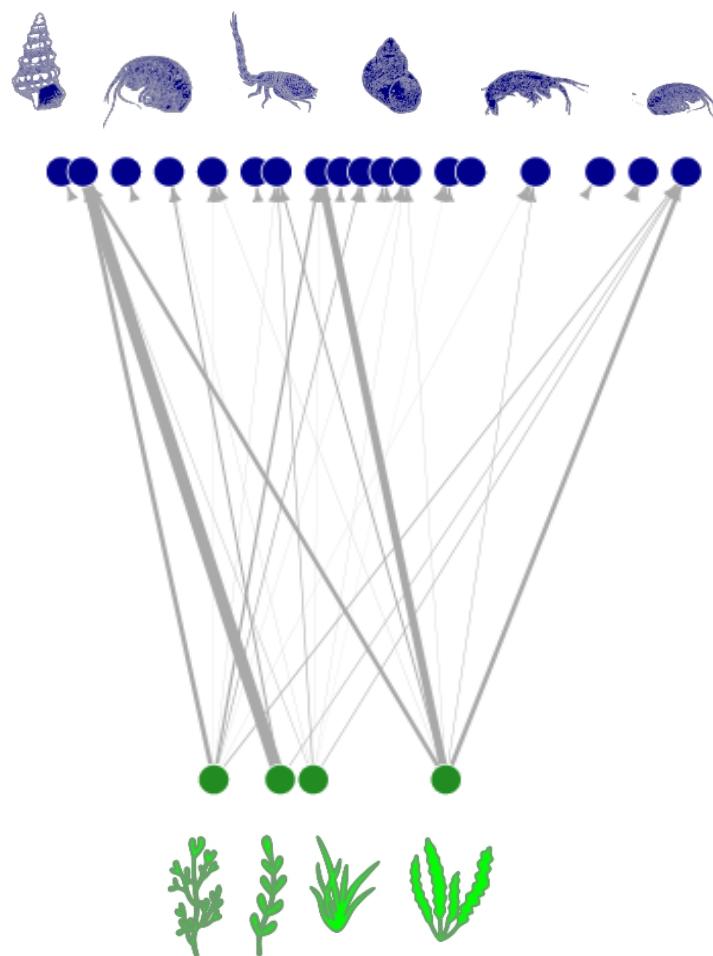
```
114 AllNets<-list() #store matrices, networks and layouts in list (for every season and site)
115 
116 
117 ▼ for (se in seasons){
118 ▼   for (s in sites){
119 
120   SubData<-subset(AllData,grepl(se,AllData$date)==T & grepl(s,AllData$sample_n)==T)
121   macro<-unique(SubData$species)
122   inv<-AllInv[which(colsSums(SubData[,5:34])>0)]
123   m<-matrix(rep(0,length(inv)*length(macro)),length(inv))
124   colnames(m)<-macro
125   rownames(m)<-inv
126   ▼ for (ma in macro) {
127     ▼ for (i in inv) {
128       m[i,ma]<-round(mean(SubData[which(SubData$species==ma),i]),2) #get average invertebrate weighted abundance for each macrophyte and invertebrate species
129     }
130   }
131 
132   g<-graph_from_incidence_matrix(m,directed=T,mode=c("in"),weighted=T)
133   V(g)$type<-FALSE
134   V(g)[which(V(g)$name %in% AllMacro)]$type<-TRUE
135   #V(g)$label.cex<-0.5 #to visualize taxa name
136   #V(g)$label.dist<-2
137   #V(g)$label.degree<-pi/2
138   V(g)$label<=""
139   V(g)$color<- "darkblue"
140   V(g)$size<-10
141   V(g)[V(g)$type==TRUE]$color<- "forestgreen"
142   V(g)$frame.size<-1
143   V(g)$frame.color<- "white"
144   E(g)$arrow.size<-0.5
145   E(g)$weight<-E(g)$weight/max(E(g)$weight) #standardize weights differently? (see Manca et al. 2022)
146   E(g)$width<-8*E(g)$weight
147 
148   lay<-make_lay(g)
149 
150   png(paste0("./FIGURES/morpho_network_ ",se,"_",s,".png"))
151   plot(g,layout=lay,main=paste(se,s))
152   dev.off()
153 
154   AllNets[[se]][[s]]<-list(m,g,lay) #store matrices, networks and layouts in list (for every season and site)
155 
156   print(paste(se,s))
157 ▲ }
158 ▲ }
```

