

Spatial clustering of richness change in coastal North America

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Abstract

North American coastal regions show long-term changes in species abundance and distribution, and changes in community diversity. What are the spatial patterns underlying these dynamics? Specifically, do changes in biodiversity occur homogenously or randomly across space, or are these processes spatially patterned?

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Data Setup

```
mapDat <- spatialDiversity::mapDat
ureg <- mapDat[,unique(reg)]
```

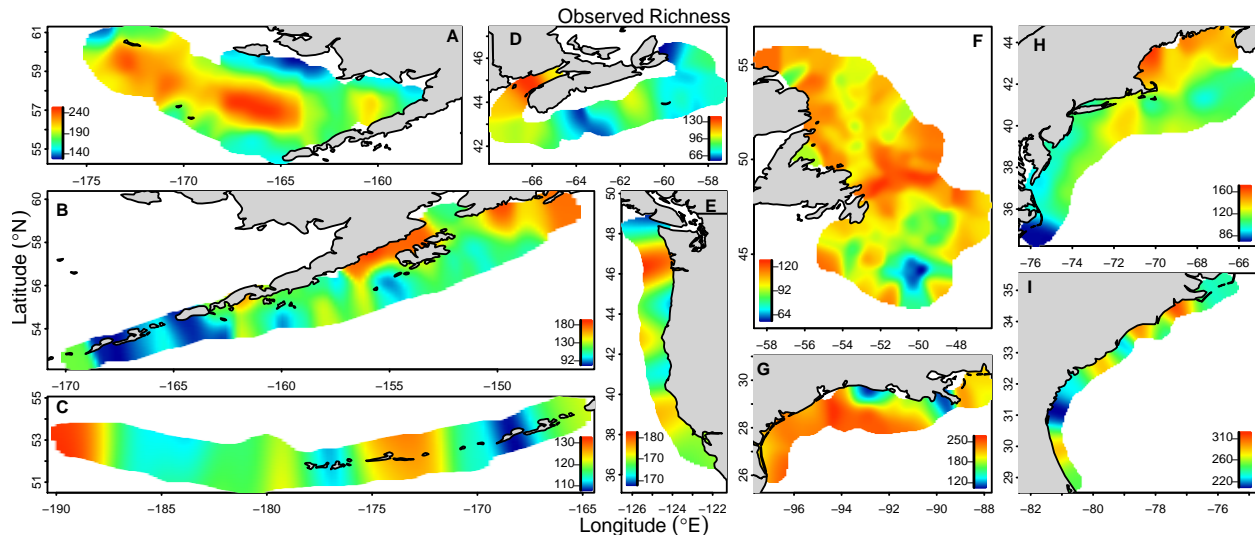


Figure 1: **Figure 1.** Maps of long-term averages of richness at each site for each region: A) E. Bering Sea, B) Gulf of Alaska, C) Aleutian Islands, D) Scotian Shelf, E) West Coast US, F) Newfoundland, G) Gulf of Mexico, H) Northeast US, I) Southeast US. Richness values were smoothed using a Gaussian kernel smoother. The smoothed richness value is indicated by the color bars in each panel; colors are scaled independently for each region.

Spatial Clustering of Colonization and Extinction

Heat Maps

Figure 1. Richness map

```
ceRate_map(ce="richness")
```

Figure 2. Colonization map

```
ceRate_map(ce="colonization")
```

Figure 2b. Unique Colonization map

```
ceRate_map(ce="uCol")
```

Figure 2c. Total Colonization map

```
ceRate_map(ce="totCol")
```

Figure 3. Extinction map

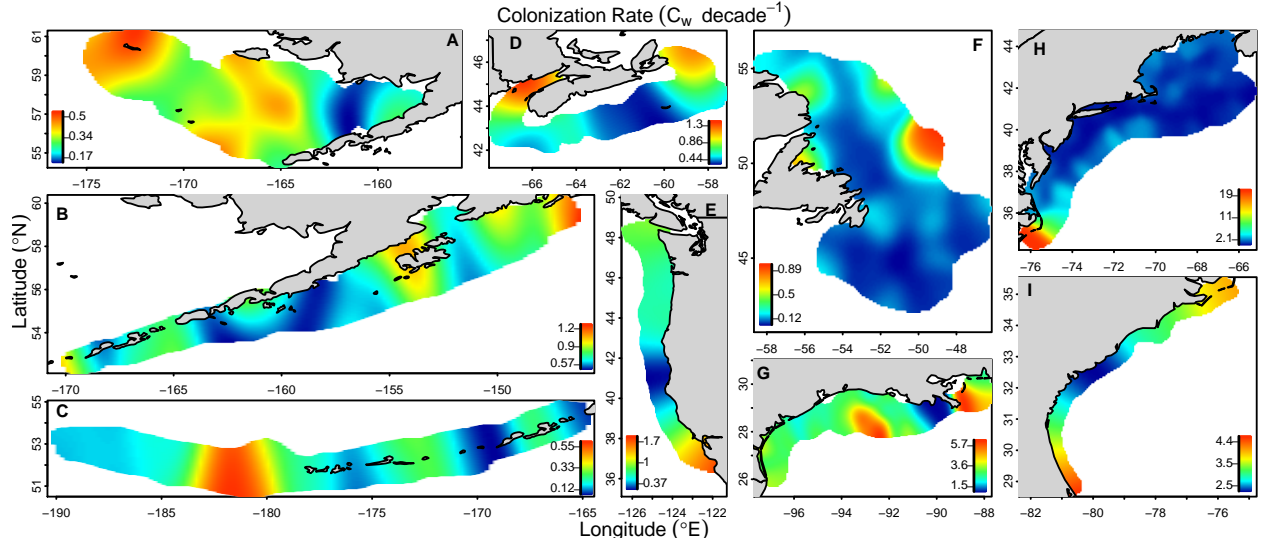


Figure 2: **Figure 2.** Maps of long-term averages of colonizations per site per decade for each region: A) E. Bering Sea, B) Gulf of Alaska, C) Aleutian Islands, D) Scotian Shelf, E) West Coast US, F) Newfoundland, G) Gulf of Mexico, H) Northeast US, I) Southeast US. Values of colonization rate were smoothed using a Gaussian kernel smoother. The smoothed colonization rate is indicated by the color bars in each panel; colors are scaled independently for each region.

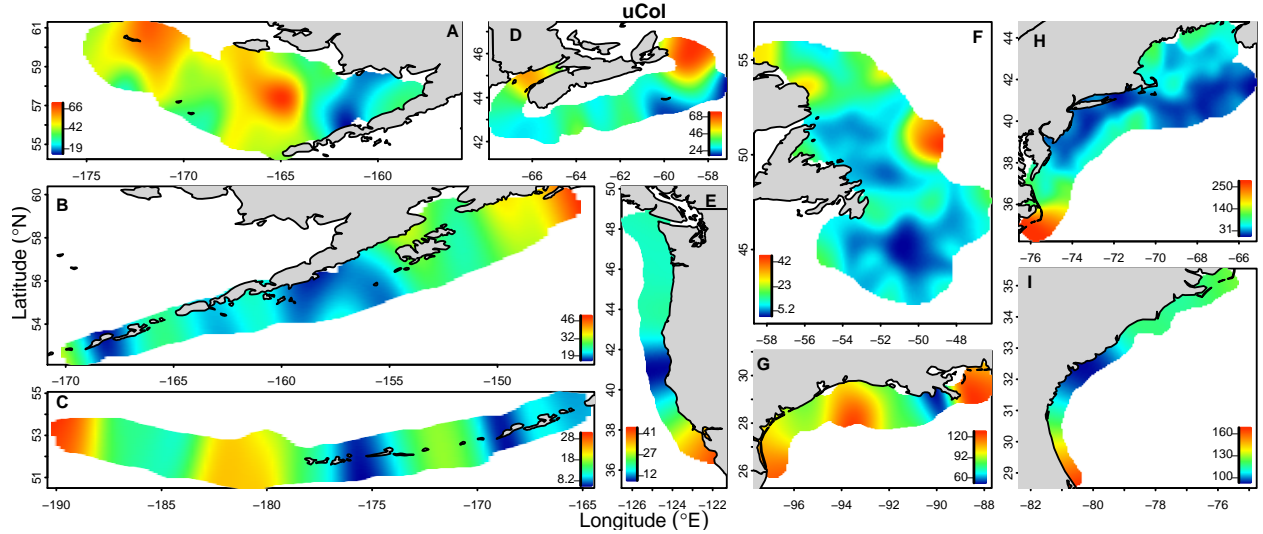


Figure 3: **Figure 2b.** Maps of the number of unique species with regional colonizations involving each site.

