



Supplement of

Reconstructions of biomass burning from sediment-charcoal records to improve data–model comparisons

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Code Description

The following is the R code for preparing and plotting the dot map figures in the manuscript. The scripts are based on the ‘paleofire’ and ‘GCD’ R packages, which were developed in conjunction with this research and are available from the Comprehensive R Archive Network (CRAN). Briefly, the first script sets up options for the gridding procedure, including the extent and resolution of the grid, target ages for analysis, binning and analysis half-window widths, the number of bootstraps to include in confidence calculations, and several graphical parameters for presenting the final plots. The script then selects data from all sites in the GCD database, processes them according to the methodology described in the main text, and saves the results for later use. The second script starts from this saved output, sets various graphical parameters, and then produces gridded dot maps of mean CHAR z-scores, number of sites contributing to each dot, and the number of dots contributed to by each site (e.g., figures 5, 6, and 7 in the main text). An option allows the plots to be displayed in the R window, or saved to PDF.

```
# STEP 1 - PREPARE BASE FIGURES
rm(list=ls())
library(devtools)
library(paleofire)
library(GCD)

#install_github("paleofire","paleofire", ref="daily")
#load_all("~/Work/research/GPWG/paleofire/")

# ----- Options and parameters
# Working directory
setwd('~/methods/charcoal/GCD v3.0 Paper figures/')

plotdata.file = "./Data/All_GCDv1.1_rawplots_BB21k_2015-09-18.rds"
#plotdata.file = "./Data/All_GCDv1.1_rawplots_BB1k_2015-09-18.rds"

# File for transformed data
TR.file = './Data/All_GCDv1.1_Transformed_BB21k.rds'
#TR.file = './Data/All_GCDv1.1_Transformed_BB1k.rds'
TR.mode = 0 #1 # 0==Run transformation, save result for later, 1==use saved data

# Figure file name base.
# - Can include a path (otherwise goes in working directory); all directories must exist.
# - Year designation and file suffix will be added automatically
# - Set to NULL to only print to screen

fig.base.name = './1perPg/GCDv3-SI-21k_'
```

```

# fig.base.name = './1perPg/GCDv3-SI-1k_'
# fig.base.name = NULL # Use for paper figures

# Base map ('coasts' or 'countries')
base.map = 'coasts'

# Grid resolution and extent (in degrees)
grd.res = 5
grd.ext = c(-180,180,-90,90) # c(lonmin, lonmax, latmin, latmax)

# Composite params
tarAge = seq(0,21000,1000) #increments = 1000 (Figs. 6 & 7 gridded maps)
#tarAge = seq(-50,1050,100) #increments = 100
hw    = 250 #10 # (v3 Figs. 6 & 7 paper setting)
binhw = 500 #50 #20 # (v3 Figs. 6 & 7 paper setting) ### THIS CHANGES THE
MAP INTERVALS & FILE NAMES
n.boot = 1000 #1000 #(v3 Fig. 6 paper setting)

# Dot size parameters
cx.mult = 1.5
cx.minsize = 0.4

# Projection for maps
# Unprojected
proj4 = "+proj=longlat"

# Robinson
# proj4 = "+proj=robin +lon_0=0 +x_0=0 +y_0=0 +ellps=WGS84 +datum=WGS84
+units=m +no_defs"

# Gall-Peters equal-area projection
# proj4 = "+proj=cea +lon_0=0 +lat_ts=45 +x_0=0 +y_0=0 +ellps=WGS84 +units=m
+no_defs"

# Lambert equal-area
# proj4 = '+proj=laea +lat_0=30 +lon_0=0 +x_0=0 +y_0=0'

# Mercator
# proj4 = "+proj=merc +lon_0=0 +k_0=1 +x_0=0 +y_0=0"

# ----- End Options
# ---- Make dir
if(!is.null(fig.base.name))
  dir.create(dirname(fig.base.name), recursive=T, showWarnings=F)

# ---- Transform records (slow, which is why TR.mode=1 is added)

```

```

if(TR.mode==0) {
  # New transform
  id = pfSiteSel() # Select all sites
  TR = pfTransform(id, method=c("MinMax","Box-Cox","Z-Score"),
BasePeriod=c(200,21000),QuantType="INFL") #Fig. 6
  #TR = pfTransform(id, method=c("MinMax","Box-Cox","Z-Score"),
BasePeriod=c(200,1000),QuantType="INFL") #Fig. BB1k
  saveRDS(TR, file=TR.file)
} else {
  # load existing
  TR = readRDS(TR.file)
}

# ----- Run pfDotMap
dotmap = pfDotMap ( TR=TR, tarAge=tarAge, binhw=binhw, hw=hw,
n.boot=n.boot,
  fig.base.name=fig.base.name, base.map=base.map,
  grd.res=grd.res, grd.ext=c(-180,180,-90,90), proj4=proj4,
  cx.minsize=cx.minsize, cx.mult=cx.mult
)

saveRDS(dotmap, plotdata.file)

# STEP 2 – MAKE PLOTS
rm(list=ls())
library(rgdal)
library(rworldmap)

# -----
setwd('~/methods/charcoal/GCD v3.0 Paper figures/')
dotmap = readRDS('./Data/All_GCDv1.1_rawplots_BB1k_2015-08-18.rds')
outdir = './PaperFigs_pfCompositeLF/'

y.lim = c(-70,80)
x.lim = c(-180,180)

##### extract 1000-year slices desired
#grd = list(dotmap$sp.grd[[1]], dotmap$sp.grd[[7]], dotmap$sp.grd[[22]])
#site = list(dotmap$sp.sites[[1]], dotmap$sp.sites[[7]], dotmap$sp.sites[[22]])
# n.bin = length(grd)
# picked 1,6,11 first

#grd = list(dotmap$sp.grd[[1]], dotmap$sp.grd[[2]], dotmap$sp.grd[[11]])
#site = list(dotmap$sp.sites[[1]], dotmap$sp.sites[[2]], dotmap$sp.sites[[11]])
# n.bin = length(grd)

```

```

# ----- Load base map
proj4 = proj4string(grd[[1]])
data(countriesCoarse) # A dataset in rworldmap used in the plots below
data(coastsCoarse) # An alternative base map. Needs one fix:
countriesCoarse = spTransform(countriesCoarse, CRS(proj4))
coastsCoarse = spTransform(coastsCoarse, CRS(proj4))

# ----- MEAN PLOT -----
dir.create(outdir, recursive=T, showWarnings=F)
file.plot = paste0(outdir, 'Mean.pdf')
file.legend = paste0(outdir, 'Mean_v3_legend.pdf')

# cols = c("#0571B0","#92C5DE",grey(0.9),"#F4A582","#CA0020") # modified from
colorbrewer
# cols = rev( c( rgb(1.000,0.250,0.000), rgb(1.000,0.501,0.144),
rgb(1.000,0.740,0.376), rgb(1.000,0.924,0.694), rgb(0.887,1.000,1.000),
rgb(0.607,0.918,1.000), rgb(0.376,0.792,1.000), rgb(0.194,0.630,1.000) ))
cols = c( rgb(0,0,1), rgb(0.194,0.630,1), rgb(0.376,0.792,1), grey(0.95),
rgb(1,0.74,0.376), rgb(1,0.501,0.144), rgb(1,0,0) )

cuts = c(-1.75,-1.25,-0.75,-0.25,0.25,0.75,1.25,1.75)
# cuts = c(-1.5,-0.9,-0.3,0.3,0.9,1.5) # Defines range and resolution of color scale
# cuts = c(-3,-1.8,-0.6,0.6,1.8,3) # Defines range and resolution of color scale
cx.sizes = c(0.75,1)

panel.labels = rep("",3) # c("Present", "6 ka", "21 ka")
grid.grey = grey(0.8)

mp = list()
for(i in 1:n.bin) {
  sp.grd = grd[[i]]

  # Assign symbol size based on whether CI contain 0
  cx = ifelse(sp.grd$CI.lower>0 | sp.grd$CI.upper<0, max(cx.sizes), min(cx.sizes))

  # The previous line will produce NA for cells with n=1 since CI are undefined. Give
  # these "non-significant" symbol size by default.
  cx[which(sp.grd$sitesPerCell==1)] = min(cx.sizes)

  # Create plot object (actually plotted later)
  mp[[i]] =

```

```

spplot(sp.grd, 'mean.CHAR', xlim=x.lim, ylim=y.lim,
cuts=cuts, colorkey=T, col.regions=cols, cex=cx, edge.col=grey(0.7), lwd=0.1,
sp.layout=list(
  list("sp.lines",coastsCoarse,col=grid.grey,lwd=0.3),
  list("sp.polygons",countriesCoarse,col=grid.grey,lwd=0.3),
  list("sp.lines",gridlines(sp.grd),col=grid.grey, lwd=0.3),
  list("sp.text",c(-150,-50), panel.labels[i], fontface=2)),
par.settings=list(
  layout.widths=list(left.padding=3, right.padding=3),
  layout.heights=list(top.padding=-3, bottom.padding=-3)),
  scales=list(alternating=0,tck=-0.5)
) # End spplot
if(i==1) mp.legend = mp[[i]]
mp[[i]]$legend = NULL
}
names(mp.legend$legend) = "bottom"
mp.legend$legend$bottom$args$key$space="bottom"

save.plot = T
if(save.plot) pdf(file.plot, width=17.5/2.54, height=11)
print(mp[[1]], position=c(0,0.635,1,0.905), panel.width=list(17.2,"cm"),
panel.height=list(17.5*0.42,"cm"), more=T)
print(mp[[2]], position=c(0,0.365,1,0.635), panel.width=list(17.2,"cm"),
panel.height=list(17.5*0.42,"cm"), more=T)
print(mp[[3]], position=c(0,0.095,1,0.365), panel.width=list(17.2,"cm"),
panel.height=list(17.5*0.42,"cm"), more=F)
if(save.plot) dev.off()

if(save.plot) {
  pdf(file.legend, width=20, height=5)
  print(mp.legend, position = c(0,0,1,1), panel.width=list(17.2,"cm"),
panel.height=list(17.5*0.42,"cm"))
  dev.off()
}

# ----- NSITES PLOT -----
file.plot = paste0(outdir, 'Nsites.pdf')
file.legend = paste0(outdir, 'Nsites_legend.pdf')

cols = grey(0.2) # Can be replaced by a vector if different colors are desired

cuts = c(0.9,1.9,9.9,1000) # Where to divide symbol sizes
cx.legend = c("1", "2-9", "10+") # legend text
cx.key = c(0.3,0.4,0.5)
n.cx = length(cuts)-1 # number of bins represented

```

```

mp = list()
for(i in 1:n.bin) {
  sp.grd = grd[[i]]

  cx = cx.key[ cut(sp.grd$sitesPerCell, cuts, labels=F) ]

  # Create plot object (actually plotted later)
  mp[[i]] =
    spplot(sp.grd, 'sitesPerCell', xlim=x.lim, ylim=y.lim,
           cex=cx, cex.key=cx.key, legendEntries=cx.legend, cuts=cuts,
           col.regions=cols, edge.col="transparent",
           sp.layout=list(
             list("sp.lines",coastsCoarse,col=grid.grey,lwd=0.3),
             list("sp.polygons",countriesCoarse,col=grid.grey,lwd=0.3),
             list("sp.lines",gridlines(sp.grd),col=grid.grey, lwd=0.3),
             list("sp.text",c(-150,-50), panel.labels[i], fontface=2, cex=0.7)),
           par.settings=list(
             layout.widths=list(left.padding=-3, right.padding=-3),
             layout.heights=list(top.padding=-3, bottom.padding=-3)),
           scales=list(alternating=0,tck=-0.5)

         )
  if(i==1) mp.legend = mp[[i]]
  mp[[i]]$legend = NULL
}

save.plot = T
if(save.plot) pdf(file.plot, width=8.5/2.54, height=5.3)

print(mp[[1]], position=c(0,0.635,1,0.905), panel.width=list(8.25,"cm"),
      panel.height=list(8.25*0.42,"cm"), more=T)
print(mp[[2]], position=c(0,0.365,1,0.635), panel.width=list(8.25,"cm"),
      panel.height=list(8.25*0.42,"cm"), more=T)
print(mp[[3]], position=c(0,0.095,1,0.365), panel.width=list(8.25,"cm"),
      panel.height=list(8.25*0.42,"cm"), more=F)
if(save.plot) dev.off()

if(save.plot) {
  pdf(file.legend, width=8.5/2.54, height=5)
  print(mp.legend, position = c(0,0,1,1), panel.width=list(8.25,"cm"),
        panel.height=list(8.25*0.42,"cm"))
  dev.off()
}