Create network from matrix

Customize network graphics

Plot & save networks

1) Assembling the networks

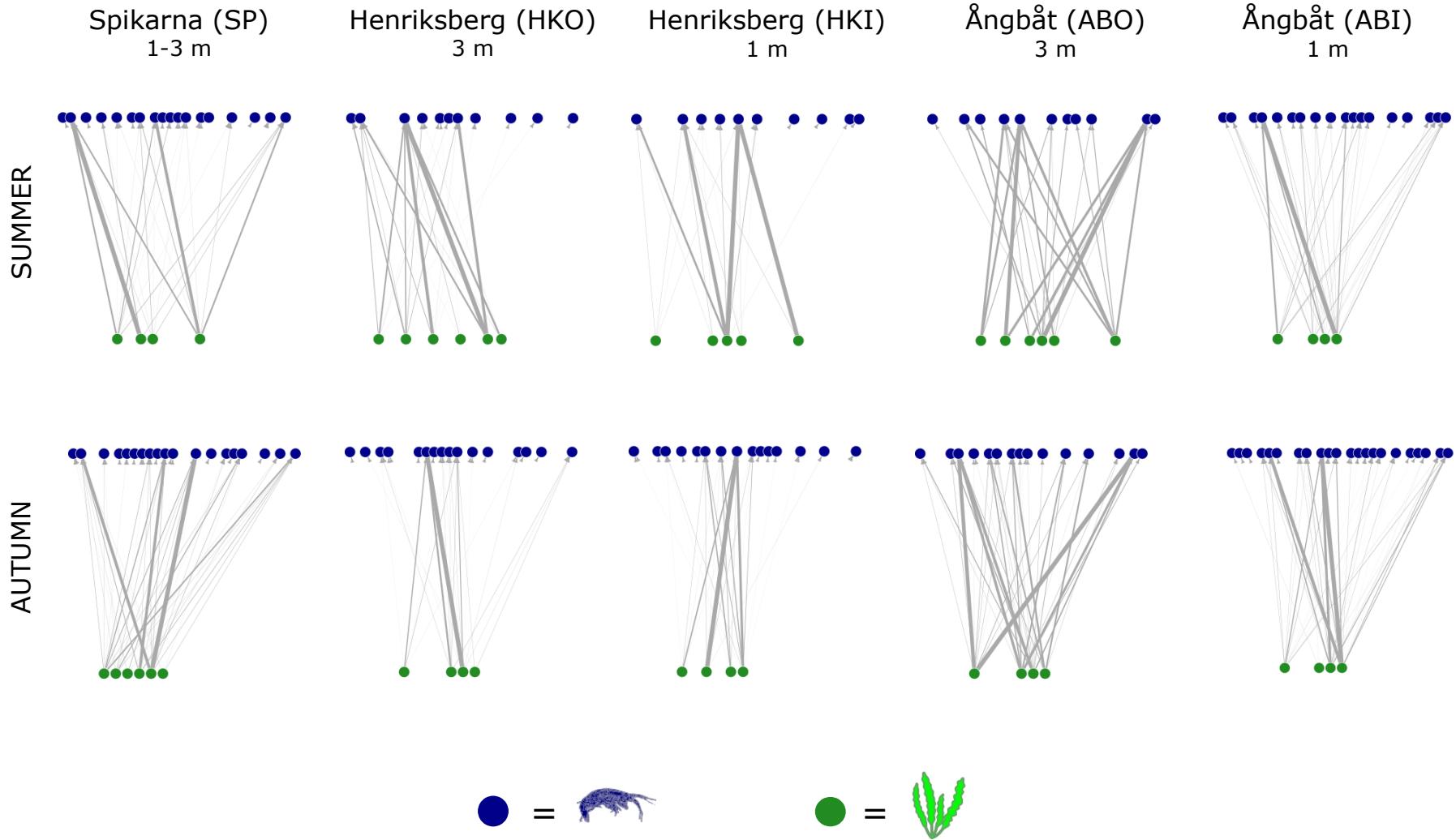


● = invertebrates

● = macrophytes

→ = association (width proportional to strength of association)

1) Assembling the networks



2) Analyze network structure

```
172 NetProp<-c()  
173 for (se in seasons){  
174   for (s in sites){  
175     g<-AllNets[[se]][[s]][[2]]  
176     m<-AllNets[[se]][[s]][[1]]  
177     n_inv<-nrow(m) #n. of invertebrate nodes (taxa)  
178     n_macro<-ncol(m) #n. of macrophyte nodes (taxa)  
179     links<-gsize(g) #n. of links (associations)  
180     conn<-links/( n_inv*n_macro)  
181     mean_lw<-mean(m[which(m>0)]) #average link weight  
182     #perhaps better to filter the links first  
183     mean_deg_inv<-mean(degree(g)[V(g)$type==FALSE]) #mean degree invertebrates  
184     mean_deg_macro<-mean(degree(g)[V(g)$type==TRUE]) #mean degree macrophytes  
185     nodf<-nestednodf(m)$statistic[3] #nestedness (compare with null models?)  
186  
187     #robustness: run co-extinction simulations (random) and calculate AUC  
188     macro<-colnames(m)  
189     inv<-rownames(m)  
190  
191     coex<-c()  
192   for(i in 1:100){  
193     g_r<-g  
194     rem_step<-0  
195     coex<-rbind(coex,c(rem_step,1))  
196   for (sp in sample(macro)){#remove macrophytes at random  
197     to_del<-which(V(g_r)$name==sp)  
198     g_r<-delete_vertices(g_r,to_del)  
199     to_del<-which(degree(g_r,mode="IN")[V(g_r)$name %in% inv]==0)  
200     g_r<-delete_vertices(g_r,to_del)  
201     inv_surv<-sum(V(g_r)$name %in% inv)/length(inv)  
202     rem_step<-rem_step+1  
203     coex<-rbind(coex,c(rem_step,inv_surv))  
204   }  
205 }  
206  
207 mean_coex<-aggregate(coex[,2]-coex[,1],FUN="mean")  
208 y<-mean_coex[,2]  
209 x<-mean_coex[,1]/length(macro)  
210 rob<-AUC(x,y) #trapezoid (default)  
211  
212 NetProp<-rbind(NetProp,c(se,  
213   s,  
214   n_inv,  
215   n_macro,  
216   links,  
217   conn,  
218   mean_lw,  
219   mean_deg_inv,  
220   mean_deg_macro,  
221   nodf,
```