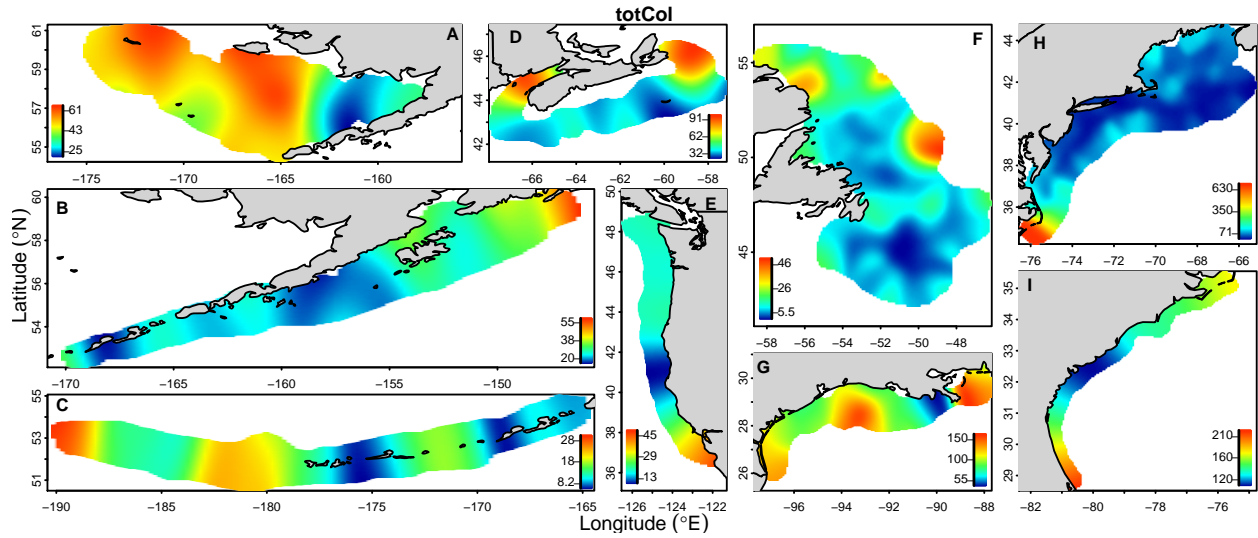


Figure 4: **Figure 2c.** Maps of total colonizations per site.

```
ceRate_map(ce="extinction")
```

46 **Figure 3b.** Unique Extinction map

```
ceRate_map(ce="uExt")
```

47 **Figure 3c.** Toal Extinction map

```
ceRate_map(ce="totExt")
```

48 Hotspots can be seen in most regions. Newfoundland also has high values around its edge (as opposed to
 49 interior), it seems. NEUS and Gmex show very strong hotspots, and other locations tend to be much much
 50 lower. Other regions show more of a continuum.

```
sppp <- function(...){spatstat::Smooth(spatstat::ppp(...), hmax=1)}
map_smooth <- function(X, val=c("n_spp_col_weighted","n_spp_ext_weighted","avgRich","uCol","uExt","totC
  val <- match.arg(val)
  r <- X[,unique(reg)]
  sppp(x=X[,lon], y=X[,lat], marks=X[,get(val)], window=map0win[[r]])
}
rel_col_ext_rate <- mapDat[,j={
  map_smooth_rich <- map_smooth(.SD, "avgRich")
  mark_range_rich <- range(map_smooth_rich, na.rm=TRUE)*10

  map_smooth_col <- map_smooth(.SD, "n_spp_col_weighted")
  mark_range_col <- range(map_smooth_col, na.rm=TRUE)*10

  map_smooth_ext <- map_smooth(.SD, "n_spp_ext_weighted")
  mark_range_ext <- range(map_smooth_ext, na.rm=TRUE)*10
```

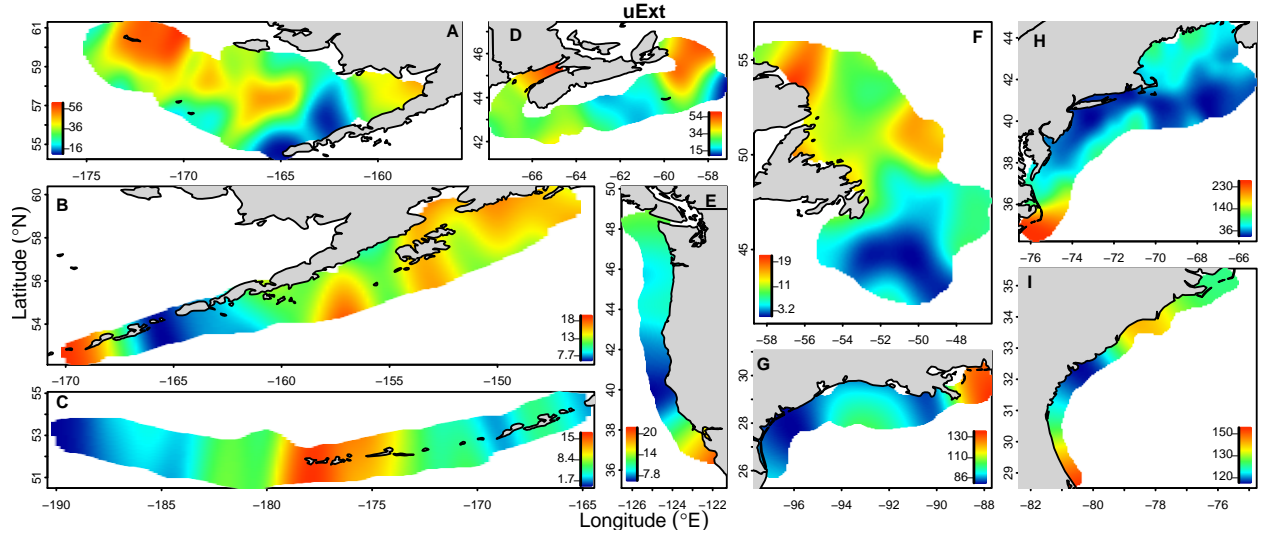
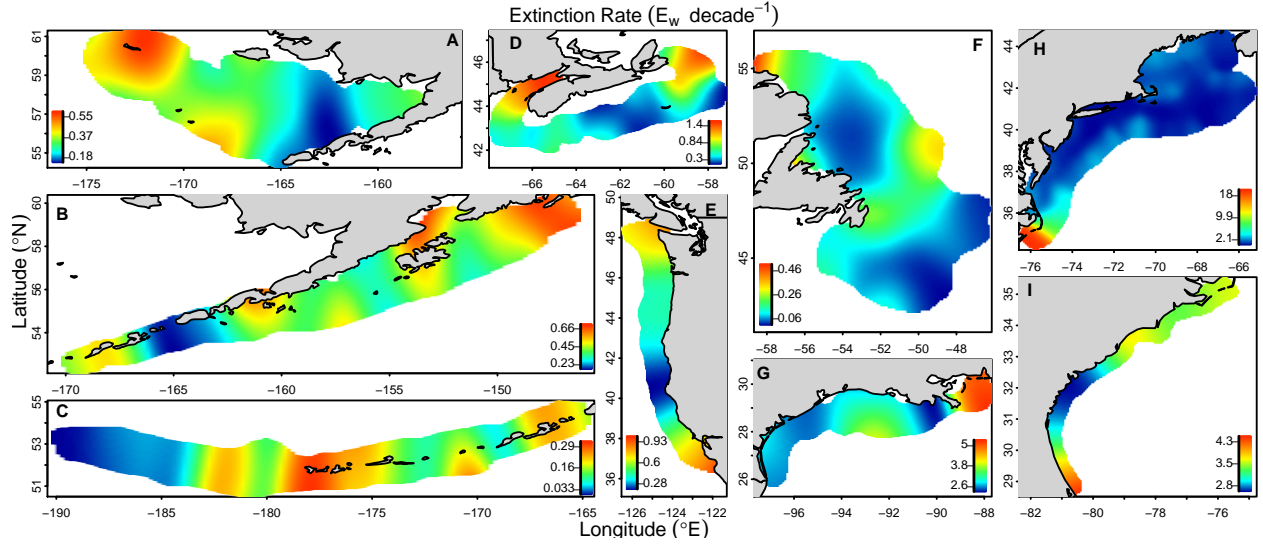


Figure 6: **Figure 3b.** Maps of the number of unique species with regional colonizations involving each site.