```

```

# ----- NSITES PLOT -----
file.plot = paste0(outdir, 'Ncells.pdf')
file.legend = paste0(outdir, 'Ncells_legend.pdf')

cols = grey(0.2) # Can be replaced by a vector if different colors are desired

cuts = c(0.9,1.9,3.9,100) # Where to divide symbol sizes
cx.legend = c("1", "2-3", "4+") # legend text
cx.key = c(0.3,0.4,0.5)
n.cx = length(cuts)-1 # number of bins represented

# ind.non0 = which(cx>0) # Don't want to change size 0 (== not plotted)
# cx[ind.non0] = cx[ind.non0] + cx.minsize - min(cx[ind.non0])

mp = list()
for(i in 1:n.bin) {
  sp.site = site[[i]]

  cx = cx.key[ cut(sp.site$cellsPerSite, cuts, labels=F) ]

  # Create plot object (actually plotted later)
  mp[[i]] =
    spplot(sp.site, 'cellsPerSite', xlim=x.lim, ylim=y.lim,
           cex=cx, cex.key=cx.key, legendEntries=cx.legend, cuts=cuts,
           col.regions=cols, edge.col="transparent",
           sp.layout=list(
             list("sp.lines",coastsCoarse,col=grid.grey,lwd=0.3),
             list("sp.polygons",countriesCoarse,col=grid.grey,lwd=0.3),
             list("sp.lines",gridlines(sp.grd),col=grid.grey, lwd=0.3),
             list("sp.text",c(-150,-50), panel.labels[i], fontface=2, cex=0.7)),
           par.settings=list(
             layout.widths=list(left.padding=-3, right.padding=-3),
             layout.heights=list(top.padding=-3, bottom.padding=-3)),
           scales=list(alternating=0,tck=-0.5)

         )
  if(i==1) mp.legend = mp[[i]]
  mp[[i]]$legend = NULL
}

save.plot = T
if(save.plot) pdf(file.plot, width=8.5/2.54, height=5.3)

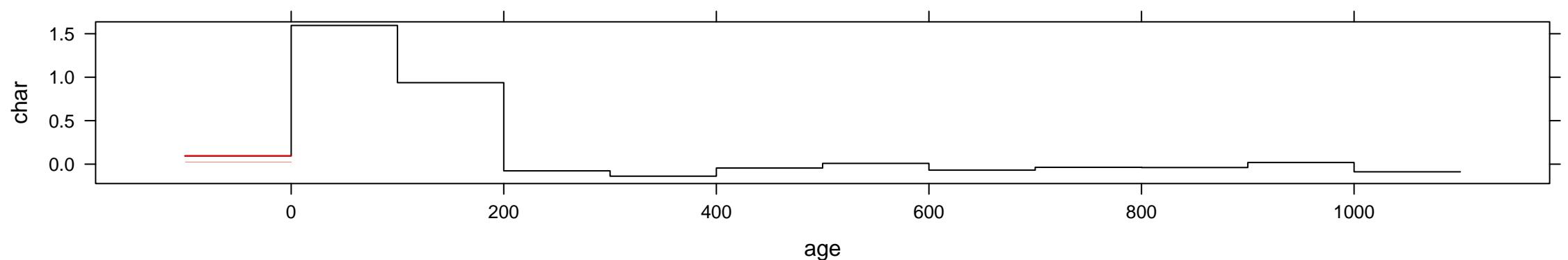
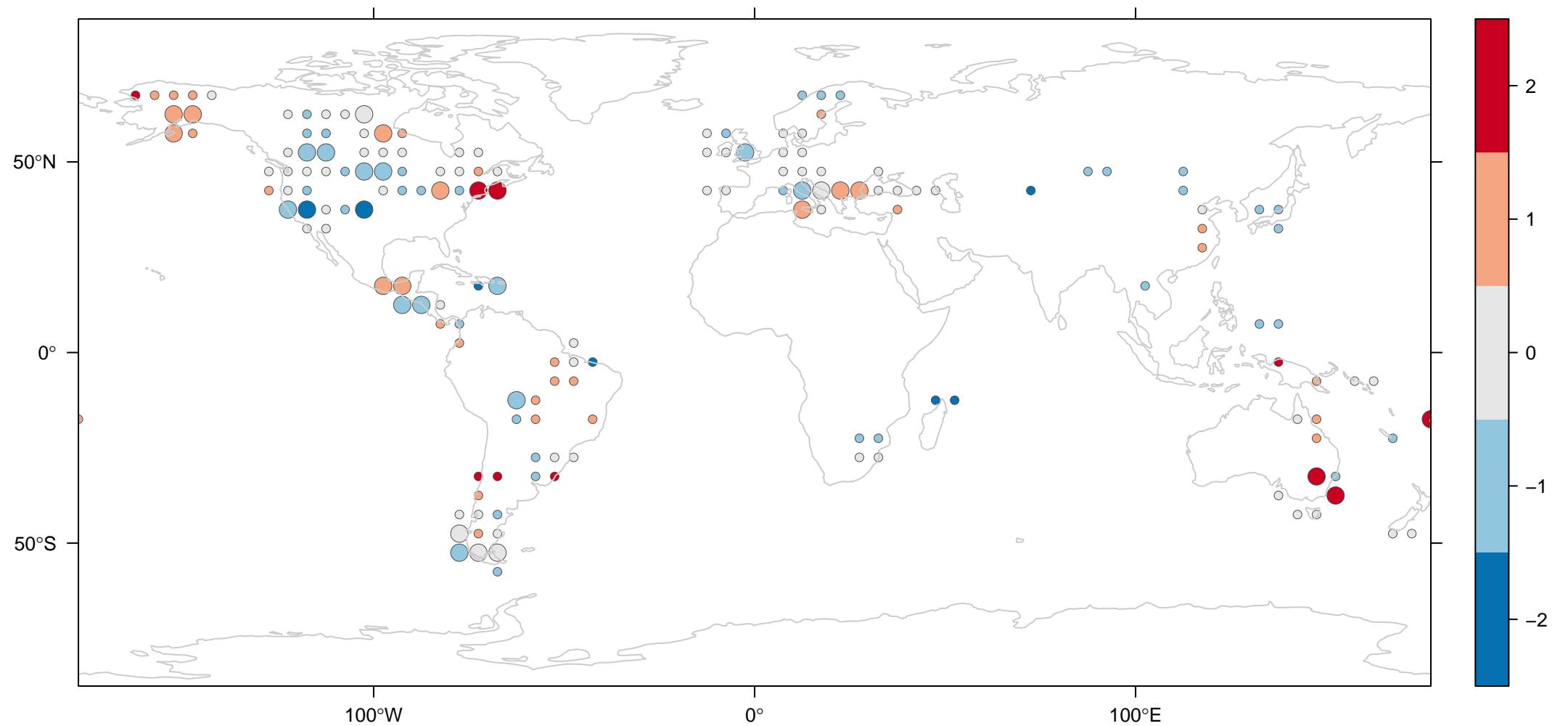
print(mp[[1]], position=c(0,0.635,1,0.905), panel.width=list(8.25,"cm"),
      panel.height=list(8.25*0.42,"cm"), more=T)

```

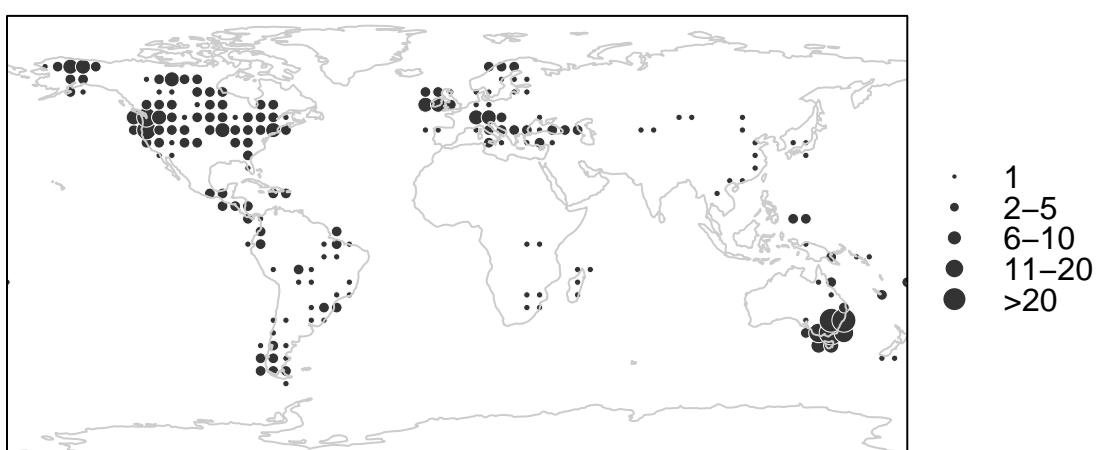
```
print(mp[[2]], position=c(0,0.365,1,0.635), panel.width=list(8.25,"cm"),
panel.height=list(8.25*0.42,"cm"), more=T)
print(mp[[3]], position=c(0,0.095,1,0.365), panel.width=list(8.25,"cm"),
panel.height=list(8.25*0.42,"cm"), more=F)
if(save.plot) dev.off()

if(save.plot) {
  pdf(file.legend, width=8.5/2.54, height=5)
  print(mp.legend, position = c(0,0,1,1), panel.width=list(8.25,"cm"),
panel.height=list(8.25*0.42,"cm"))
  dev.off()
}
```

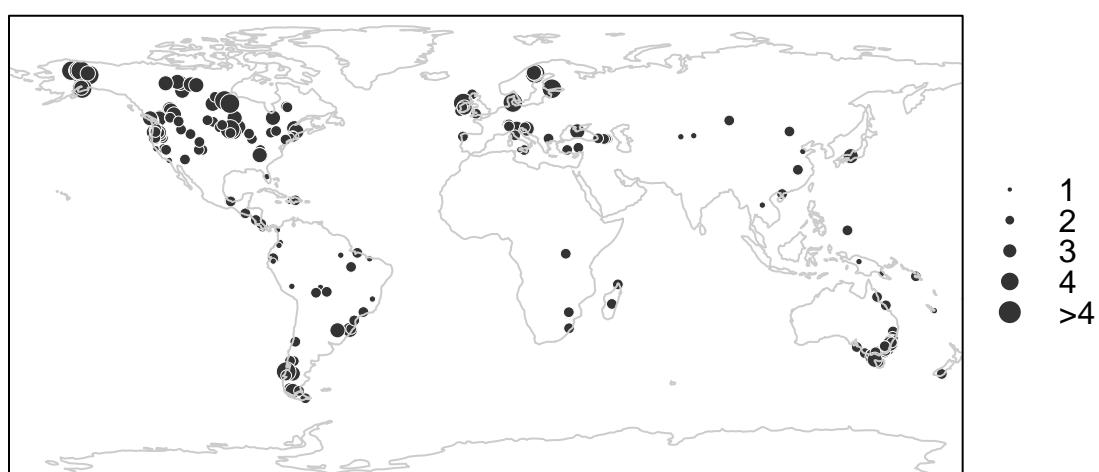
Charcoal Influx z-Scores: -100–0 BP



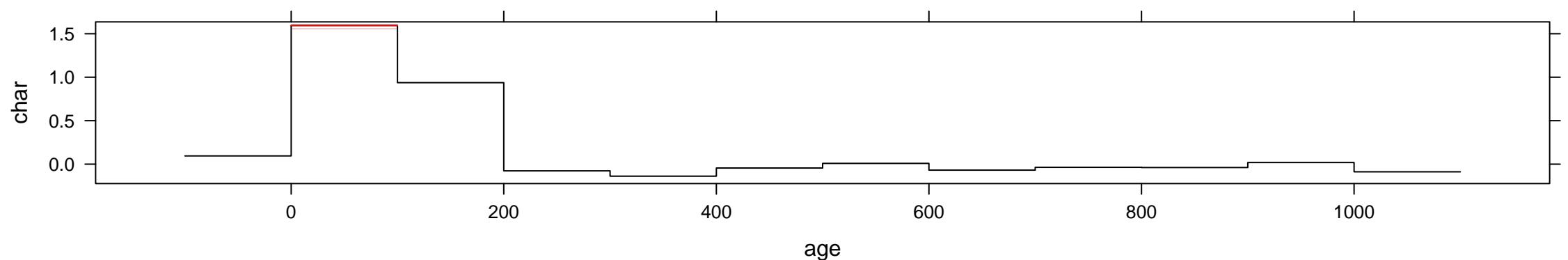
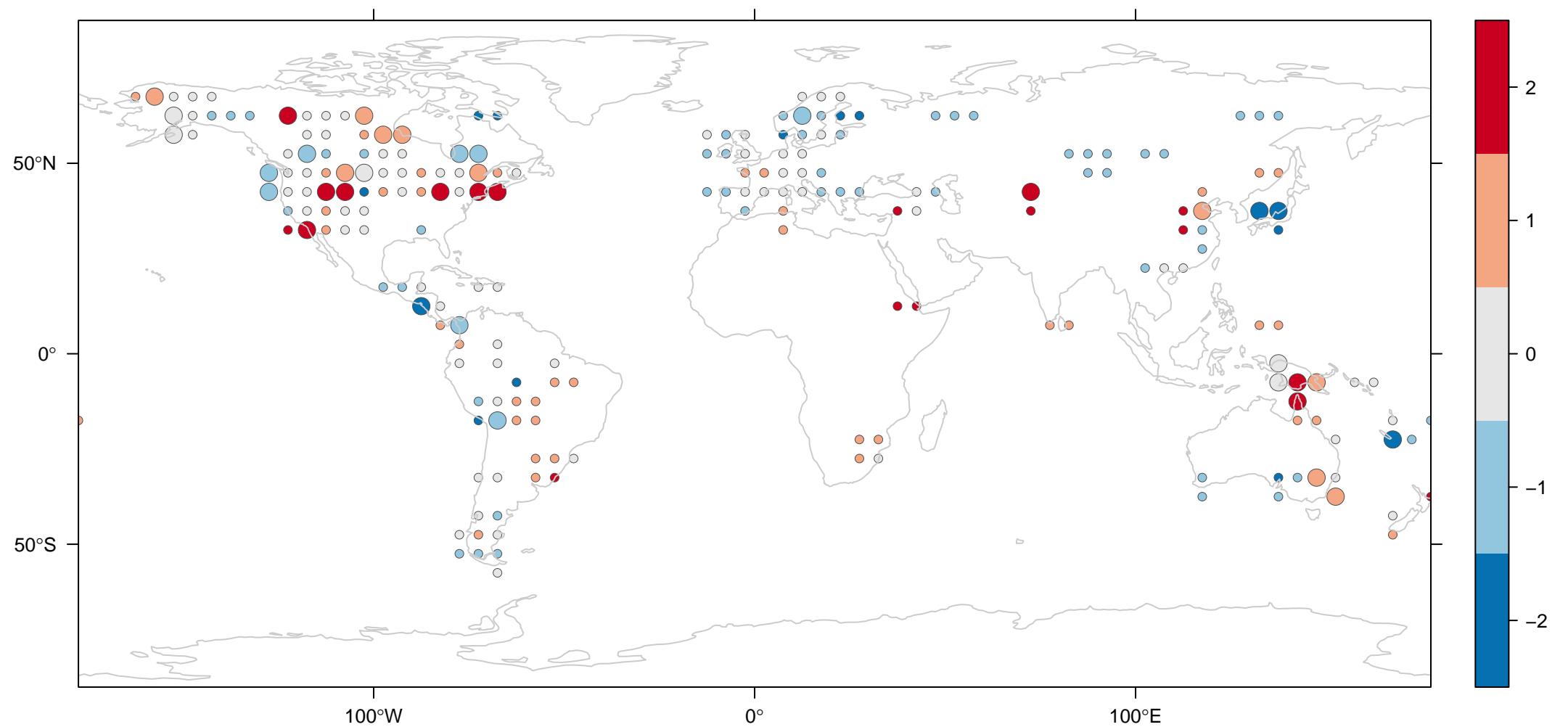
Number of sites per grid cell