Compute different network properties

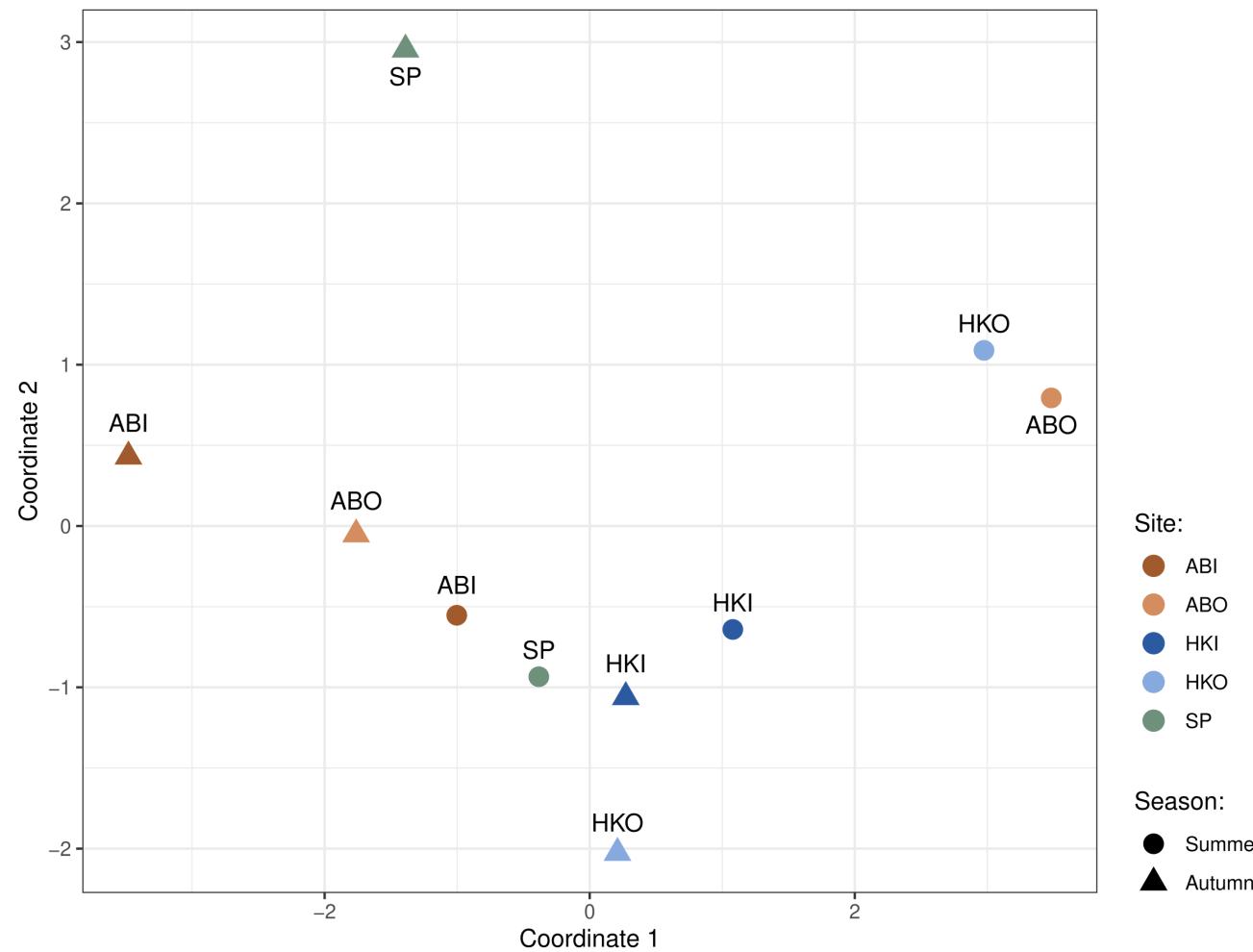
2) Analyze network structure

```
277 #Euclidean distance + MDS network properties
278
279
280 #normalize data
281 for_mds<-scale(for_pca)
282
283 ed<-dist(for_mds) #euclidean distance matrix
284 write.csv(as.matrix(round(ed,2)), "./DATA/Clean/network_properties_distance_matrix.csv", row.names=T)
285 mds<-cmdscale(ed,eig=TRUE,k=2) #multidimensional scaling
286 mds
287
288 #plot results
289 x<-mds$points[,1]
290 y<-mds$points[,2]
291 plot(x,y,xlab="Coordinate 1",ylab="Coordinate 2",main="Metric MDS",type="n")
292 text(x,y,labels=row.names(for_mds),cex=0.7)
293
294 #ggplot
295 mds.data<-data.frame(site=NetProp$site, #sites (labels)
296                         season=NetProp$date, #season (shape)
297                         X=x, #coordinate 1
298                         Y=y) #coordinate 2
299
300 mds.plot<-ggplot(data=mds.data, aes(x=X, y=Y, label=site)) +
301     geom_point(aes(shape=season,color=site),size=4) +
302     geom_text() +
303     xlab(paste("Coordinate 1")) +
304     ylab(paste("Coordinate 2")) +
305     theme_bw() +
306     scale_color_manual(values=c("#A05A2C", "#D38D5F", "#2C5AA0", "#87AADE", "#6F917C"))
307
308 pdf("./FIGURES/mds_network_properties.pdf",height=6,width=8)
309 mds.plot
310 dev.off()
311
```