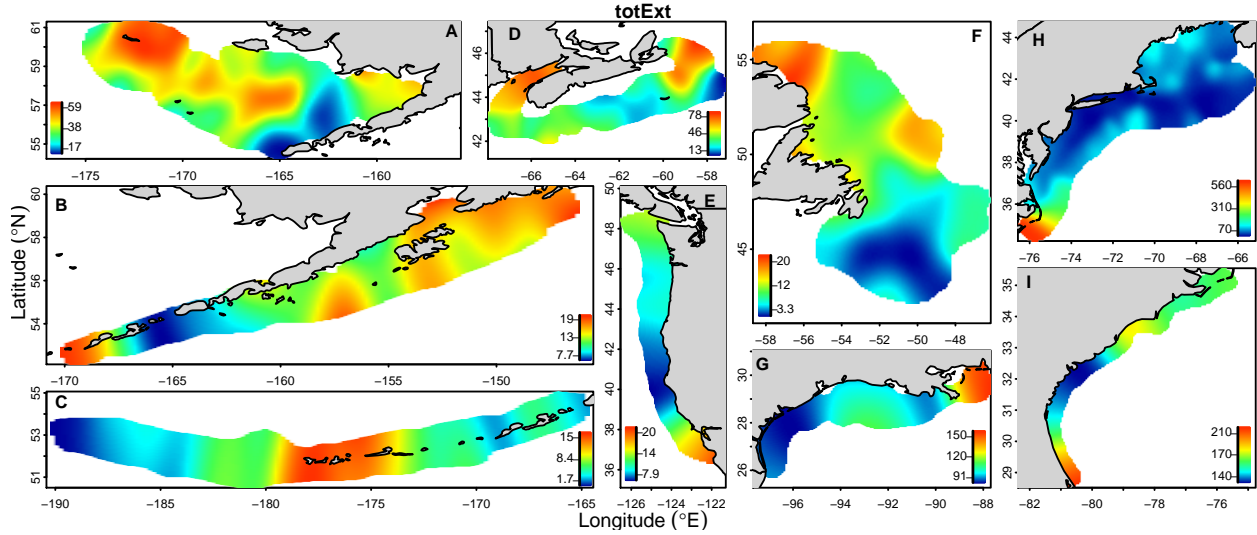


Figure 7: **Figure 3c.** Maps of the total number of regional extinctions involving each site.

```
map_smooth_uCol <- map_smooth(.SD, "uCol")
mark_range_uCol <- range(map_smooth_uCol, na.rm=TRUE)*10

map_smooth_uExt <- map_smooth(.SD, "uExt")
mark_range_uExt <- range(map_smooth_uExt, na.rm=TRUE)*10

map_smooth_totCol <- map_smooth(.SD, "totCol")
mark_range_totCol <- range(map_smooth_totCol, na.rm=TRUE)*10

map_smooth_totExt <- map_smooth(.SD, "totExt")
mark_range_totExt <- range(map_smooth_totExt, na.rm=TRUE)*10

ol <- list(
  minval_rich=mark_range_rich[1], maxval_rich=mark_range_rich[2],
  max_o_min_rich=do.call("/",as.list(rev(mark_range_rich))),
  minval_col=mark_range_col[1], maxval_col=mark_range_col[2],
  max_o_min_col=do.call("/",as.list(rev(mark_range_col))),
  minval_ext=mark_range_ext[1], maxval_ext=mark_range_ext[2],
  max_o_min_ext=do.call("/",as.list(rev(mark_range_ext))),
  minval_uCol=mark_range_uCol[1], maxval_uCol=mark_range_uCol[2],
  max_o_min_uCol=do.call("/",as.list(rev(mark_range_uCol))),
  minval_uExt=mark_range_uExt[1], maxval_uExt=mark_range_uExt[2],
  max_o_min_uExt=do.call("/",as.list(rev(mark_range_uExt))),
  minval_totCol=mark_range_totCol[1], maxval_totCol=mark_range_totCol[2],
  max_o_min_totCol=do.call("/",as.list(rev(mark_range_totCol))),
  minval_totExt=mark_range_totExt[1], maxval_totExt=mark_range_totExt[2],
  max_o_min_totExt=do.call("/",as.list(rev(mark_range_totExt)))
)

lapply(ol, function(x)if(is.numeric(x)){signif(x,3)}else{x})
},by=c("reg"), .SDcols=names(mapDat))
# #+ col-ext-intensities-table, echo=FALSE
# kable(
#   rbind(rel_col_ext_rate, rel_col_ext_rate[,lapply(.SD, median)][,reg=="MEDIAN"]),
```

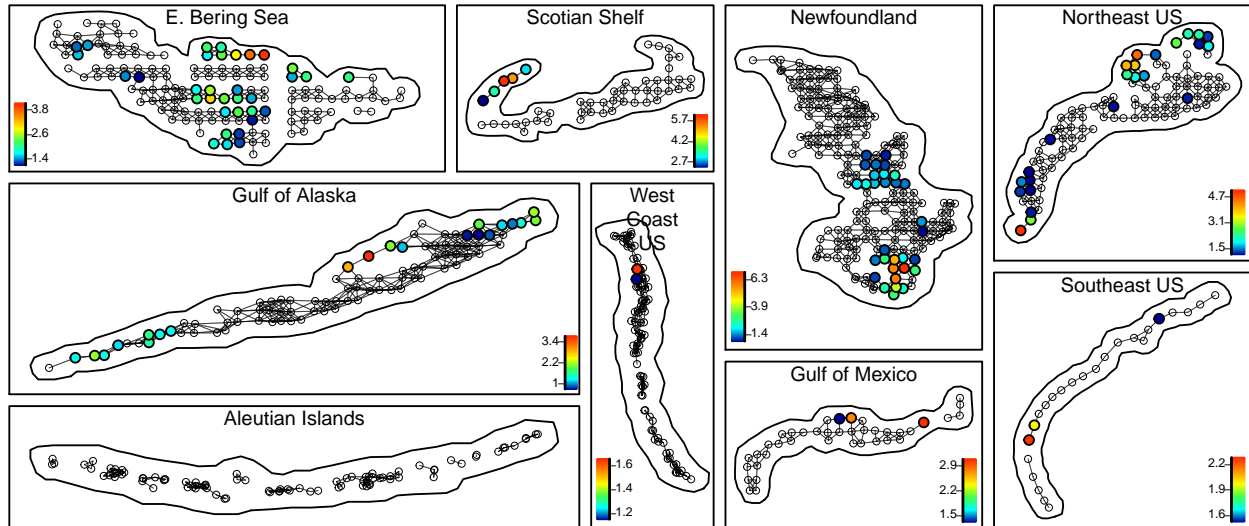


Figure 8: **Figure 4.** Connectivity and local spatial autocorrelation of richness in each region. Each site is represented by a point. Points connected by a line are neighbors. For each region, neighbors were determined by first calculating the minimum distance required to allow each site to have at least 1 neighbor. Neighbors of a focal point were then defined as the points within this minimum distance from the focal point. Local spatial autocorrelation is local Moran's I, significant LMI is indicated by a solid point, the color of which indicates the value of the LMI statistic. The outline is the region boundary used for smoothing in Figure 3 (main text), but does not affect calculations of LMI.

```
# caption="The colonization and extinction intensity range and max/min ratio, and median among region."
# )
```

Neighborhoods and Local Moran's I

Figure 4. Richness neighborhood

```
nb_moranI(ce="richness")
```

Figure 5. Colonization neighborhood

```
nb_moranI(ce="colonization")
```

Figure 5b. Unique Colonization neighborhood

```
nb_moranI(ce="uCol")
```

Figure 5c. Total Colonization neighborhood

```
nb_moranI(ce="totCol")
```

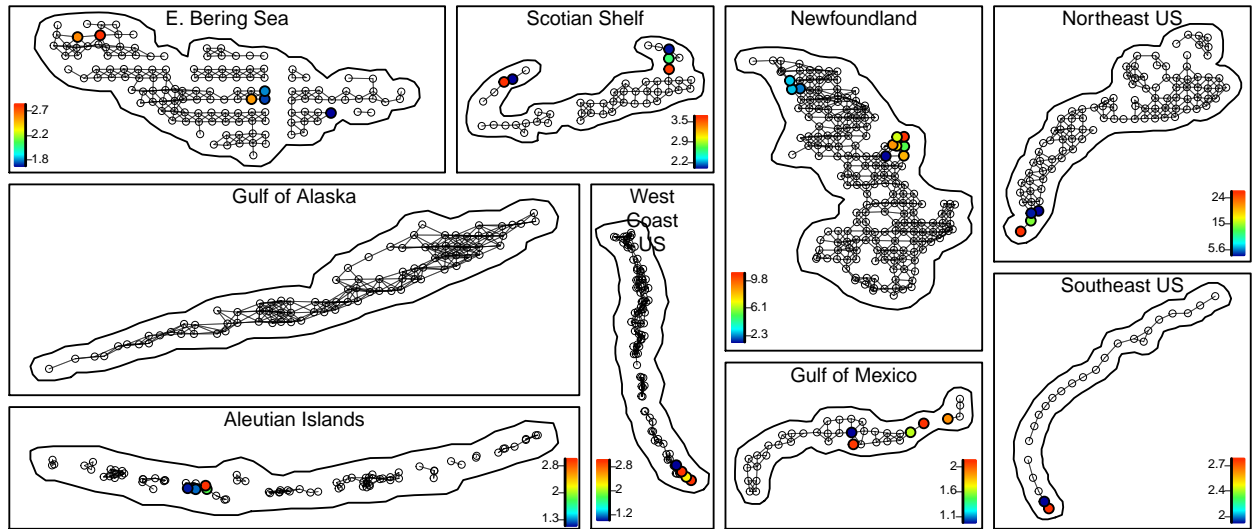



Figure 9: **Figure 5.** Connectivity and local spatial autocorrelation of colonization events in each region.