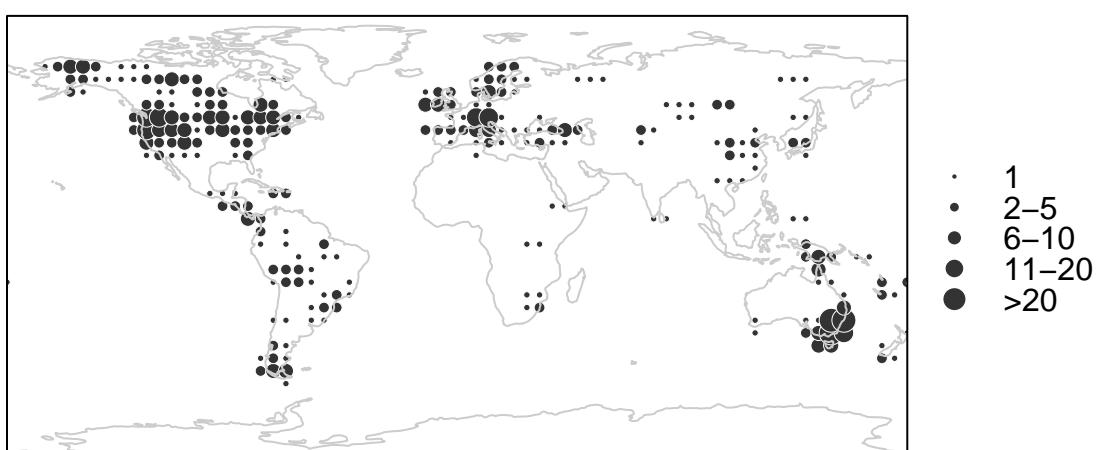
Number of grid cells influenced by each site



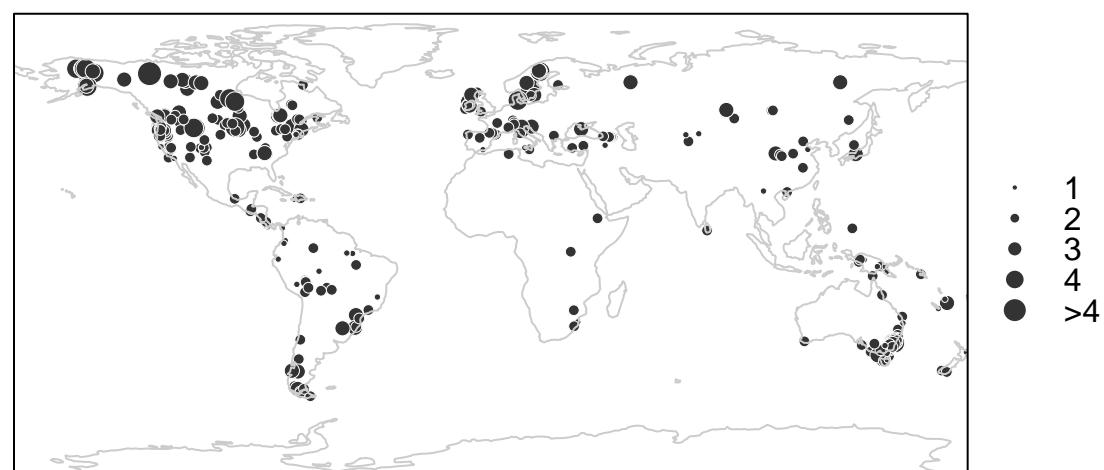
Charcoal Influx z-Scores: 0–100 BP



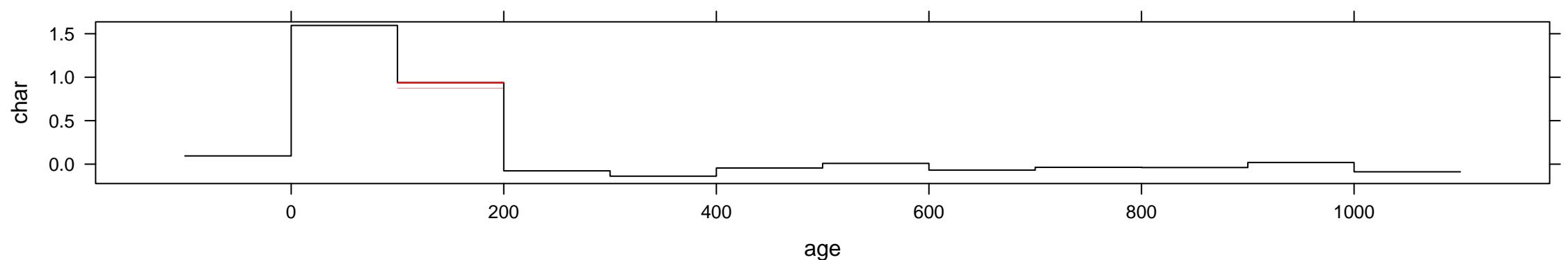
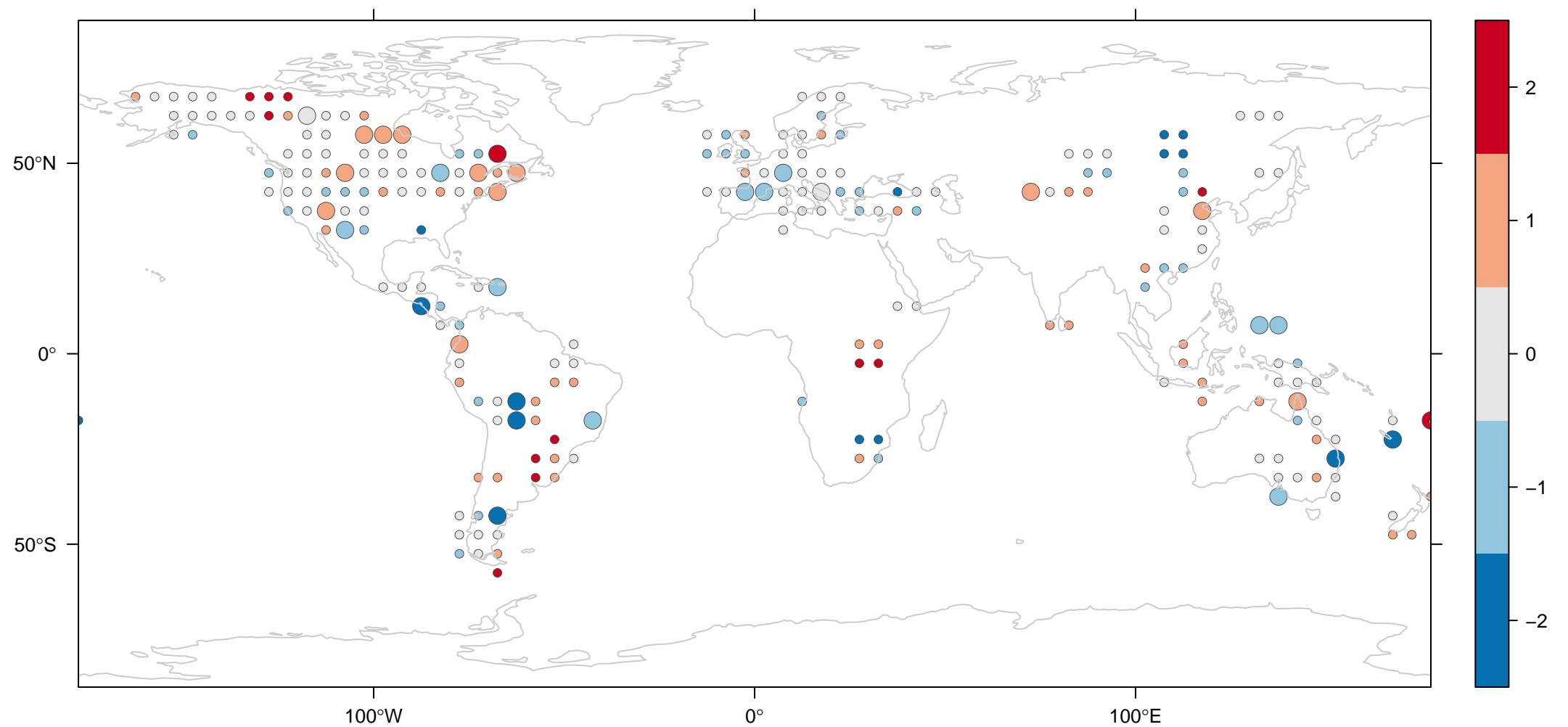
Number of sites per grid cell



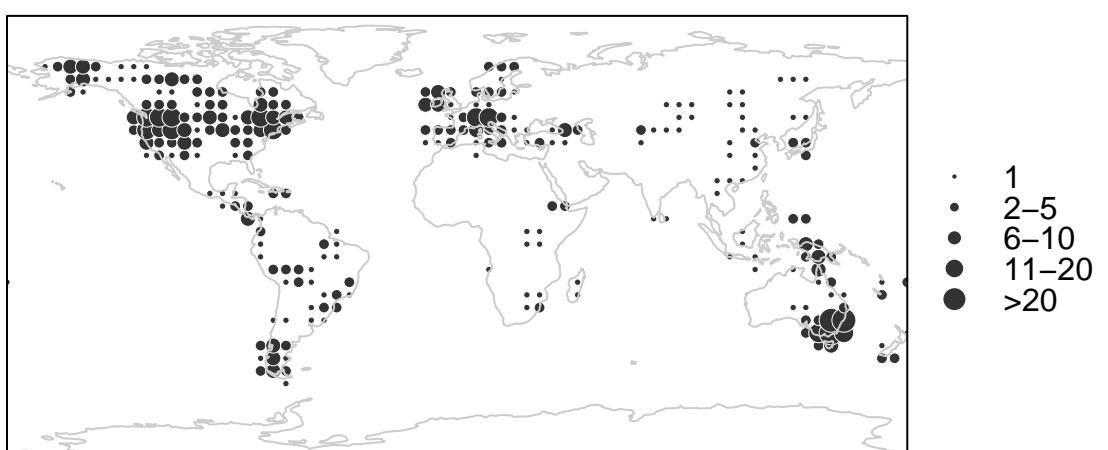
Number of grid cells influenced by each site



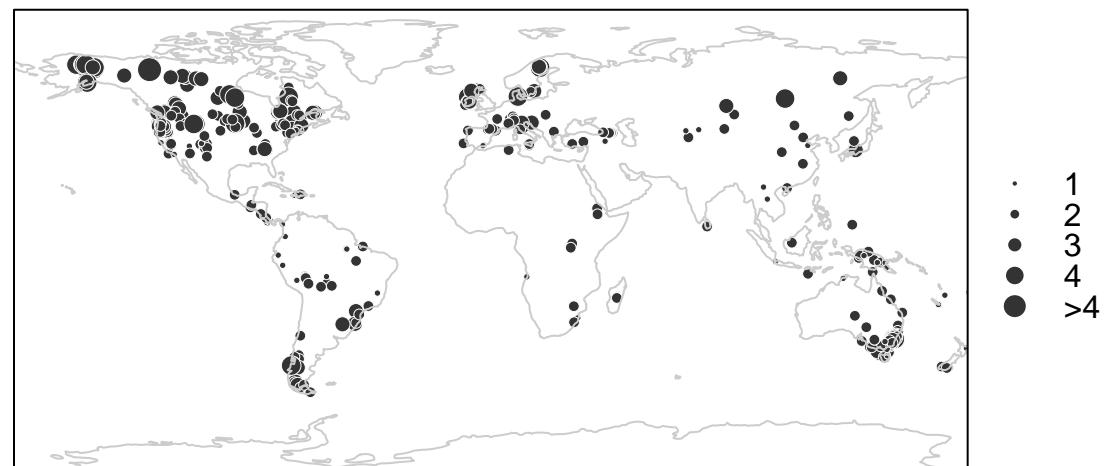
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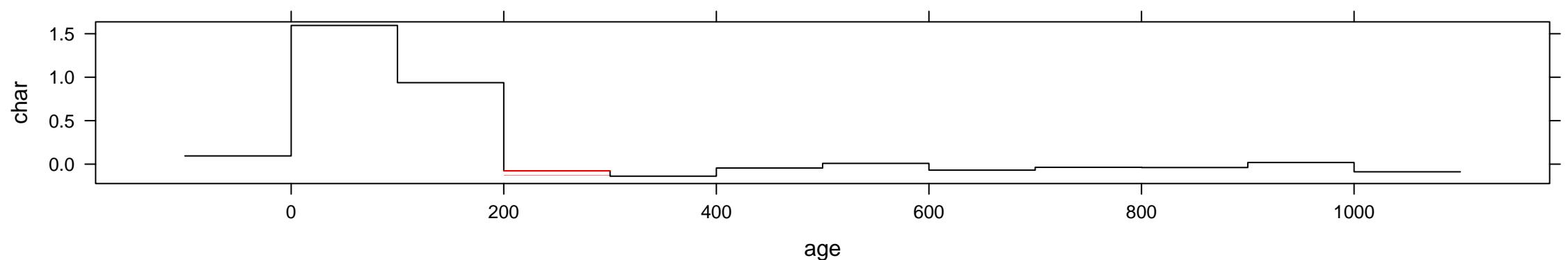
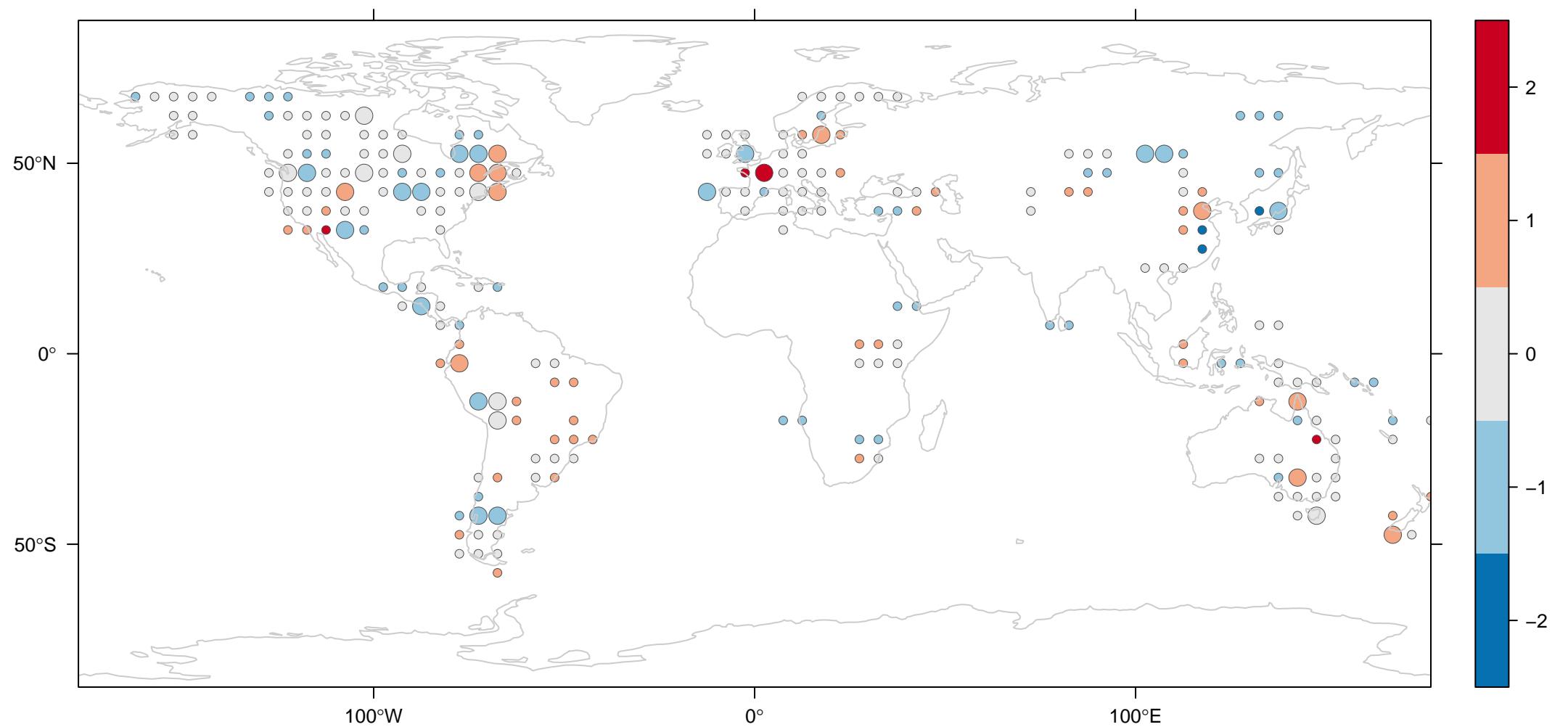
Number of sites per grid cell