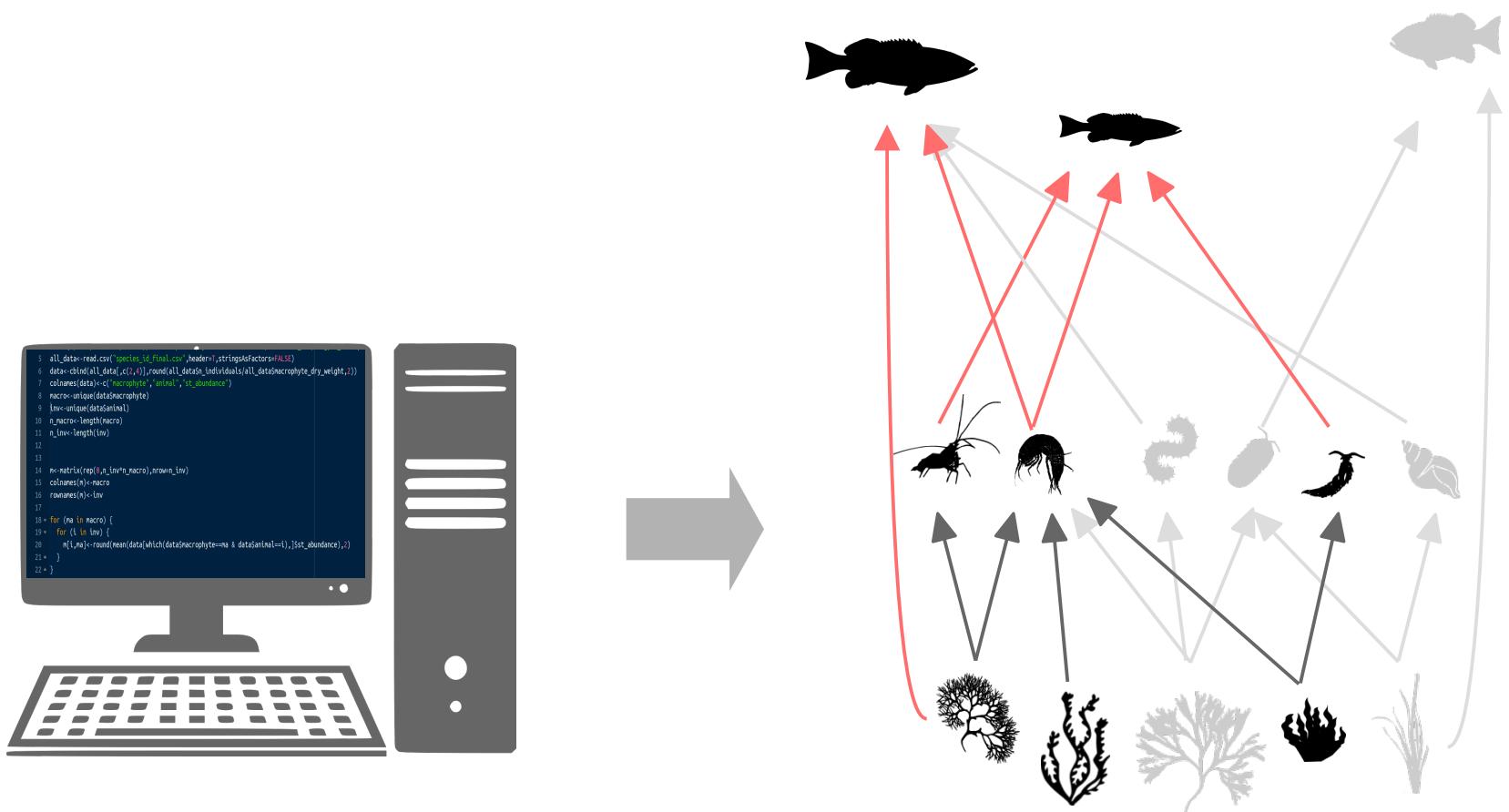
Compute similarity
between networks

Plot their position

2) Analyze network structure