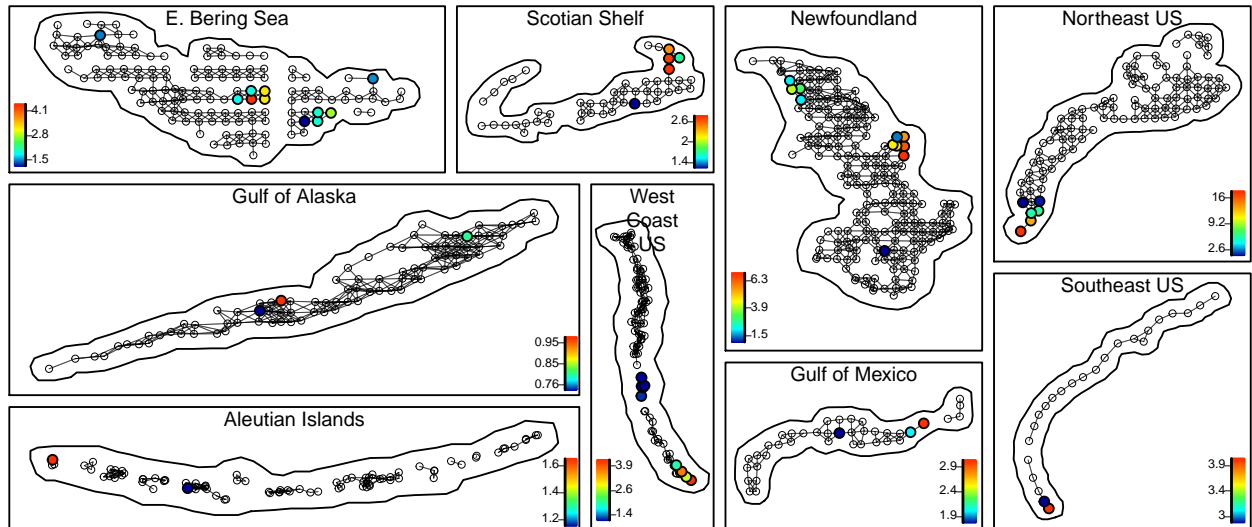


Figure 10: **Figure 5b.** Connectivity and local spatial autocorrelation of colonization events (each species only counted once per stratum) in each region.

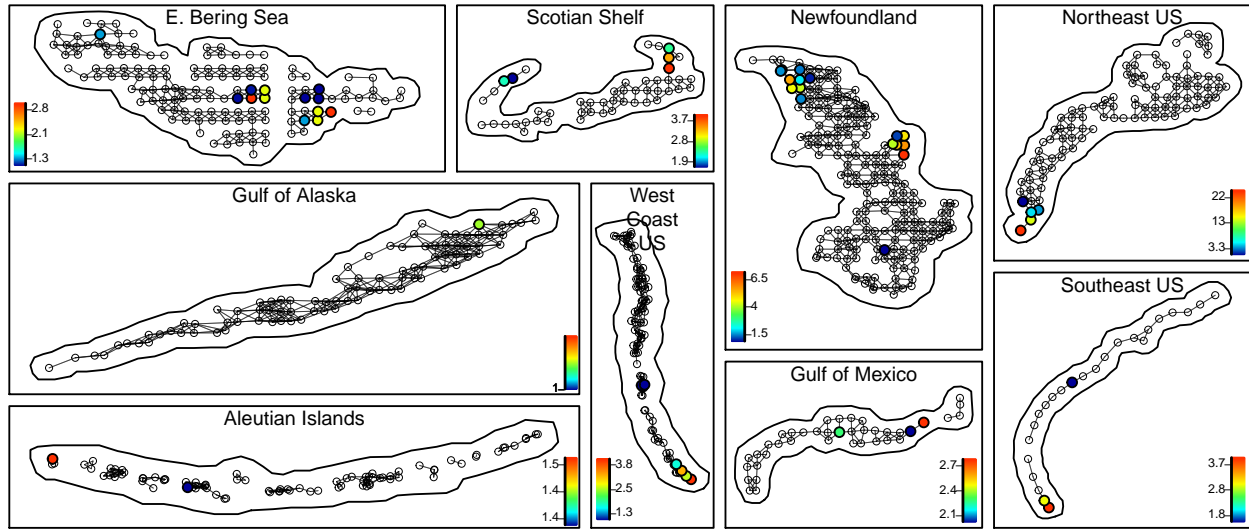


Figure 11: **Figure 5c.** Connectivity and local spatial autocorrelation of colonization events (each species possibly counted more than once per stratum) in each region.

56 **Figure 6. Extinction neighborhood**

```
nb_moranI(ce="extinction")
```

57 **Figure 6b. Unique Extinction neighborhood**

```
nb_moranI(ce="uExt")
```

58 **Figure 6c. Total Extinction neighborhood**

```
nb_moranI(ce="totExt")
```

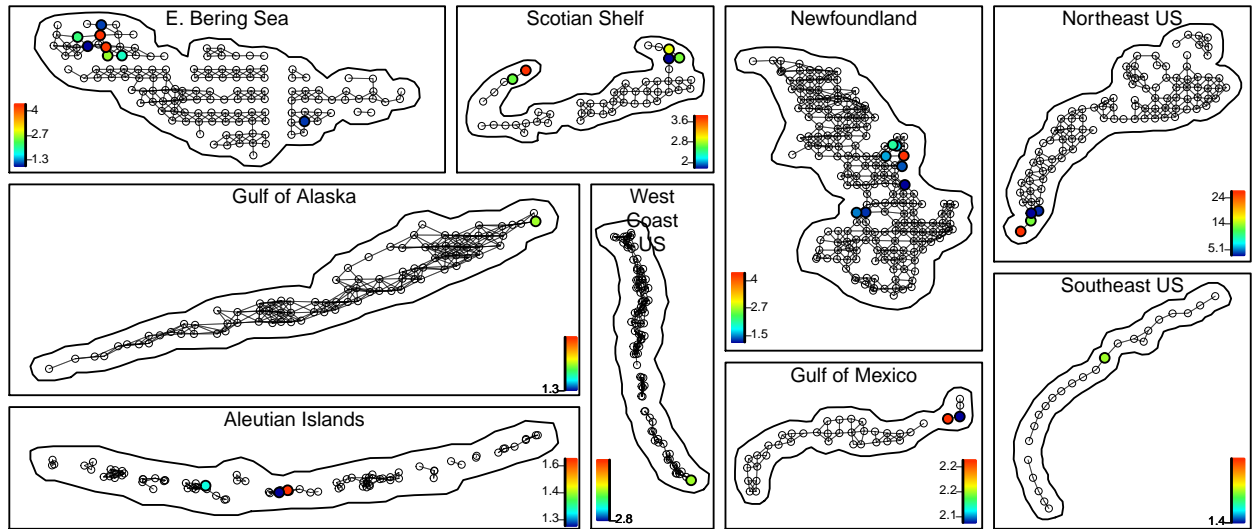


Figure 12: **Figure 6.** Connectivity and local spatial autocorrelation of extinction events in each region.

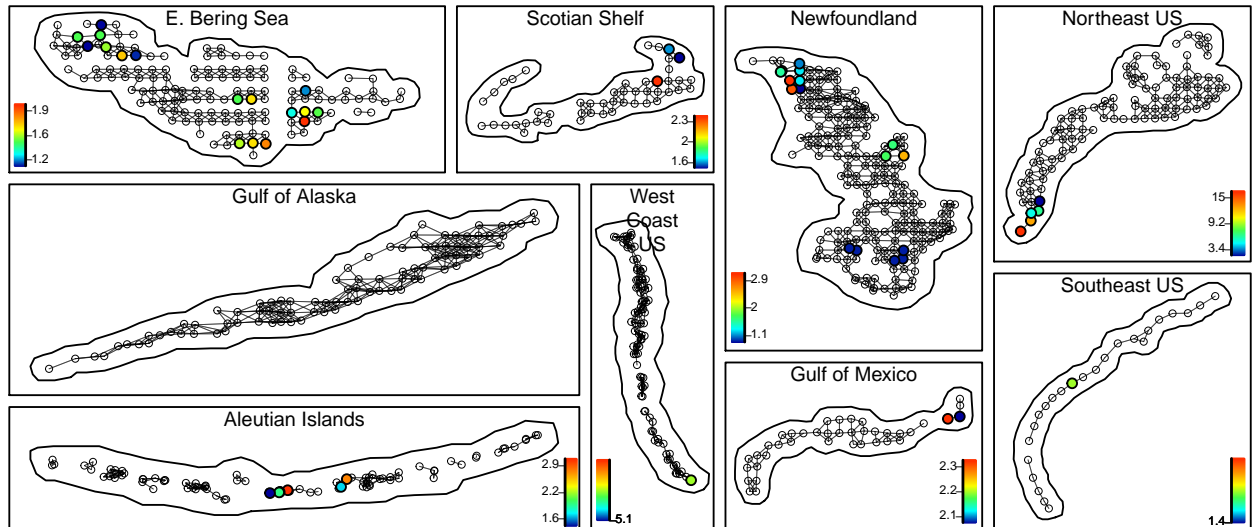


Figure 13: **Figure 6b.** Connectivity and local spatial autocorrelation of extinction events (each species only counted once per stratum) in each region.