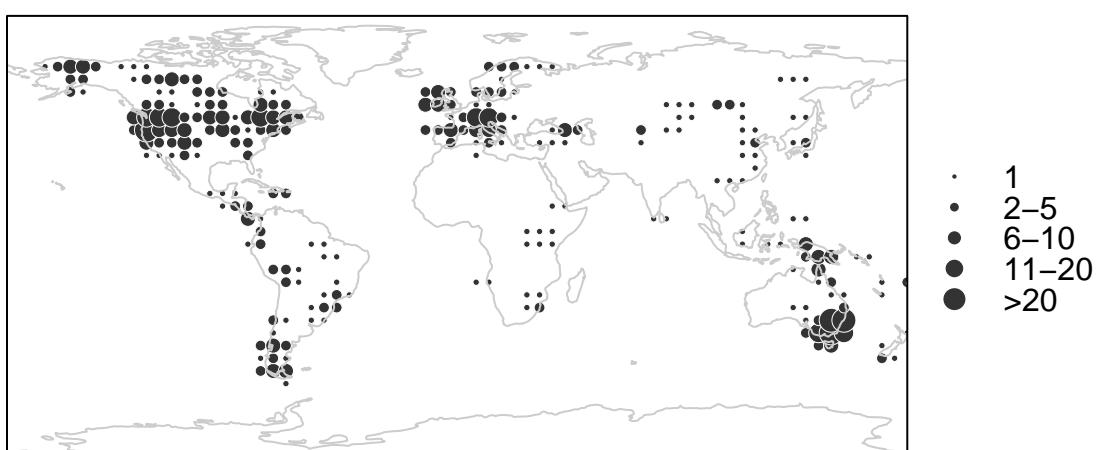
Number of grid cells influenced by each site



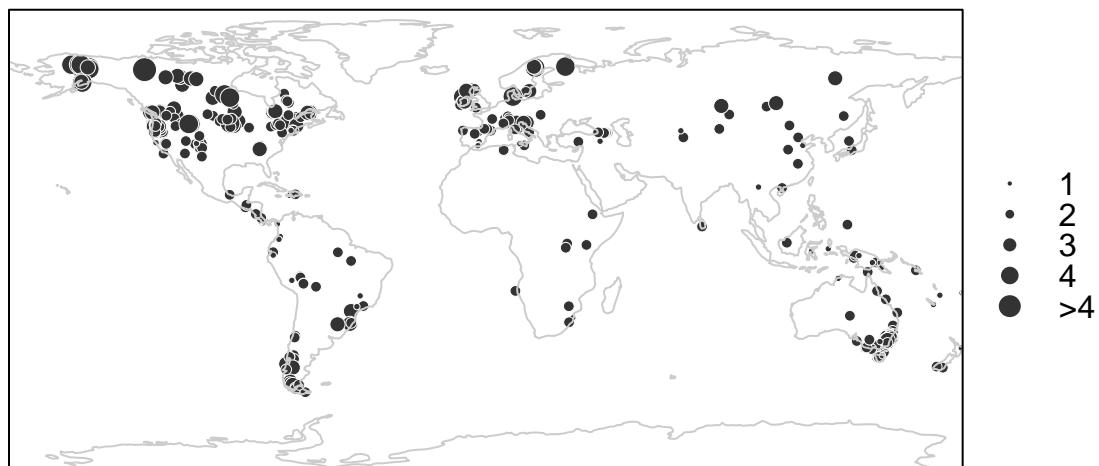
Charcoal Influx z-Scores: 200–300 BP



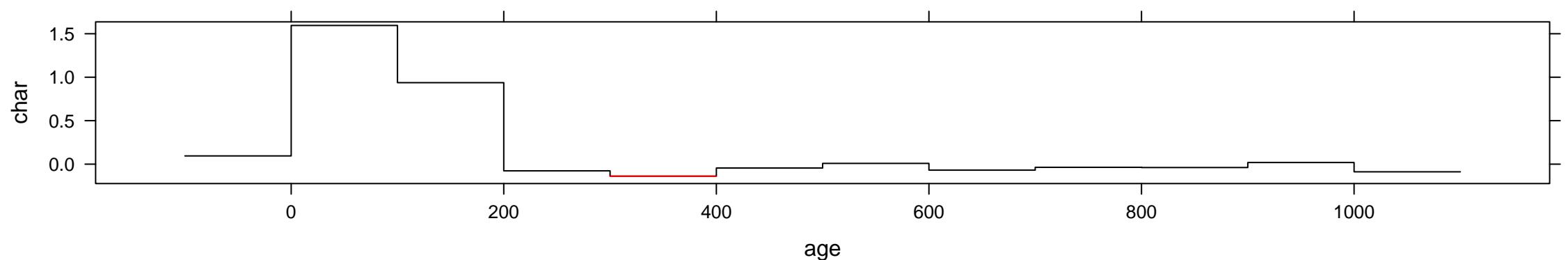
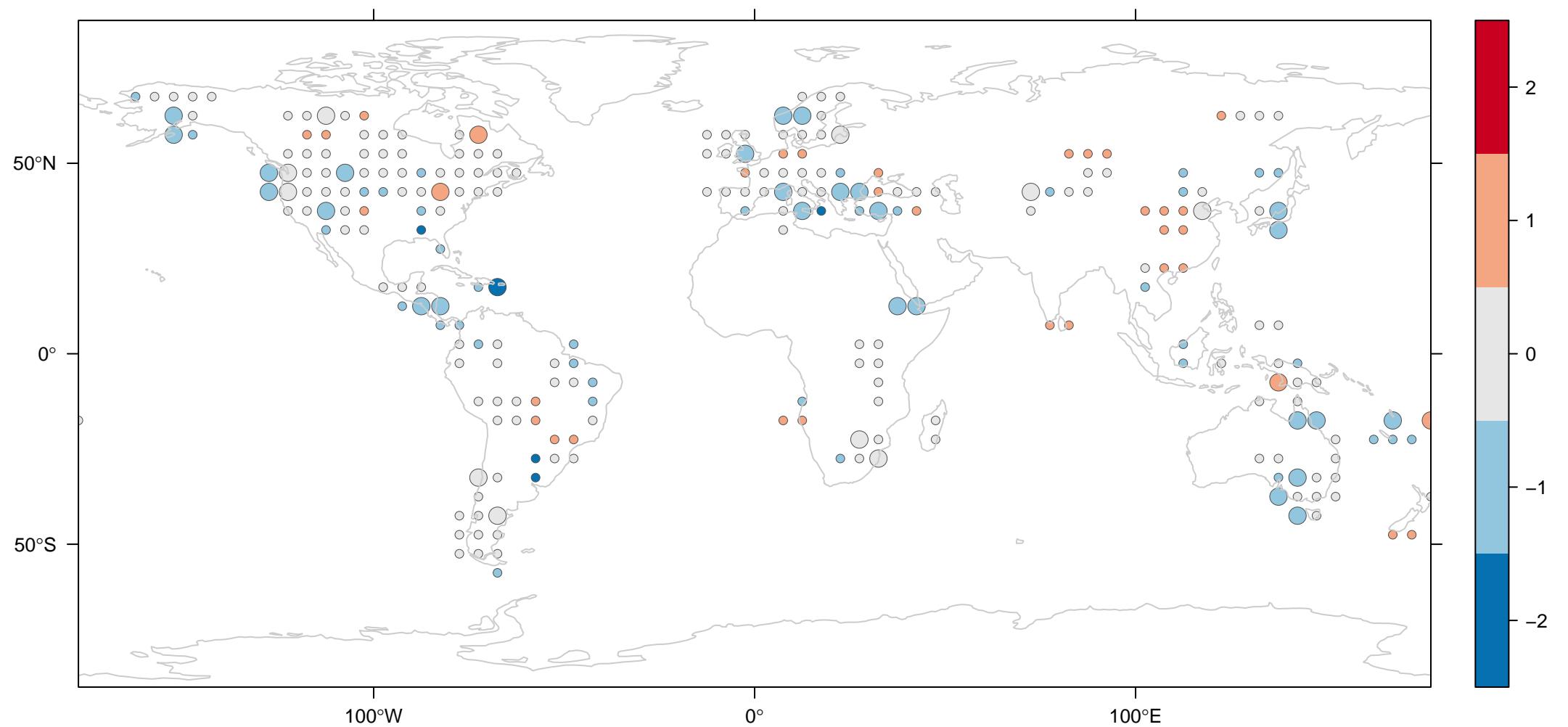
Number of sites per grid cell



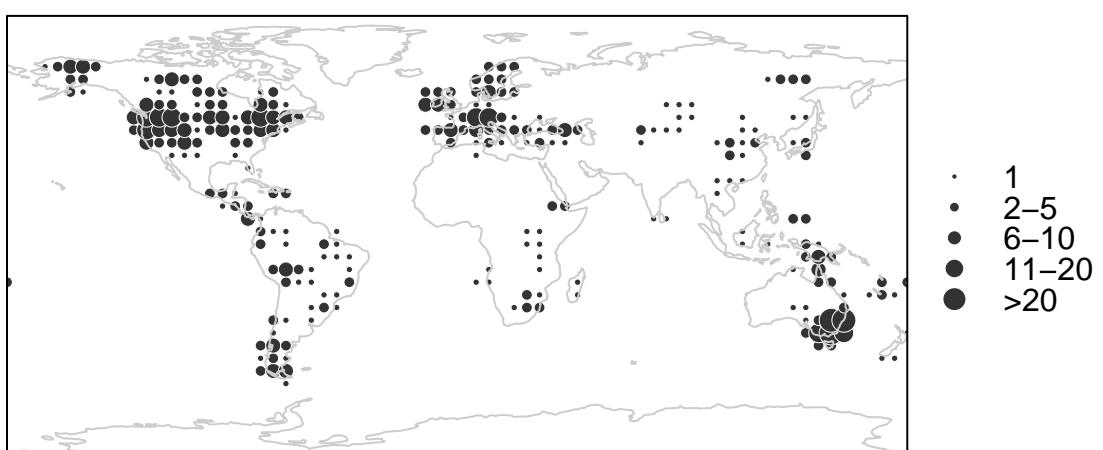
Number of grid cells influenced by each site