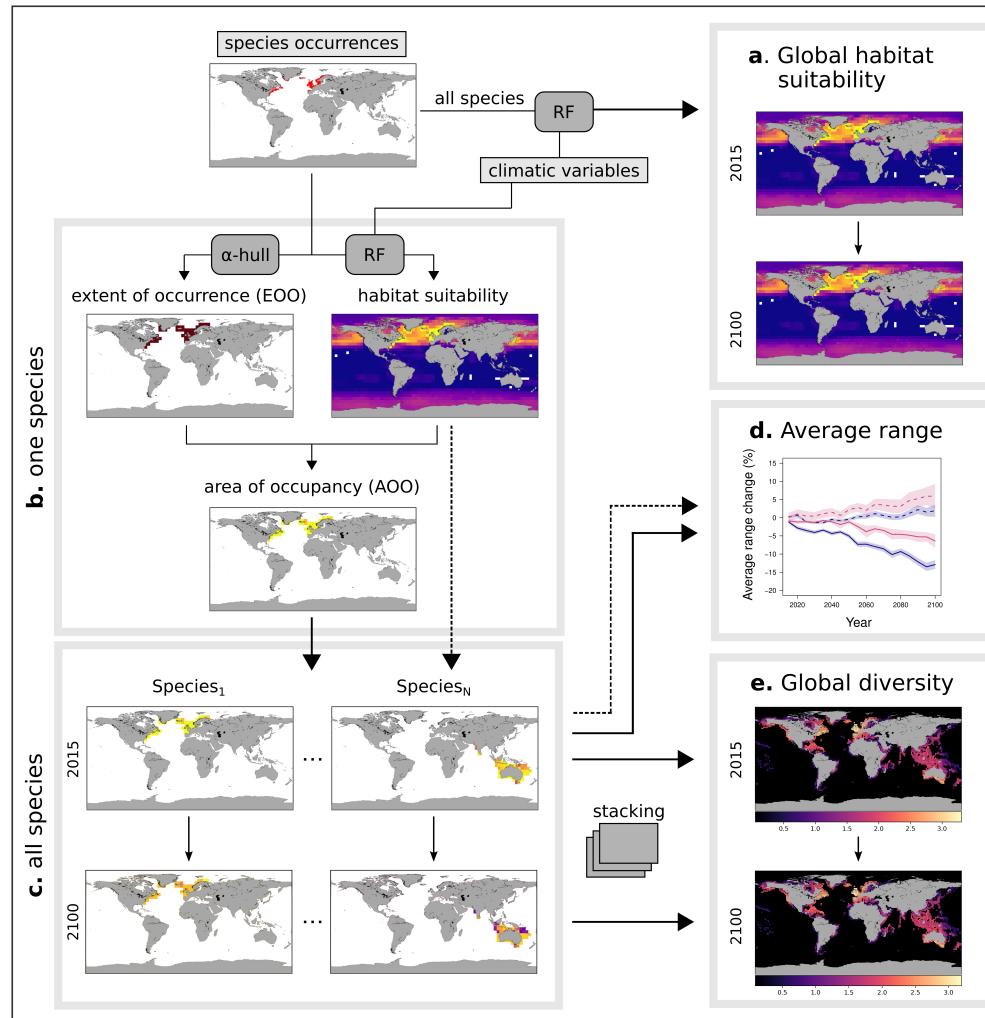


3) Modeling the effect of climate change



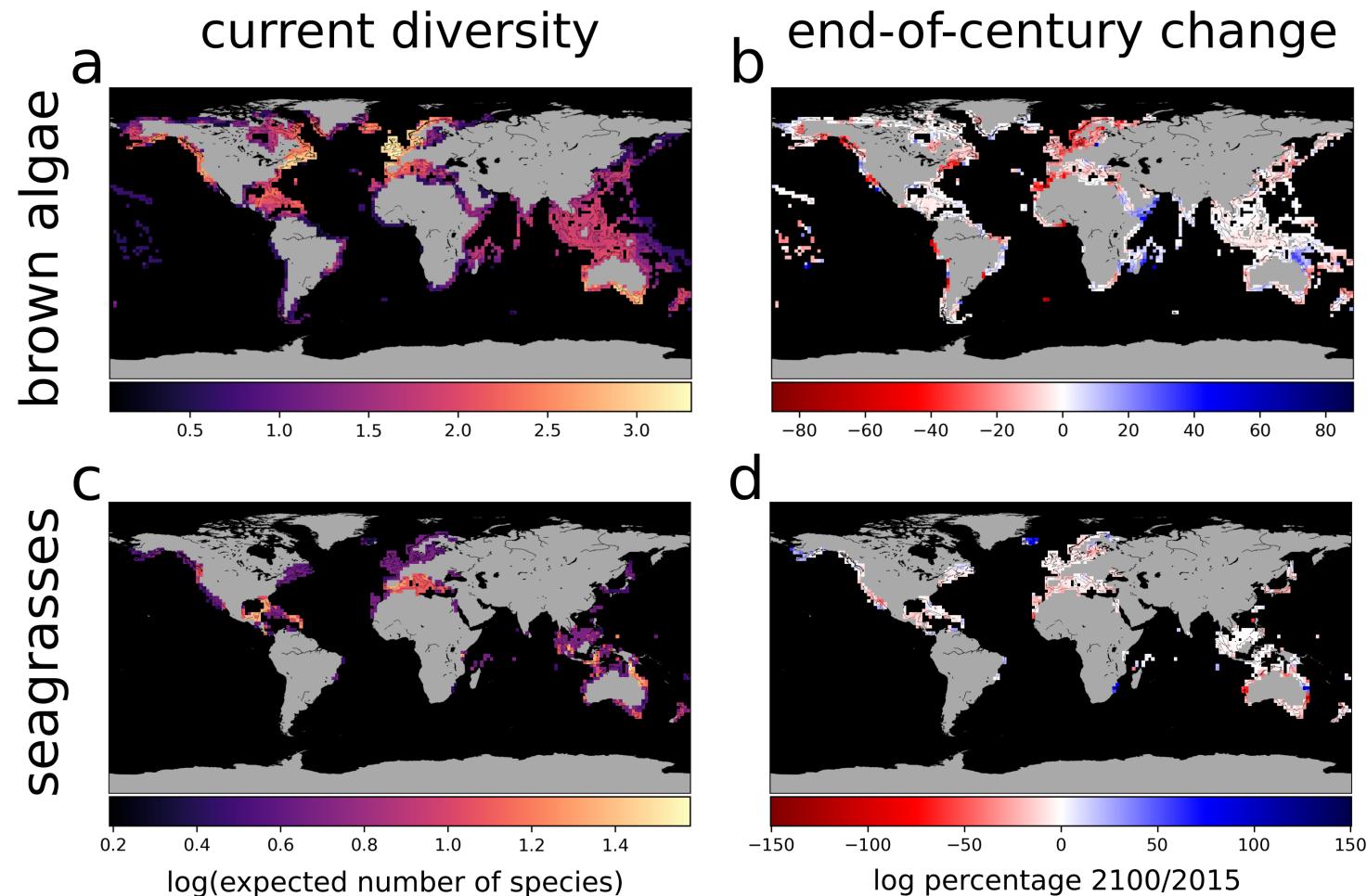
3) Modeling the effect of climate change