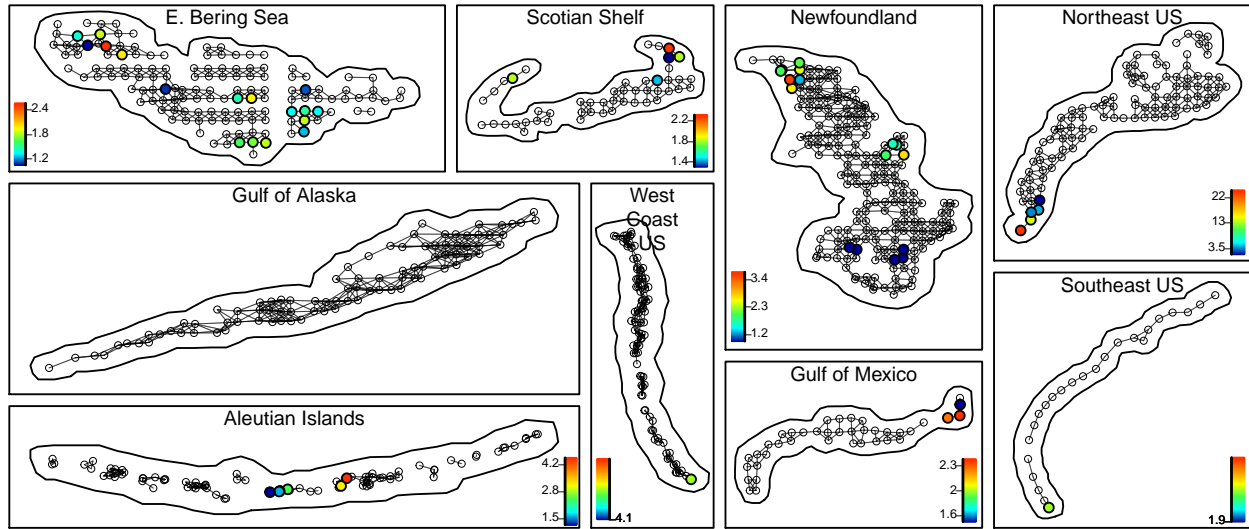


Figure 14: **Figure 6c.** Connectivity and local spatial autocorrelation of extinction events (each species possibly counted more than once per stratum) in each region.

59

60 Scatterplots involving colonization, richness, extinction

61 **Figure 7. Richness vs Depth**

```
par(mfrow=c(3,3))
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j]={
    plot(depth, avgRich);
    mtext(ureg[r],side=3,line=0.5,font=2);
    lines(sort(depth),predict(lm(avgRich~depth+I(depth^2),data=.SD[order(depth)])))
  }
}
```

par(mfrow=c(3,3));mapDat[,j]={plot(depth, uCol);mtext(reg,side=3,line=0.5,font=2)},by='reg'] # no rela

62 **Figure 8. Unique Colonization vs Richness**

```
par(mfrow=c(3,3))
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j]={
    plot(avgRich, uCol)
    mtext(ureg[r],side=3,line=0.5,font=2)
  }
}
```

63 **Figure 9. Unique Extinction vs Richness**

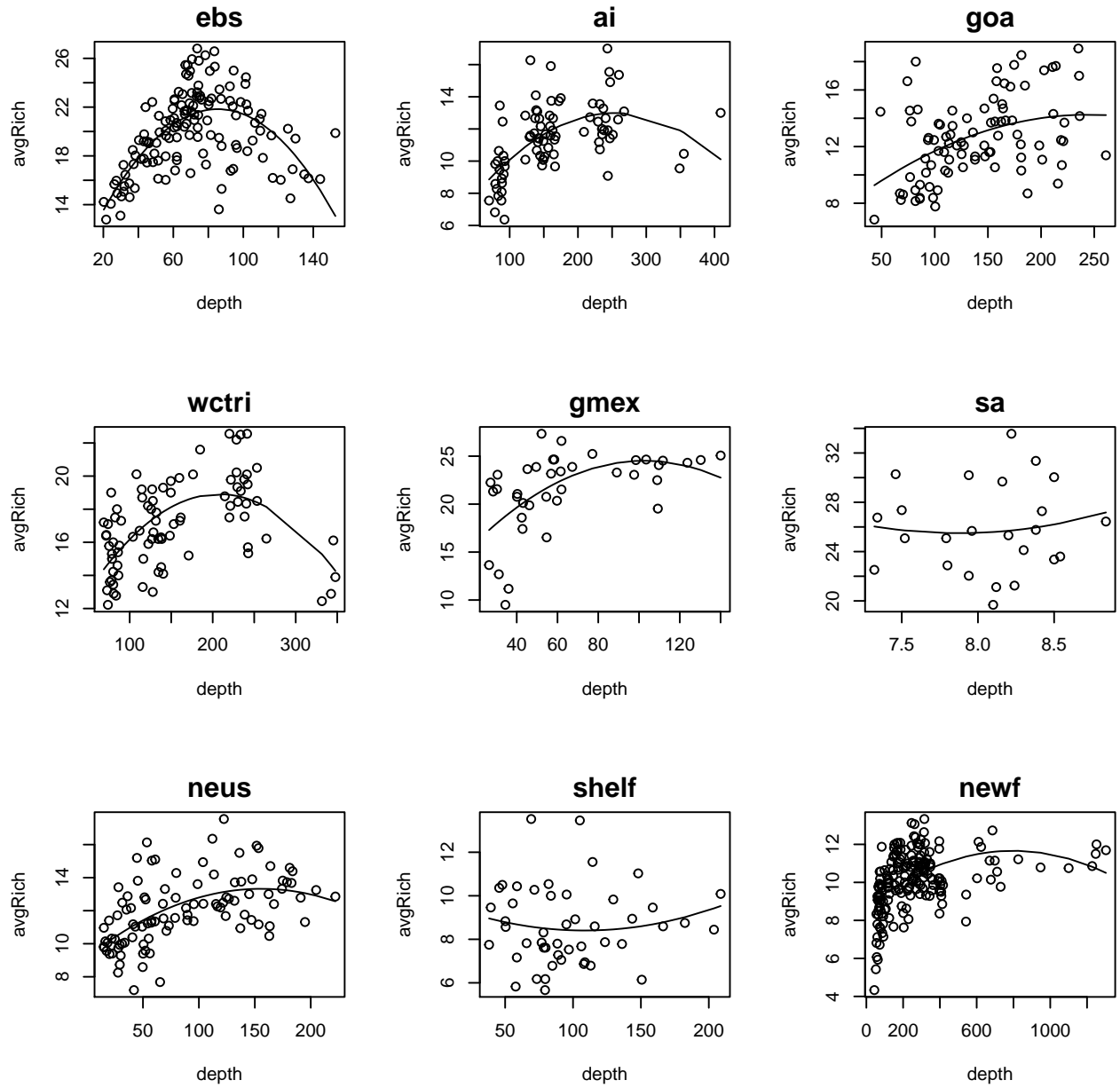


Figure 15: **Figure 7.** Long-term average of per-site species richness vs the depth (m) of the site. Fitted line is a regression of $\text{richness} \sim \text{depth} + \text{depth}^2$.