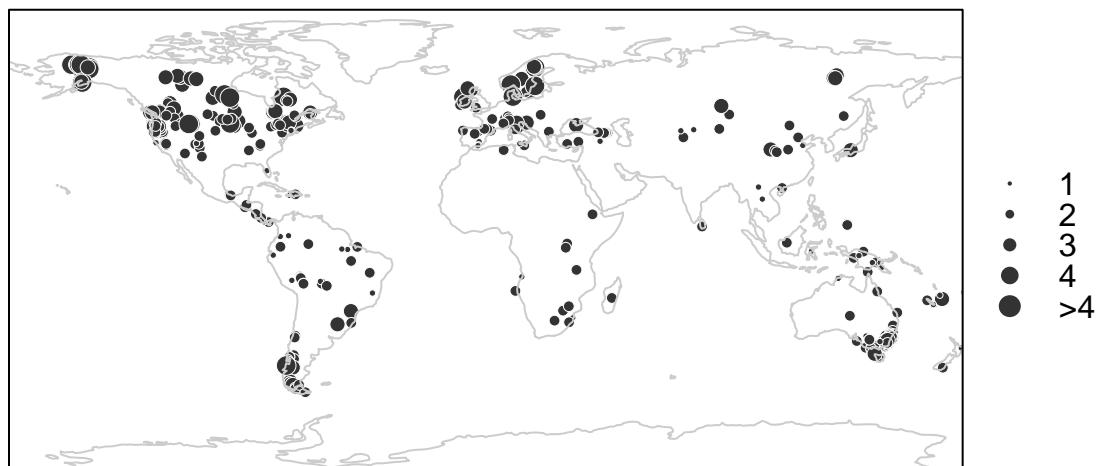
Charcoal Influx z-Scores: 300–400 BP



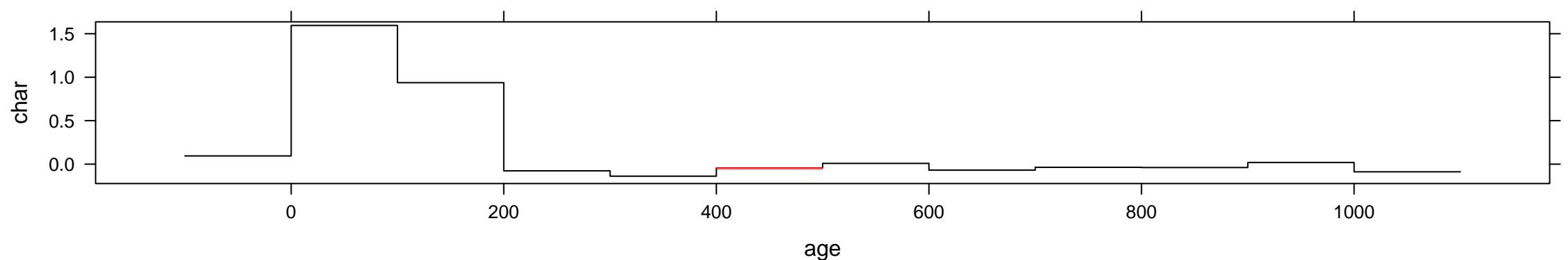
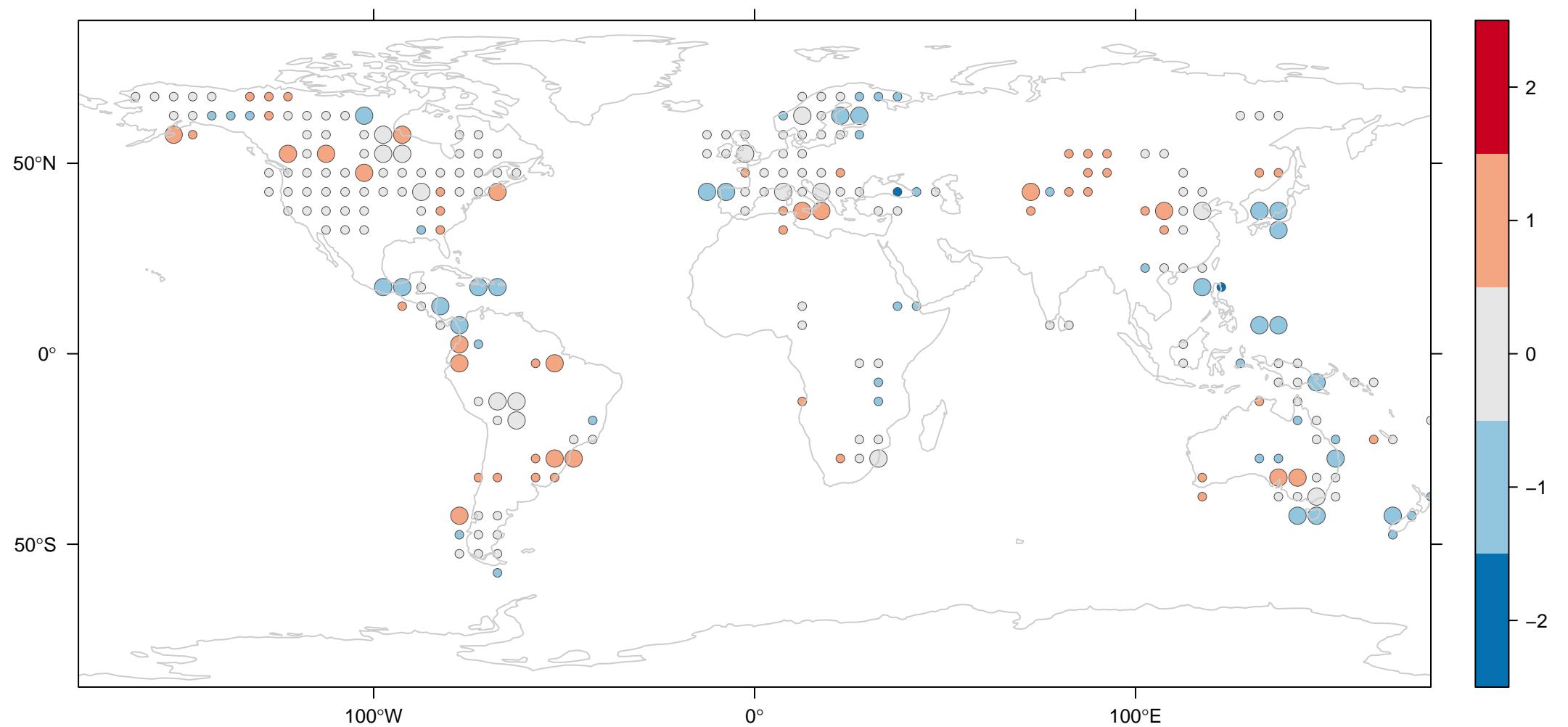
Number of sites per grid cell



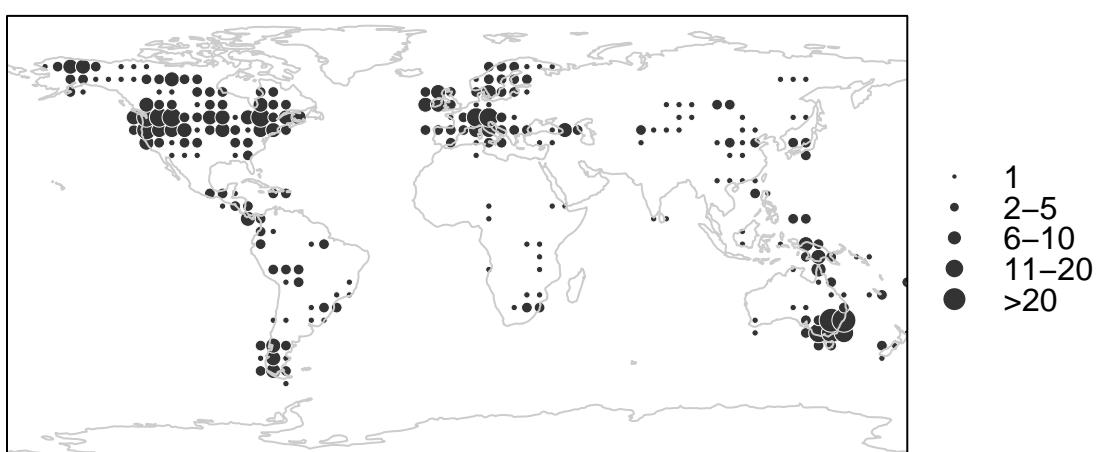
Number of grid cells influenced by each site



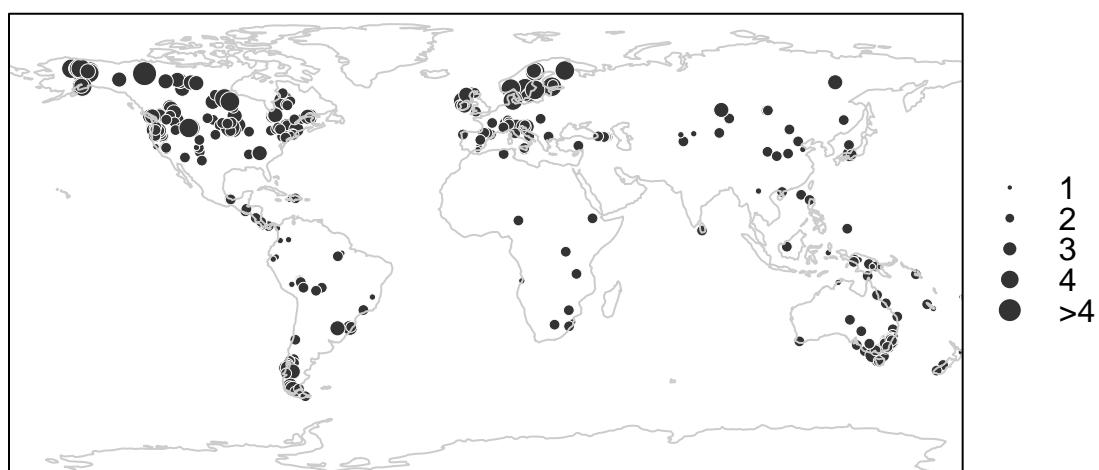
Charcoal Influx z-Scores: 400–500 BP



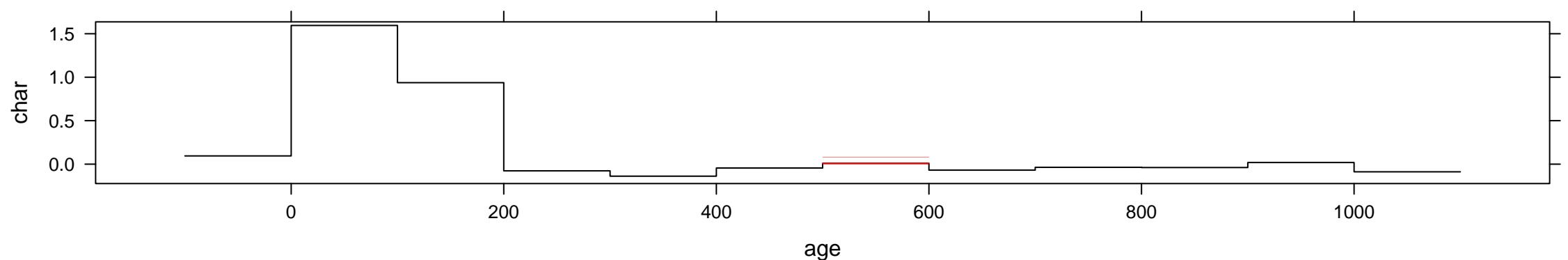
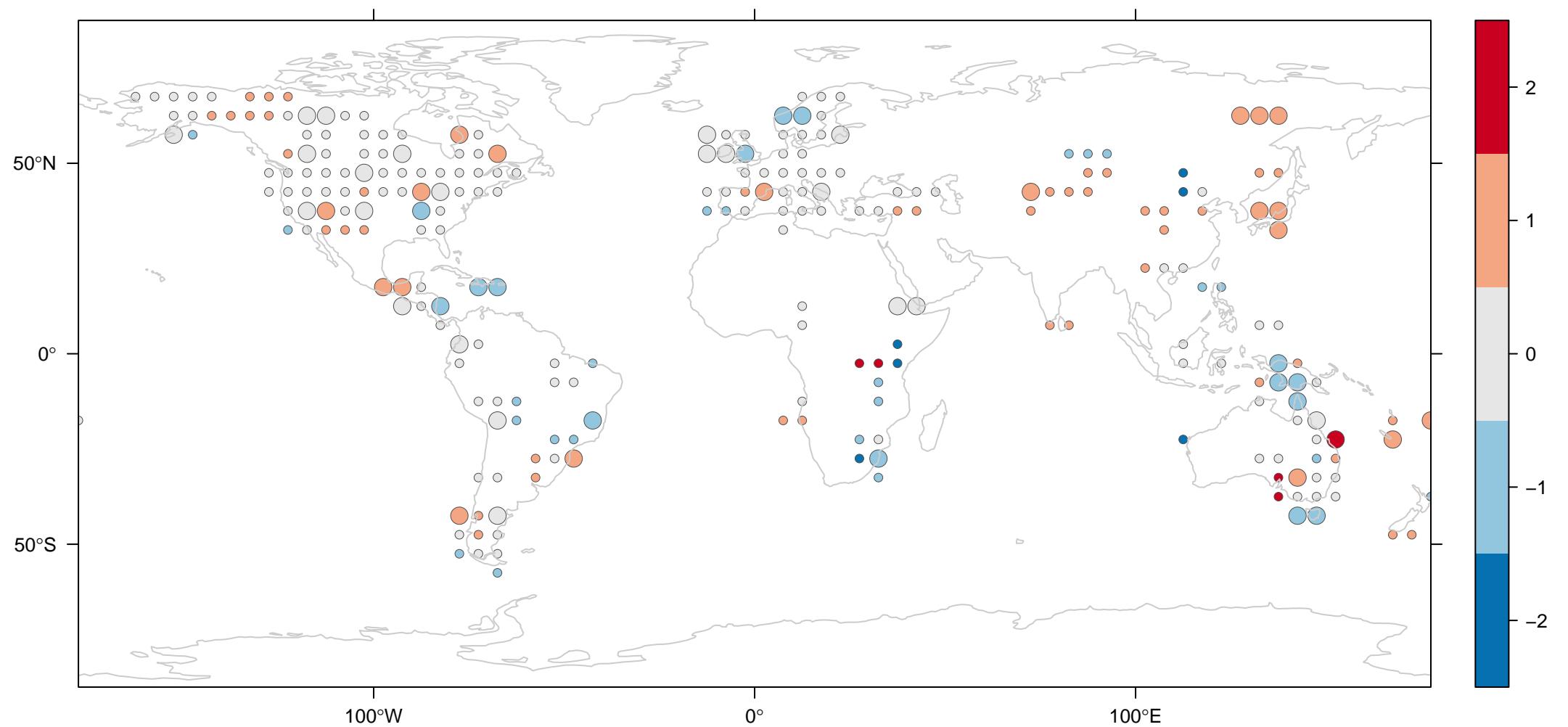
Number of sites per grid cell



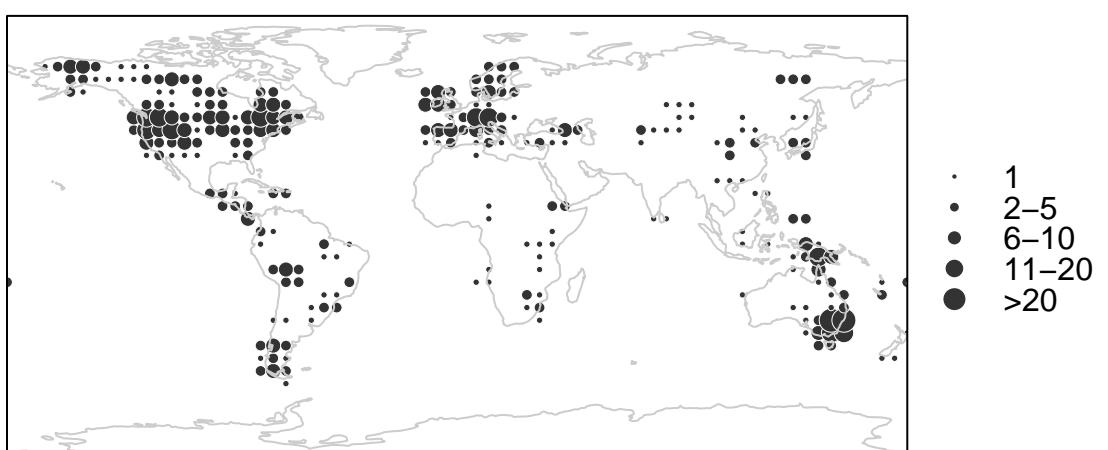
Number of grid cells influenced by each site