Projected future global distribution and diversity of marine macrophytes



3) Modeling the effect of climate change

Global species diversity



3) Modeling the effect of climate change

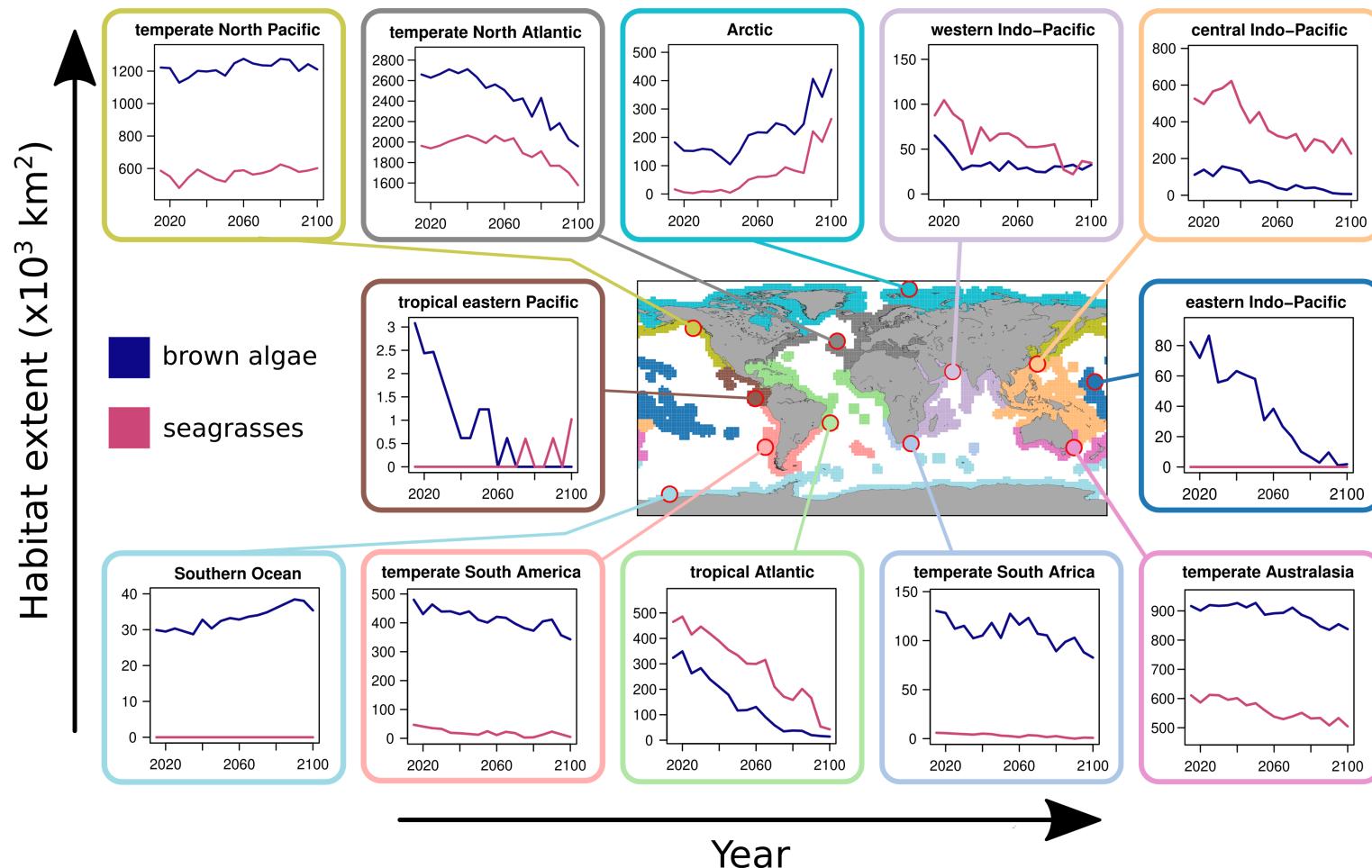
```
138  ##Fig.4:  
139  
140  
141 #panel a:marine regions macrophyte habitat trajectories (km2)  
142  
143 regions<-unique(a$region)  
144 regions<-subset(regions,regions!="global")  
145  
146 c<-c()  
147  
148 for (sc in scenarios){  
149   #print(sc)  
150  
151 pdf(paste0("./Figures/pdf/Fig.4a_ ",sc,".pdf"),height=8,width=12)  
152 par(mfrow=c(3,5))  
153  
154 a_sc<-a[a$ssp==sc,]  
155  
156 for (re in regions){  
157   #print(re)  
158   a_reg<-a_sc[a_sc$region==re,]  
159   plot(0,0,type='n',xlim=c(2015,2100),ylim=c(0.001*min(a_reg[,"X60"],na.rm=T),0.001*max(a_reg[,"X60"],na.rm=T)),  
160     las=1,cex.axis=1,cex.lab=1,xlab='year',ylab='Habitat extent (km2*10e-3)',main=re)  
161   sc_col<-1  
162   for (ta in taxa){  
163     a_ta<-a_reg[a_reg$kingdom==ta,]  
164     x_m<-aggregate(0.001*a_ta$X60-round(a_ta$year/t_res),FUN='mean',na.rm=T)  
165     lines(x_m[,1]*t_res,x_m[,2],lwd=2,col=plasma(3)[sc_col])  
166     sc_col<-sc_col+1  
167   }  
168 }  
169  
170 dev.off()  
171  
172  
173 #panel b:% of global macrophyte habitat hosted in each marine regions (macrophyte habitat trajectories (years 2015,2100))  
174  
175 cols<-c("#17becfff", "#888888ff", "#caca50ff", "#b0e7a5ff", "#d2c1deff", "#ffc790ff",  
176 "#1f77b4ff", "#905c52ff", "#ffb0a0ff", "#aec7e8ff", "#e995cff", "#9edae5ff")  
177  
178 pdf(paste0("./Figures/pdf/Fig.4b_ ",sc,".pdf"),height=8,width=12)  
179 par(mfrow=c(2,1))  
180  
181
```