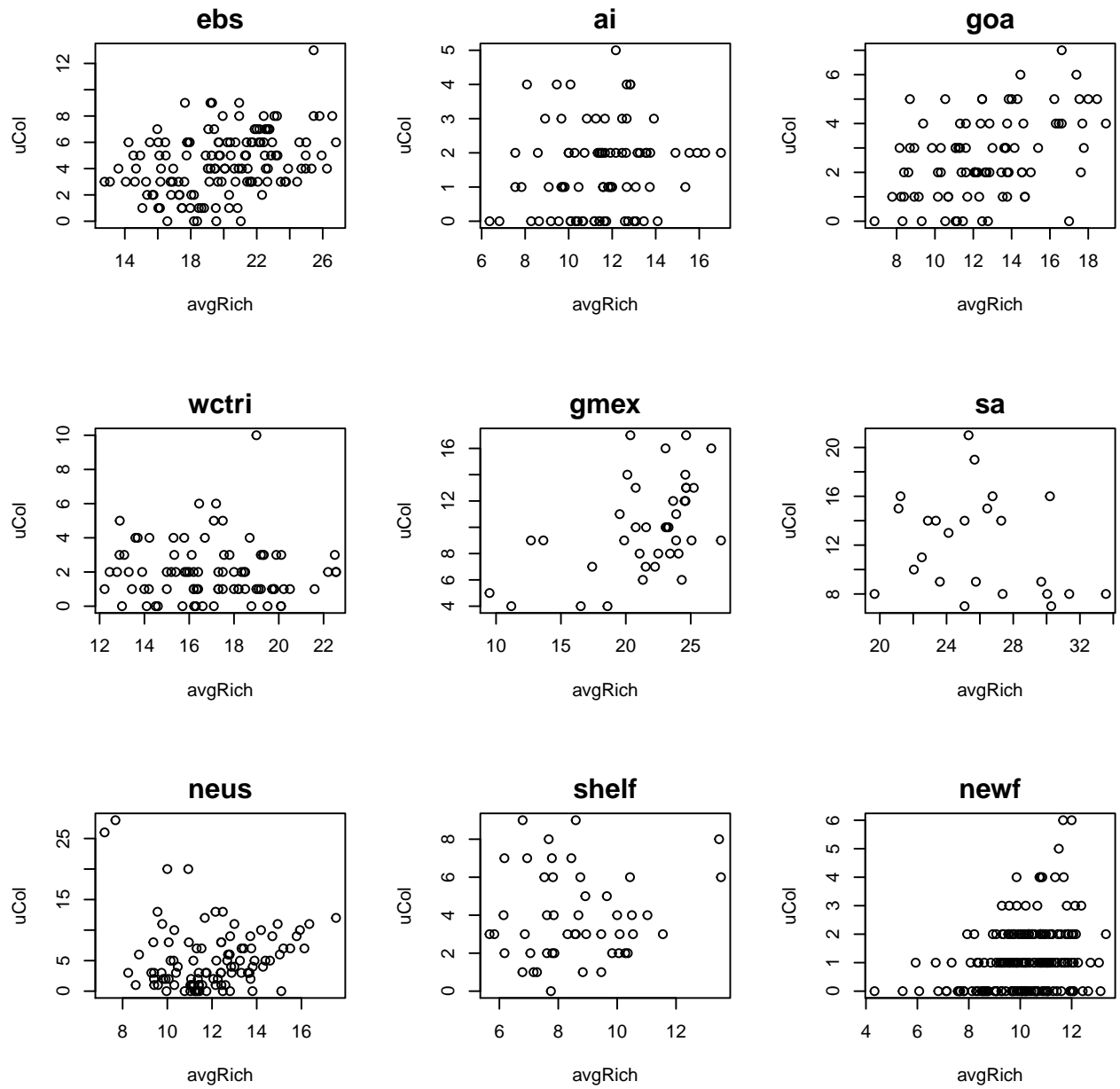


Figure 16: **Figure 8.** The number of species that ever had a regional colonization event involving that site vs long-term average of each site's richness.

```

par(mfrow=c(3,3))
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j]={
    plot(avgRich, uExt)
    mtext(ureg[r],side=3,line=0.5,font=2)
  }
}

```

64 **Figure 10. Unique Colonization vs Unique Extinction**

```

eval(figure_setup())
par(mfrow=c(3,3), mar=c(2.15,2.15,1.15,0.5), cex=1, mgp=c(1,0.25,0), tcl=-0.15, ps=10)
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j]={
    sigColInd <- lI_pvalue_uCol<0.05
    sigExtInd <- lI_pvalue_uExt<0.05
    muCol <- mean(uCol)
    muExt <- mean(uExt)
    hotspotIndCol <- sigColInd #& (totCol > muCol)
    hotspotIndExt <- sigExtInd #& (totExt > muExt)
    both <- hotspotIndExt&hotspotIndCol
    neither <- !hotspotIndExt&!hotspotIndCol

    cols <- vector("character", length(hotspotIndCol))
    cols[hotspotIndCol] <- "blue"
    cols[hotspotIndExt] <- "red"
    cols[both] <- "purple"
    cols[neither] <- "black"

    pchs <- vector("integer", length(hotspotIndCol))
    pchs[hotspotIndCol] <- 3
    pchs[hotspotIndExt] <- 4
    pchs[both] <- 5
    pchs[neither] <- 1

    # print(all(hotspotIndCol | hotspotIndExt | both | neither))

    # pchs <- rep(21, length(hotspotIndExt))
    # pchs[!neither] <- 19

    plot(uExt, uCol, col=cols, pch=pchs, cex=1.2)
    mtext(pretty_reg[ureg[r]],side=3,line=0.01,font=2)

    sigRichInd <- lI_pvalue_rich<0.05
    hotspotIndRich <- sigRichInd
    points(uExt[hotspotIndRich], uCol[hotspotIndRich], col='gray', pch=20, cex=0.7)
  }
}

```

65 **Figure 10b. Total Colonization vs Total Extinction**

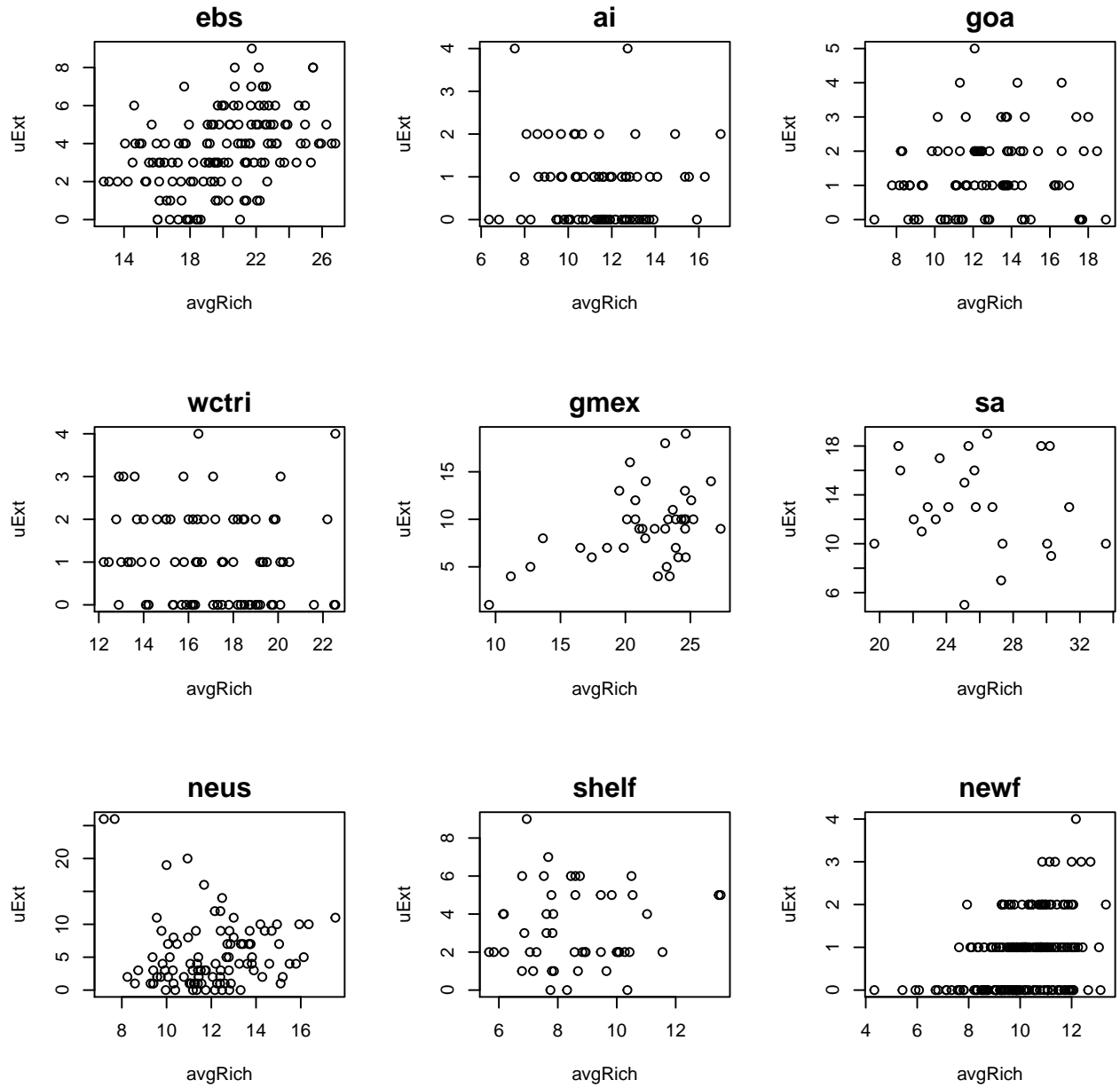


Figure 17: **Figure 9.** The number of species that ever had a regional extinction event involving that site vs long-term average of each site's richness.