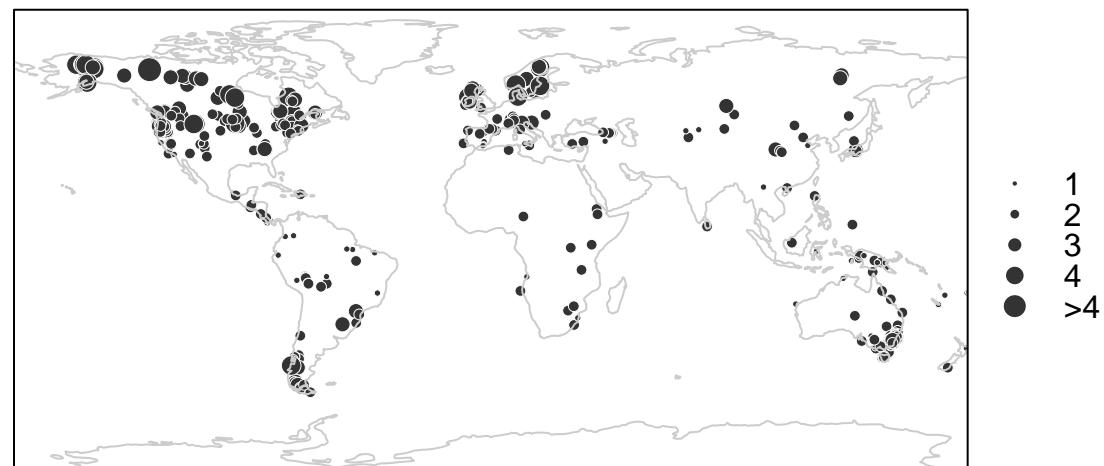
Charcoal Influx z-Scores: 500–600 BP



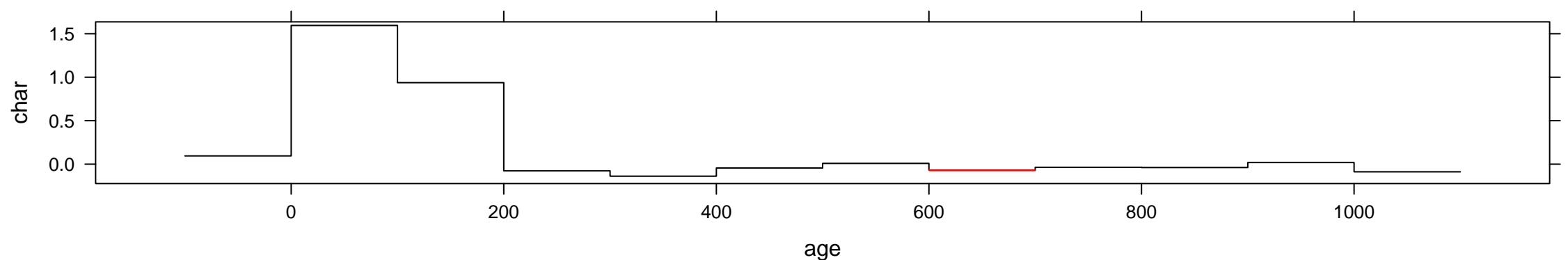
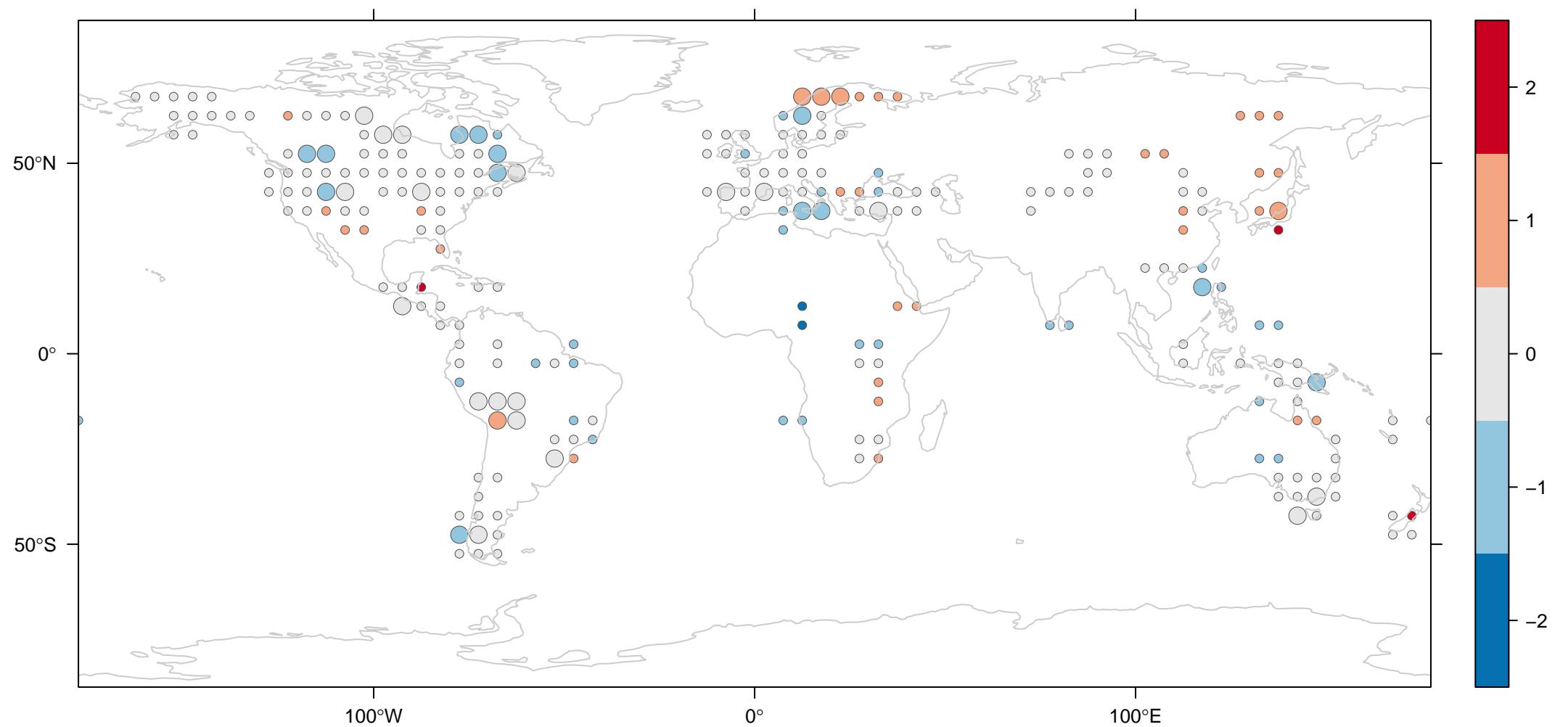
Number of sites per grid cell



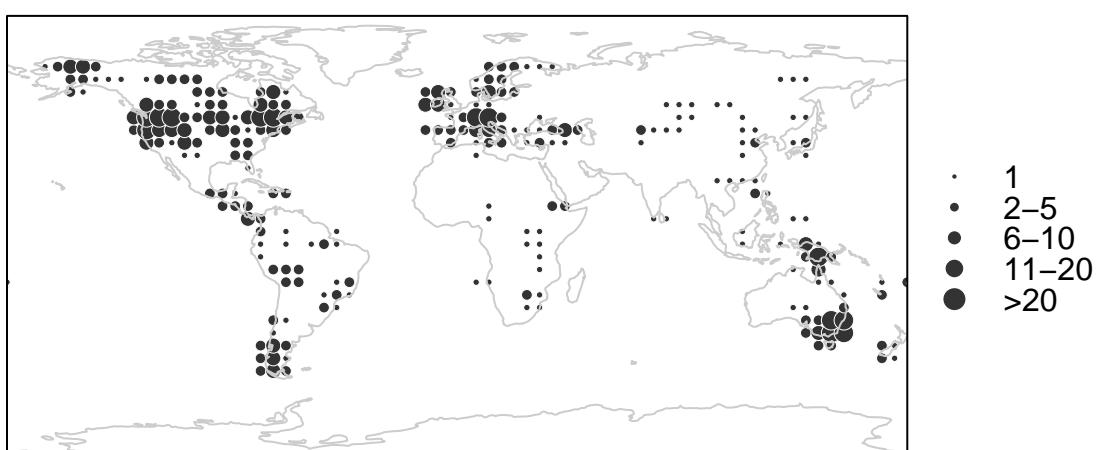
Number of grid cells influenced by each site



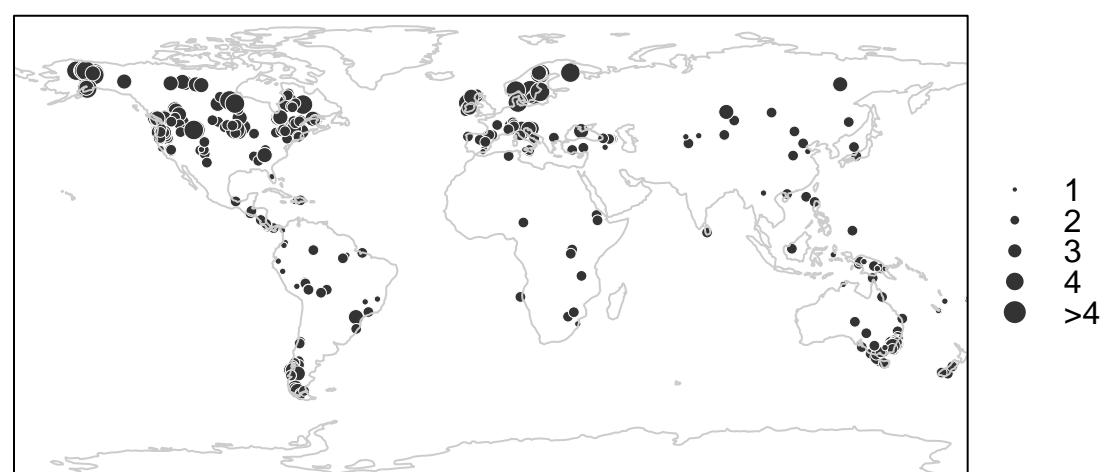
Charcoal Influx z-Scores: 600–700 BP



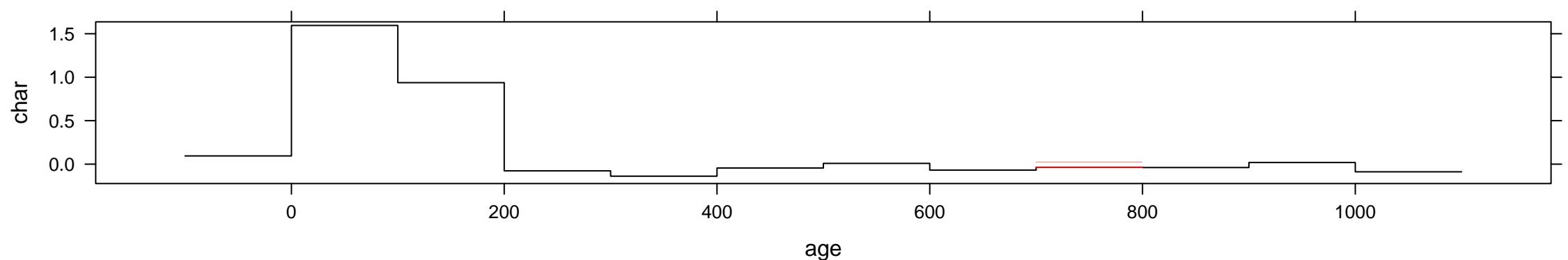
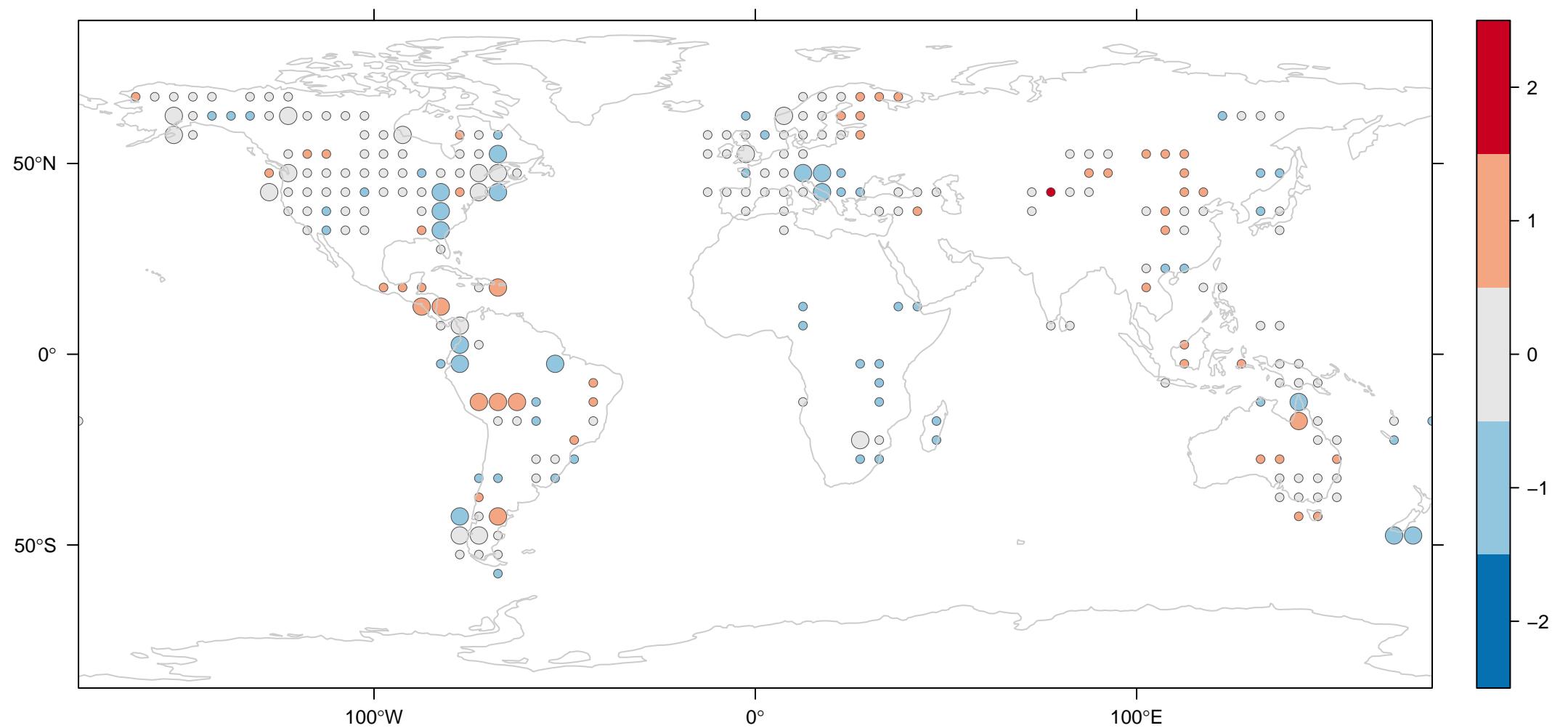
Number of sites per grid cell