Plot change in
macrophyte habitat

3) Modeling the effect of climate change

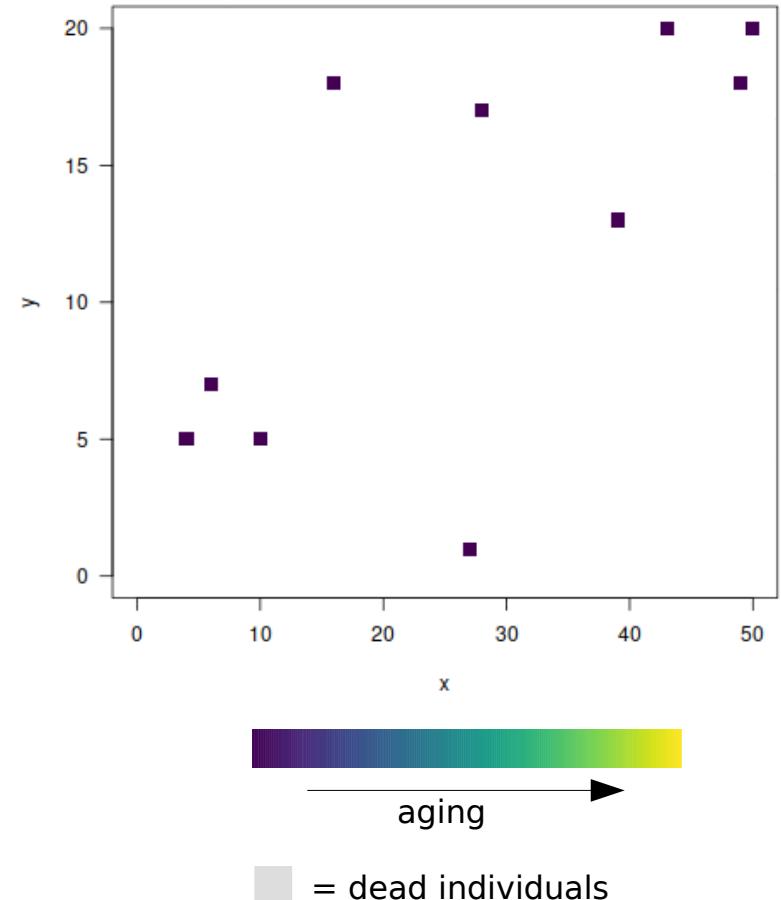
Global macrophyte habitat



Introduction to ecological modeling

Single species population model

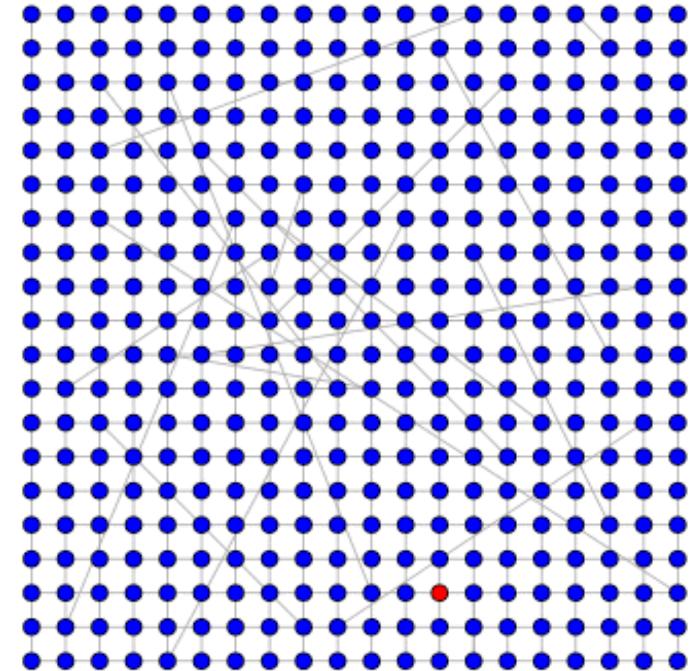
```
301 library(viridis)
302 b_rate<-0.5
303 max_age<-5
304 time_steps<-100
305 w_w<-50
306 w_h<-20
307 space_mat<-matrix(rep(0,w_w*w_h),nrow=w_h)
308 pop<-10
309
310 plot(0,0,type='n',xlim=c(0,w_w),ylim=c(0,w_h),xlab='x',ylab='y',las=1)
311 pop<-c()
312 while (sum(space_mat)<pop[0]){
313   r_row<-sample(1:w_h,1)
314   r_col<-sample(1:w_w,1)
315   if (space_mat[r_row,r_col]==0){
316     pop<-rbind(pop,c(r_row,r_col,0)) #add age
317     space_mat[r_row,r_col]<-1
318   }
319 }
320
321 points(pop[,2],pop[,1],pch=15,cex=1.5,col=viridis(6)[pop[,3]+1])
322
323 pop_size<-c()
324 for (i in 1:time_steps){
325   new_pop<-c()
326   emptied<-c()
327   for (j in 1:dim(pop)[1]){
328     r_row<-sample(1:w_h,1)
329     r_col<-sample(1:w_w,1)
330     if (space_mat[r_row,r_col]==0){
331       if (runif(1)<=b_rate){
332         space_mat[r_row,r_col]<-1
333         new_pop<-rbind(new_pop,c(r_row,r_col,0))
334       }
335     }
336     if (runif(1)>pop[j,3]/max_age){
337       new_pop<-rbind(new_pop,c(pop[j,1:2],pop[j,3]+1))
338     } #aging
339   else {
340     space_mat[pop[j,1],pop[j,2]]<-0
341     emptied<-rbind(emptied,c(pop[j,2],pop[j,1]))
342   }
343 }
344 pop<-new_pop
345 points(emptied,col='lightgrey',pch=15,cex=1.5)