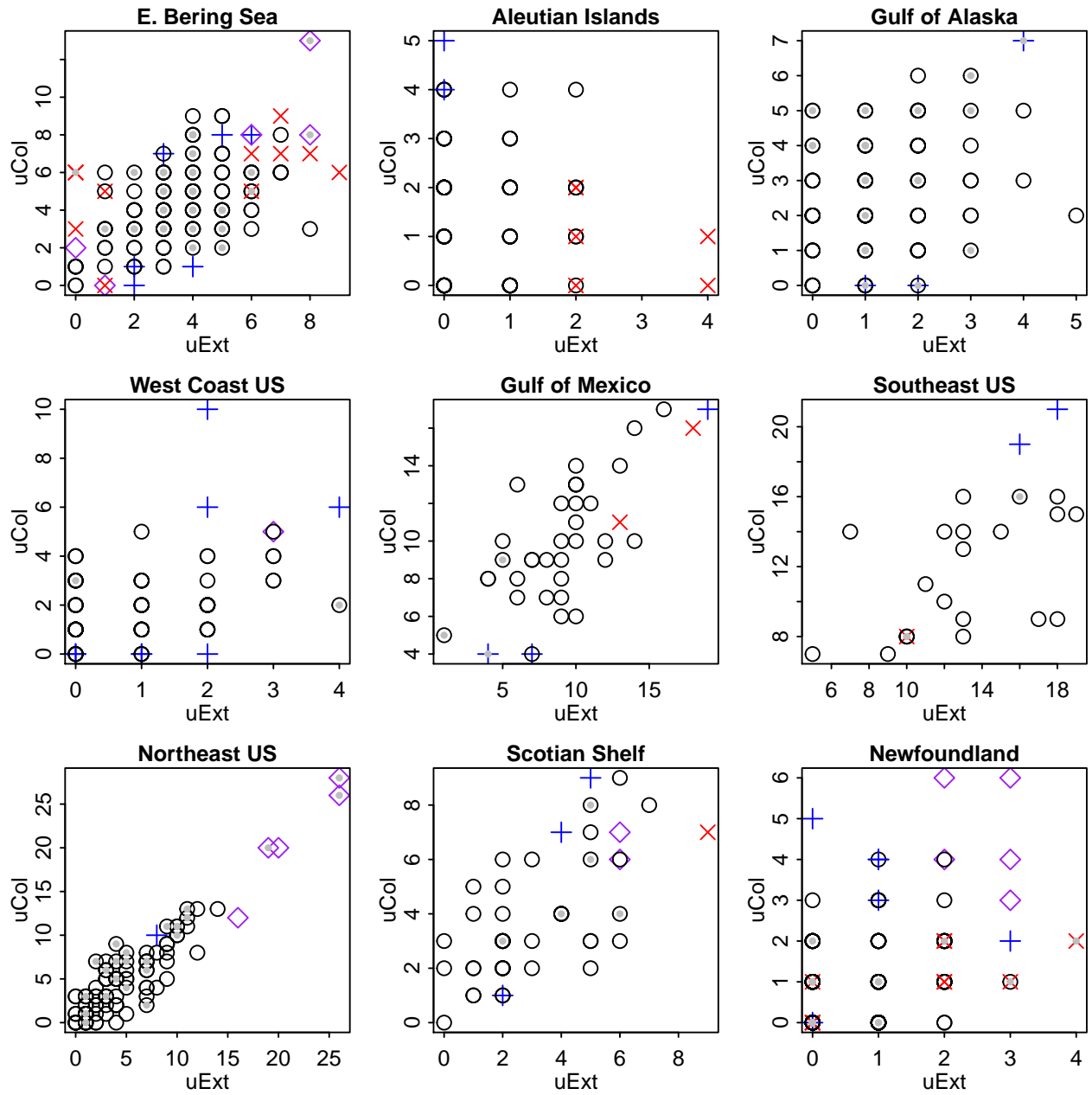


Figure 18: **Figure 10.** Numbers of colonizations versus extinctions at each site. Species were only counted once per site (even if that species colonized or went extinct from the region multiple times, each time involving the site). Colors and shapes indicate the metrics with significant local spatial autocorrelation at the site: Blue +’s are colonization only, red x’s are extinction only, purple diamonds are both colonization and extinction, and black circles are neither colonization nor extinction. Gray circles were overlaid on sites with significant clustering in local species richness.

```

eval(figure_setup())
par(mfrow=c(3,3), mar=c(2.15,2.15,1.15,0.5), cex=1, mgp=c(1,0.25,0), tcl=-0.15, ps=10)
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j]={
    sigColInd <- lI_pvalue_totCol<0.05
    sigExtInd <- lI_pvalue_totExt<0.05

    muCol <- mean(totCol)
    muExt <- mean(totExt)
    hotspotIndCol <- sigColInd #& (totCol > muCol)
    hotspotIndExt <- sigExtInd #& (totExt > muExt)

    both <- hotspotIndExt&hotspotIndCol
    neither <- !hotspotIndExt&!hotspotIndCol

# print(all(hotspotIndCol | hotspotIndExt | both | neither))

    cols <- vector("character", length(hotspotIndCol))
    cols[hotspotIndCol] <- "blue"
    cols[hotspotIndExt] <- "red"
    cols[both] <- "purple"
    cols[neither] <- "black"

    pchs <- vector("integer", length(hotspotIndCol))
    pchs[hotspotIndCol] <- 3
    pchs[hotspotIndExt] <- 4
    pchs[both] <- 5
    pchs[neither] <- 1

# pchs <- rep(21, length(hotspotIndExt))
# pchs[!neither] <- 19

    plot(totExt, totCol, col=cols, pch=pchs, cex=1.2)
    mtext(pretty_reg[ureg[r]],side=3,line=0.01,font=2)

    sigRichInd <- lI_pvalue_rich<0.05
    hotspotIndRich <- sigRichInd
    points(totExt[hotspotIndRich], totCol[hotspotIndRich], col='gray', pch=20, cex=0.7)
  }
}

```

66 Figure 11. Total Colonization vs Unique Colonization

```

par(mfrow=c(3,3))
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j]={
    plot(uCol, totCol)
    abline(a=0, b=1)
    mtext(ureg[r],side=3,line=0.5,font=2)
  }
}

```

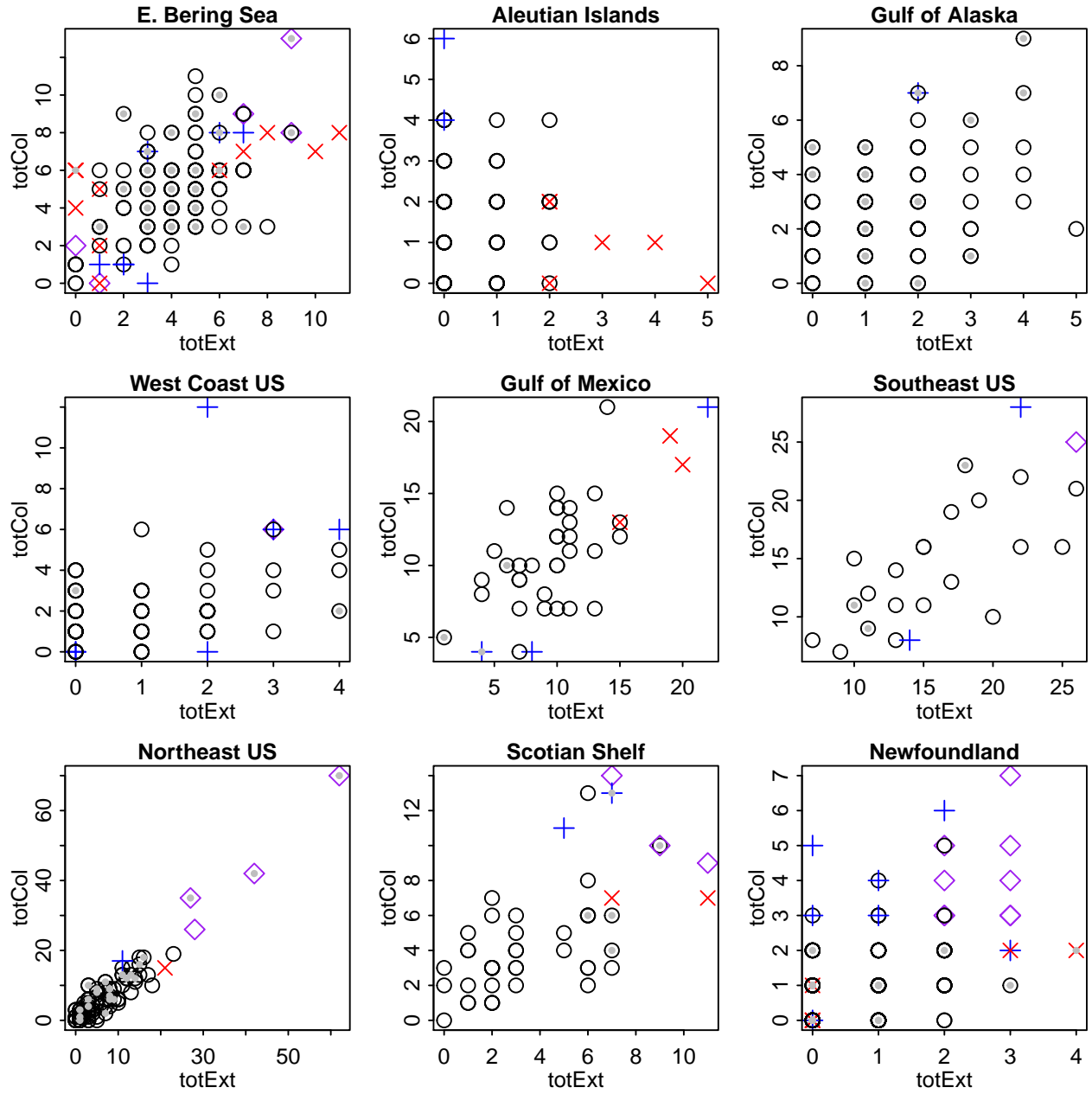


Figure 19: **Figure 10b.** Total numbers of colonizations versus extinctions at each site. Colors and shapes indicate the metrics with significant local spatial autocorrelation at the site: Blue +’s are colonization only, red x’s are extinction only, purple diamonds are both colonization and extinction, and black circles are neither colonization nor extinction. Gray circles were overlaid on sites with significant clustering in local species richness.