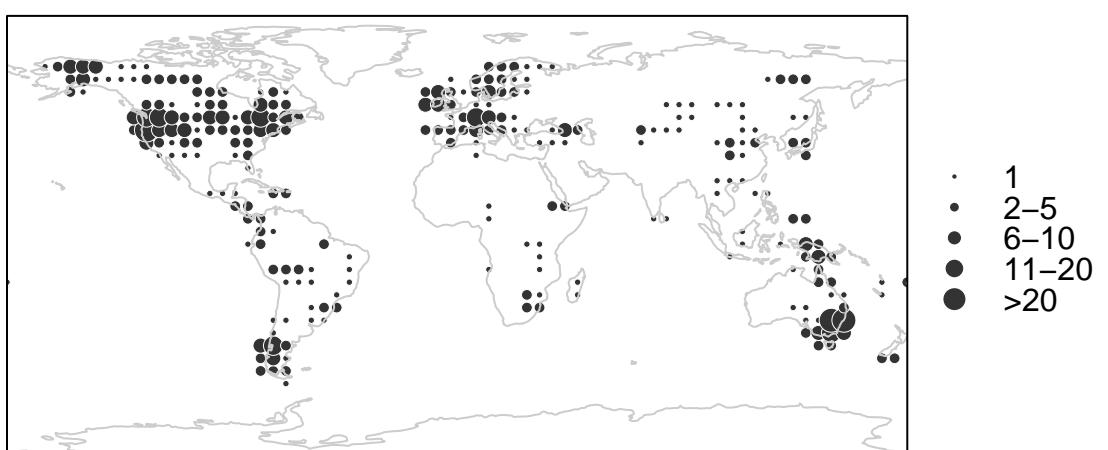
Number of grid cells influenced by each site



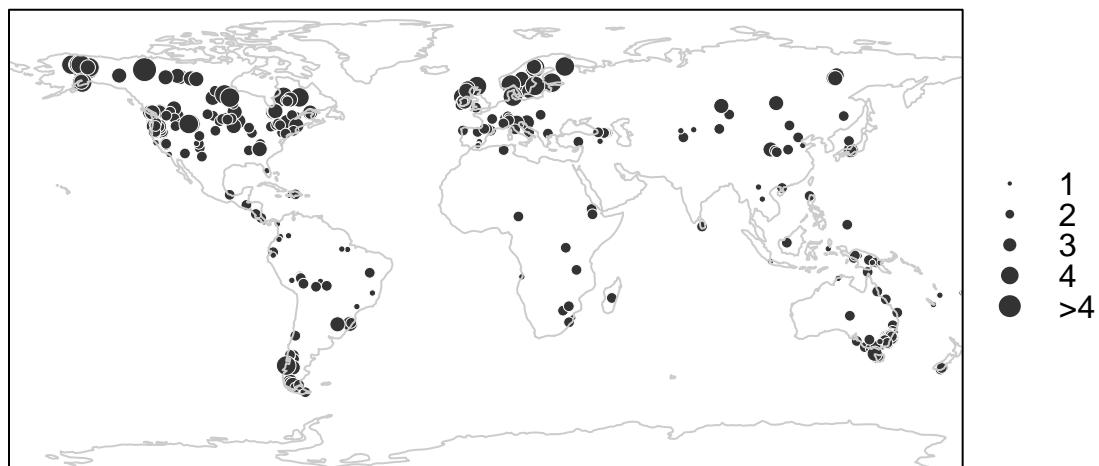
Charcoal Influx z-Scores: 700–800 BP



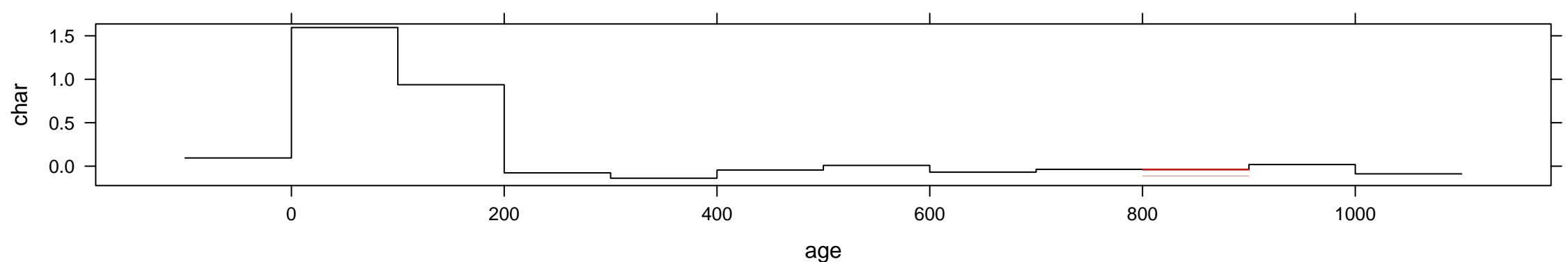
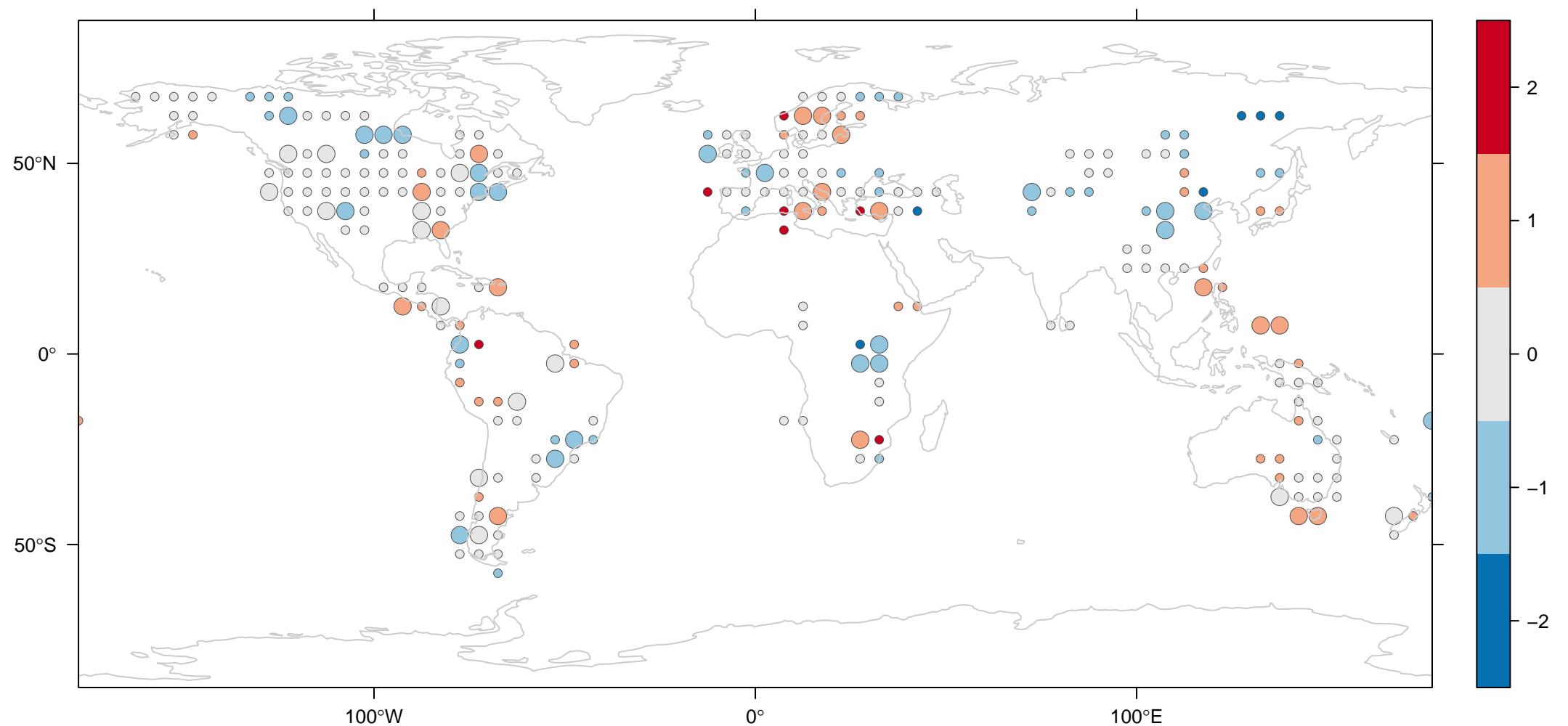
Number of sites per grid cell



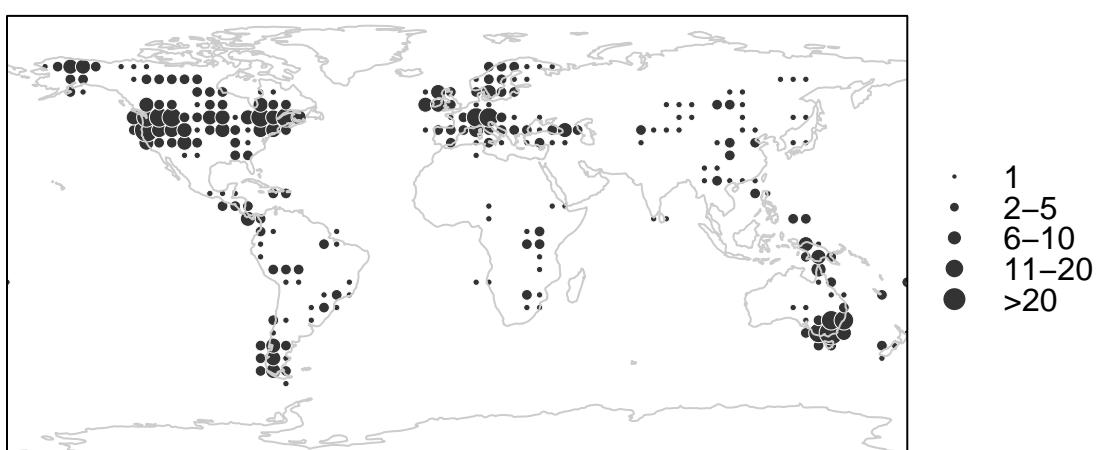
Number of grid cells influenced by each site



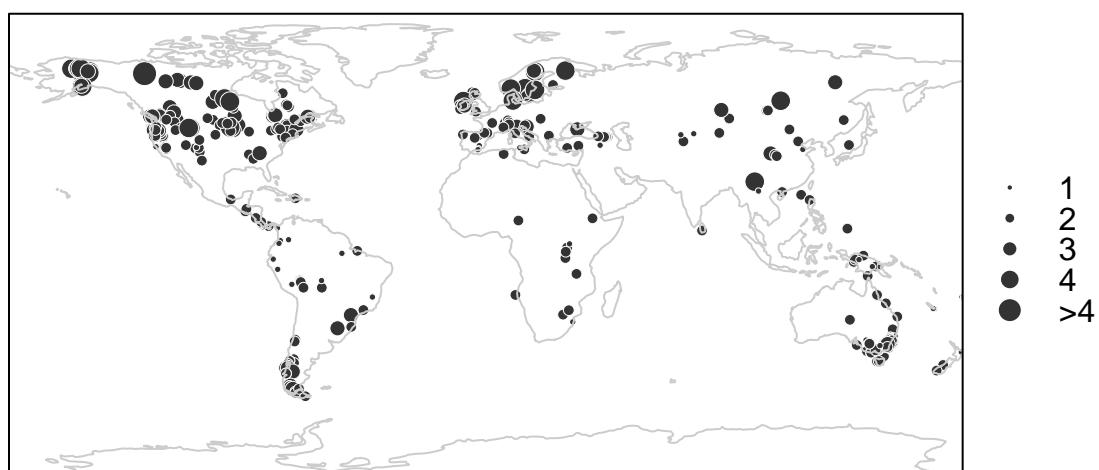
Charcoal Influx z-Scores: 800–900 BP



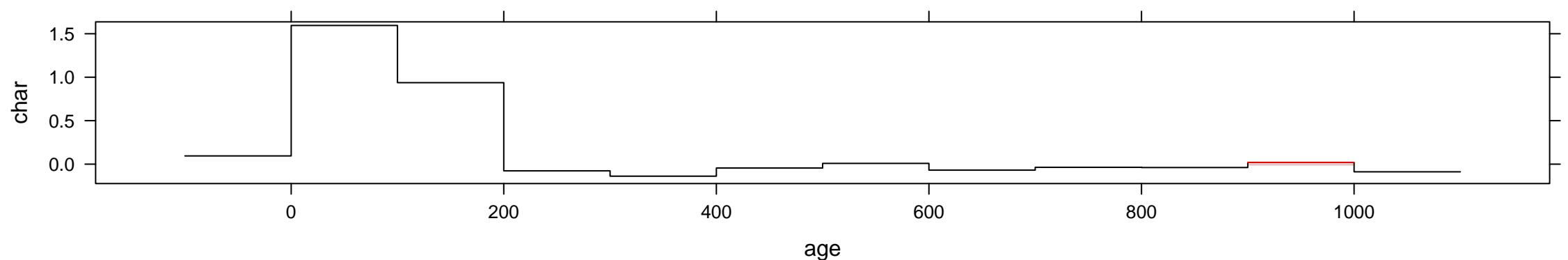
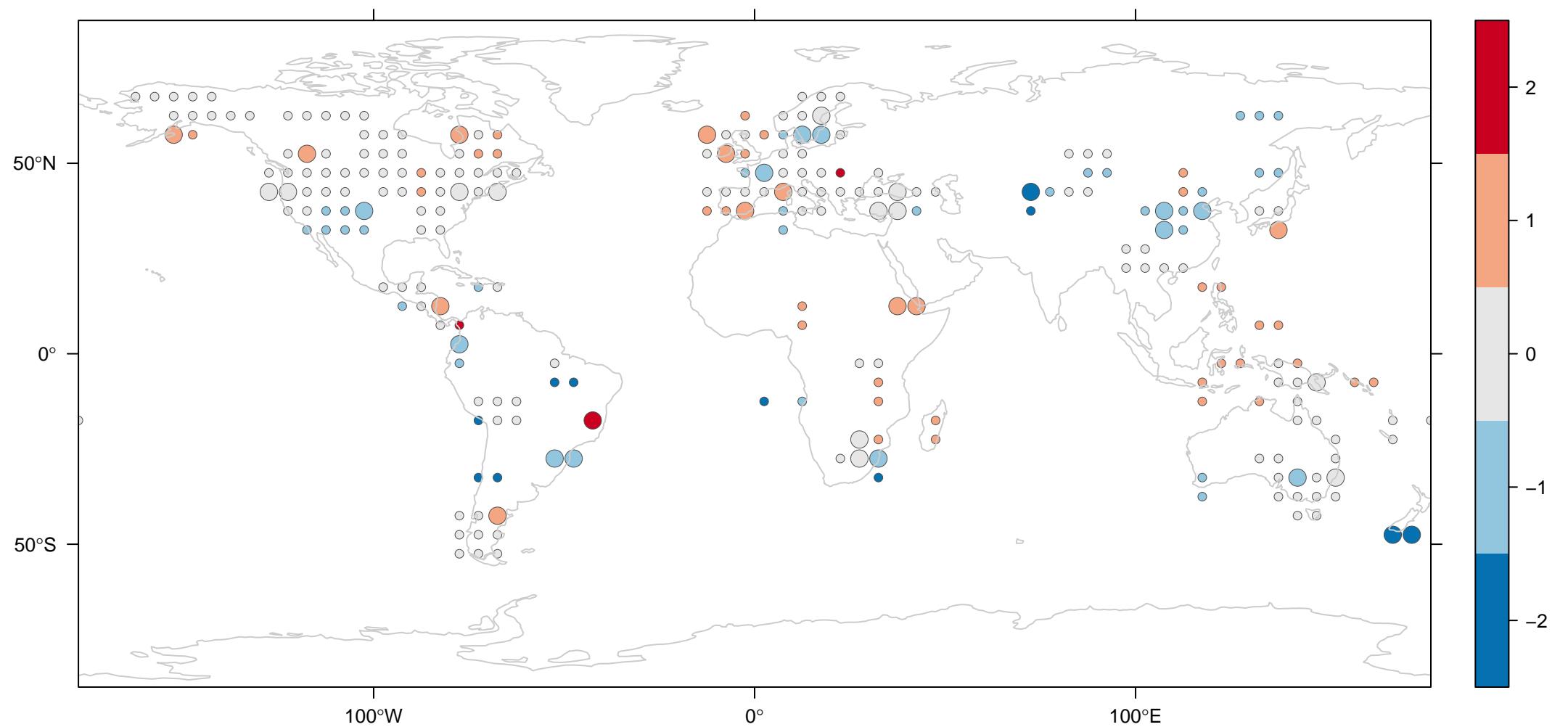
Number of sites per grid cell