346 points(pop[,c(2,1)],col=viridis(6)[pop[,3]+1],pch=15,cex=1.5)
347 pop_size<-c(pop_size,dim(pop)[1]) #we need the number of rows in pop
348 Sys.sleep(0.3)
349 print (paste('step no.',i))
350 }
```



Introduction to ecological modeling

Epidemic model

```
1  ##### EPIDEMIC MODELS
2  library(igraph)
3
4  n<-20
5  tot_n<-n**2
6  g<-make_lattice(c(n,n),nei=1)
7  g<-delete.vertices(g,which(degree(g)==0))
8
9  V(g)$size<-5
10 V(g)$label<-''
11 V(g)$color<-white
12 lay<-layout.grid(g,20,20)
13 plot(g,layout=lay)
14
15 #for (new_edge in 1:20){
16 #  g<-add.edges(g,sample(1:length(V(g)),2))
17 #}
18
19 plot(g,layout=lay)
20
21 #S-->I
22 #S-->I-->R-->S
23
24 V(g)$status<-'S'
25 V(g)$color=blue
26
27 p0<-sample(1:tot_n,1)
28 V(g)[p0]$status<-'I'
29 V(g)[p0]$color=red
30
31 plot(g,layout=lay)
32
33 i_nodes<-c(1)
34 steps<-1
35 while(sum(V(g)$status=='S')>0){
36   iii<-which(V(g)$status=='I')
37   new_i<-c()
38   for (node in iii){
39     if (runif(1)<0.5{
40       new_i<-c(new_i,sample(as.vector(neighbors(g,node)),size = 1,replace=T))
41       #new_i<-c(new_i,neighbors(g,node))
42     }
43   }
44   for (node in new_i){
45     V(g)[node]$status='I'
46     V(g)[node]$color=red
47   }
48   i_nodes<-c(i_nodes,sum(V(g)$status=='I'))
49   dev.off()
50   plot(g,layout=lay)
51   Sys.sleep(0.4)
52   steps<-steps+1
53 }
```



● = not infected

● = infected

When it's been 7 hours and you still
can't understand your own code



Thank you!

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