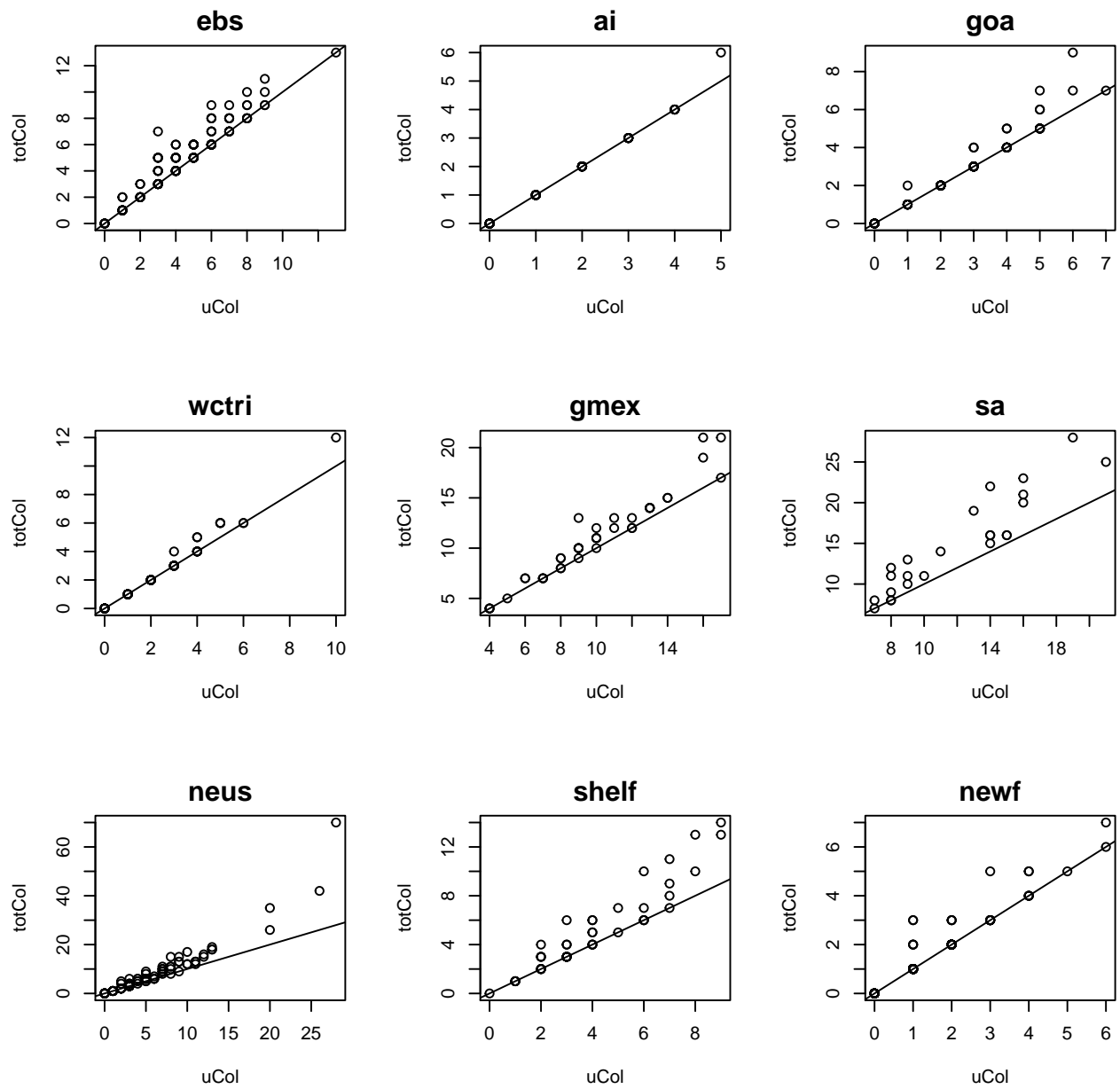


Figure 20: **Figure 11.** The total number of colonization events at each site vs the number of species that ever had a colonization event involving the site.

67 **Figure 12. Total Extinction vs Unique Extinction**

```
par(mfrow=c(3,3))
for(r in 1:length(ureg)){
  mapDat[reg==ureg[r],j={
    plot(uExt, totExt)
    abline(a=0, b=1)
    mtext(ureg[r],side=3,line=0.5,font=2)
  }]
}
```

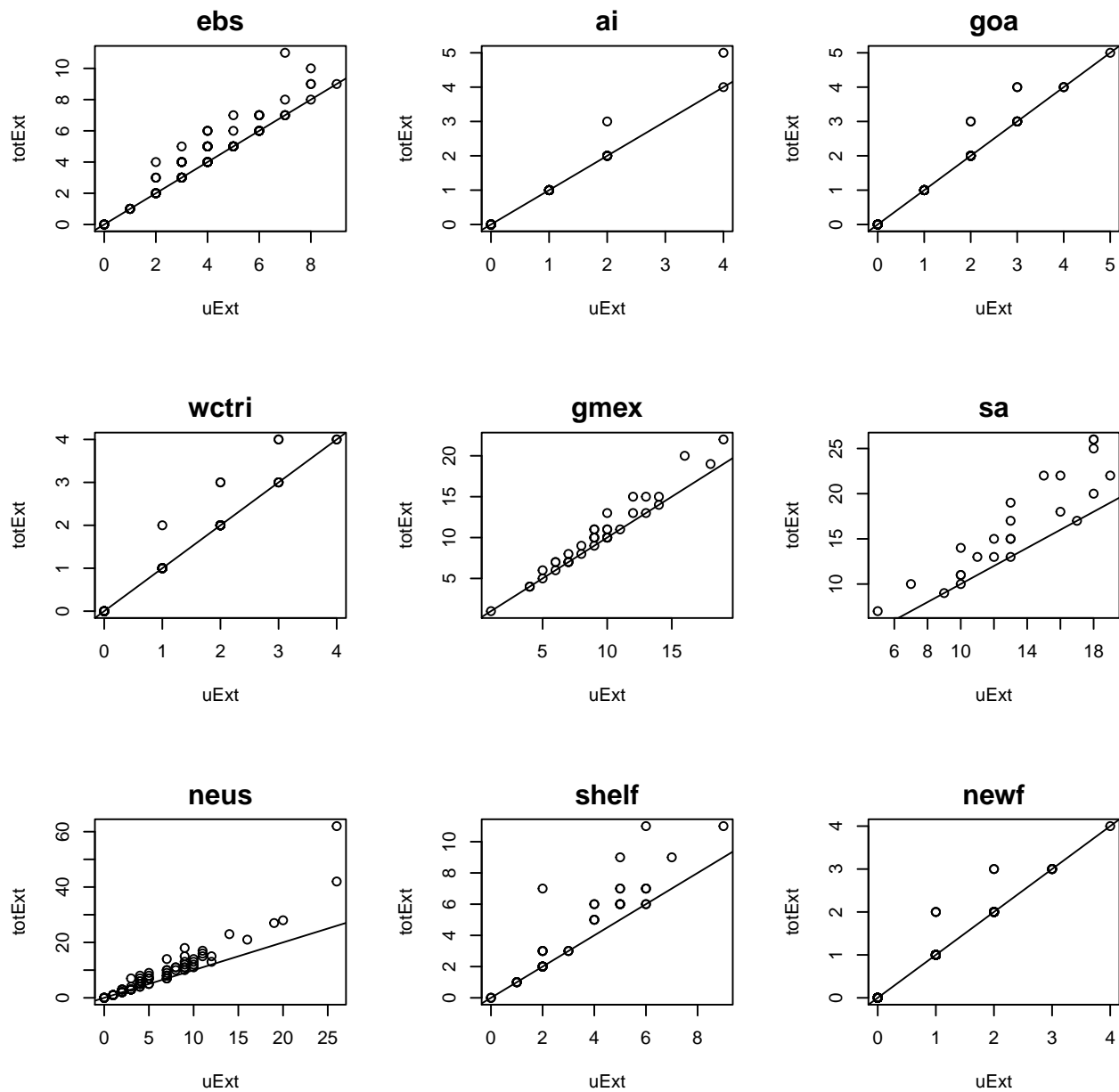


Figure 21: **Figure 12.** The total number of extinction events at each site vs the number of species that ever had an extinction event involving the site.

```

fracHotspot <- mapDat[,j]={
  sigColInd <- lI_pvalue_totCol<0.05
  sigExtInd <- lI_pvalue_totExt<0.05
  muCol <- mean(totCol)
  muExt <- mean(totExt)
  hotspotIndCol <- sigColInd & (totCol > muCol)
  hotspotIndExt <- sigExtInd & (totExt > muExt)

  list(
    hotspotFracCol=sum(totCol[hotspotIndCol])/sum(totCol),
    hotspotFracColNSPots=sum(hotspotIndCol)/length(stratum),
    hotspotFracExt=sum(totExt[hotspotIndExt])/sum(totExt),
    hotspotFracExtNSPots=sum(hotspotIndExt)/length(stratum)
  )
},by=c("reg")]
kable(fracHotspot)

```

reg	hotspotFracCol	hotspotFracColNSPots	hotspotFracExt	hotspotFracExtNSPots
ebs	0.079	0.043	0.123	0.058
ai	0.083	0.024	0.310	0.073
goa	0.029	0.011	0.000	0.000
wctri	0.170	0.048	0.032	0.012
gmex	0.049	0.026	0.137	0.077
sa	0.148	0.083	0.067	0.042
neus	0.260	0.050	0.249	0.050
shelf	0.246	0.104	0.232	0.104
newf	0.264	0.079	0.184	0.058