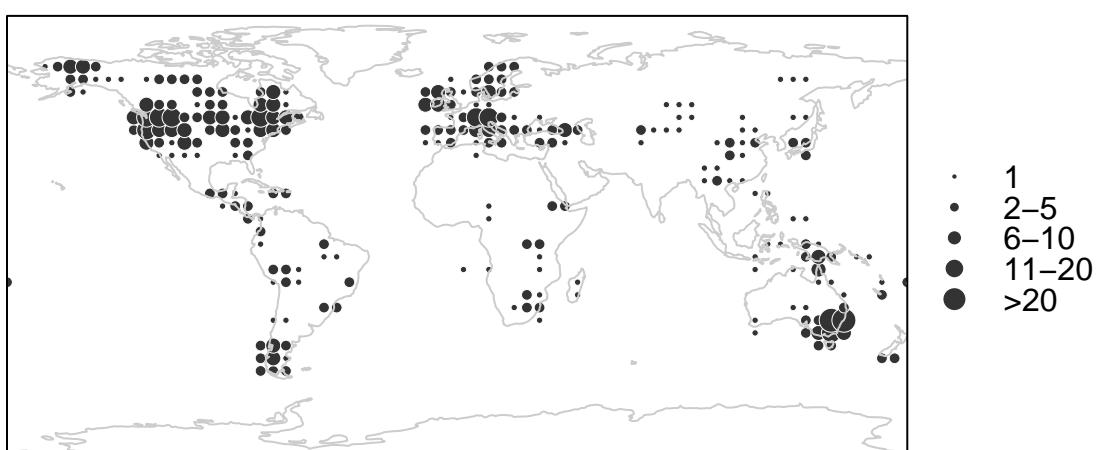
Number of grid cells influenced by each site



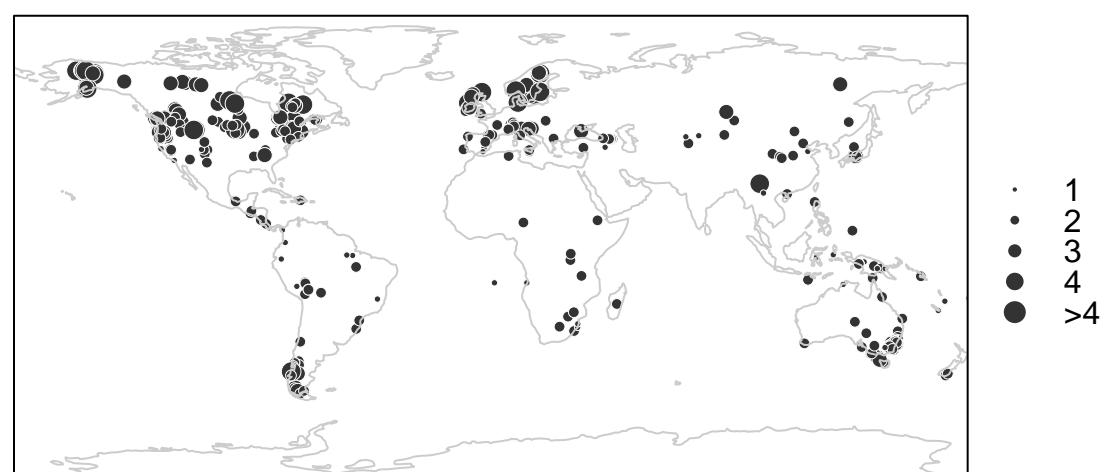
Charcoal Influx z-Scores: 900–1000 BP



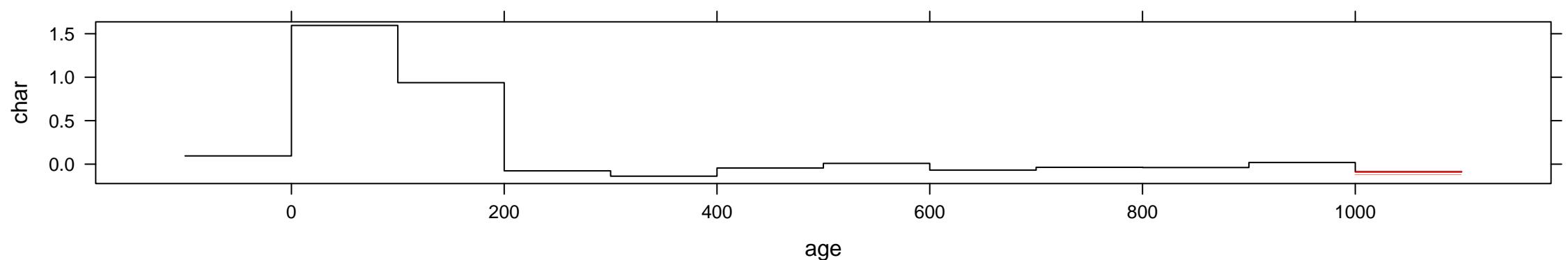
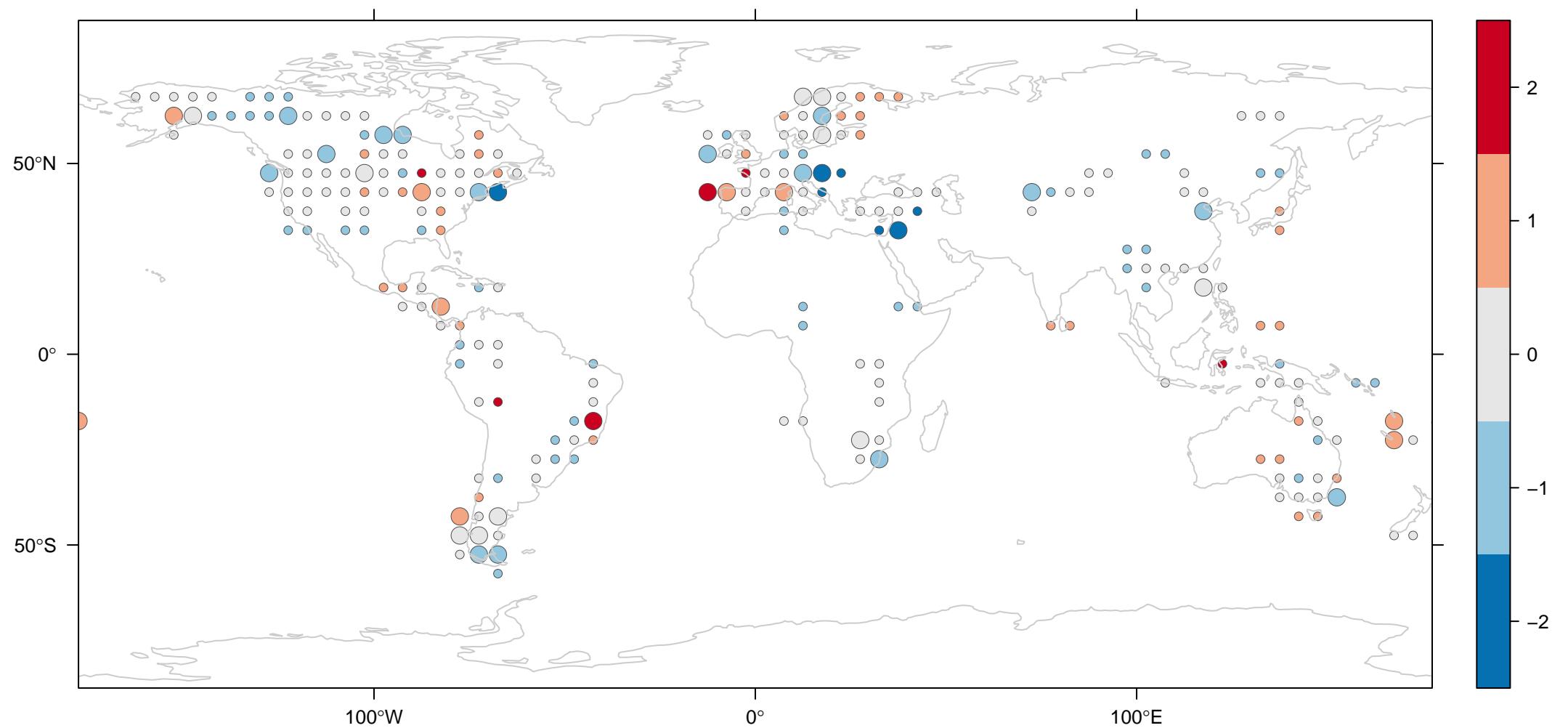
Number of sites per grid cell



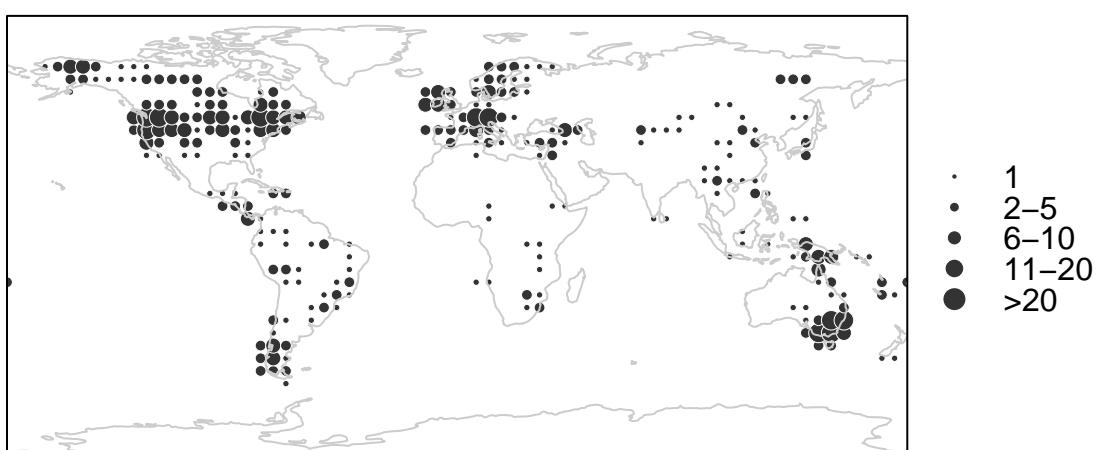
Number of grid cells influenced by each site



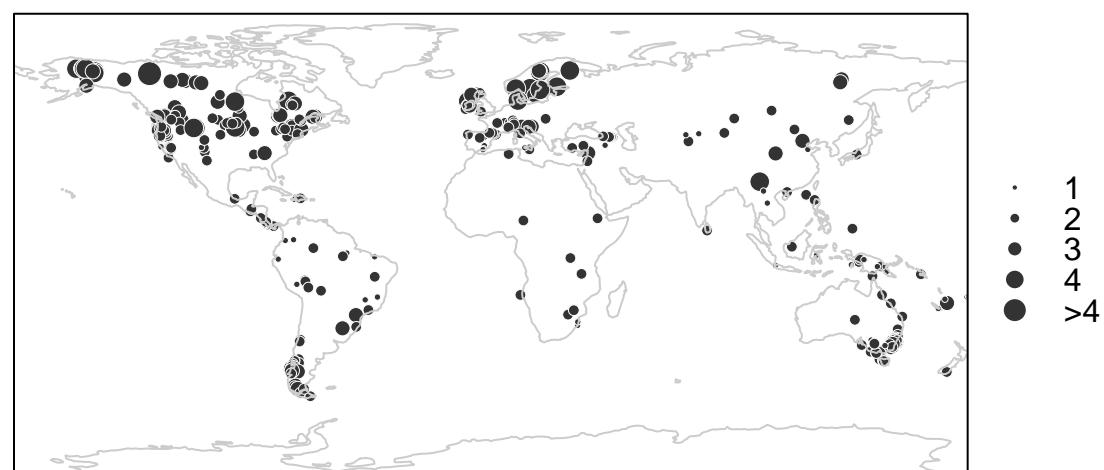
Charcoal Influx z-Scores: 1000–1100 BP



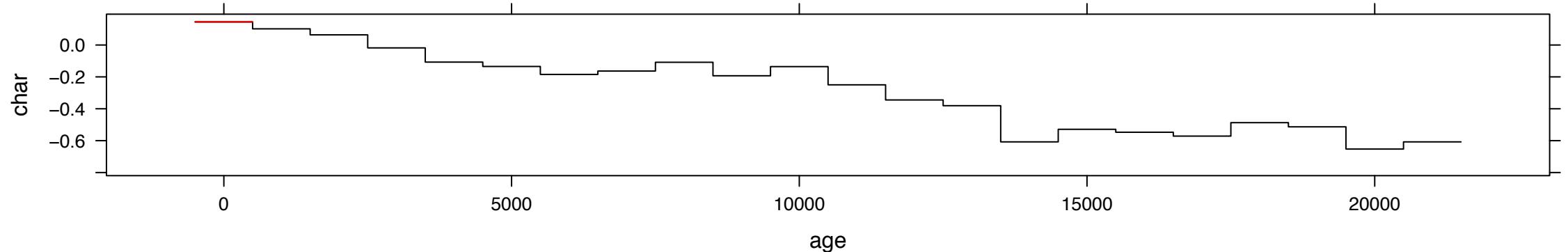
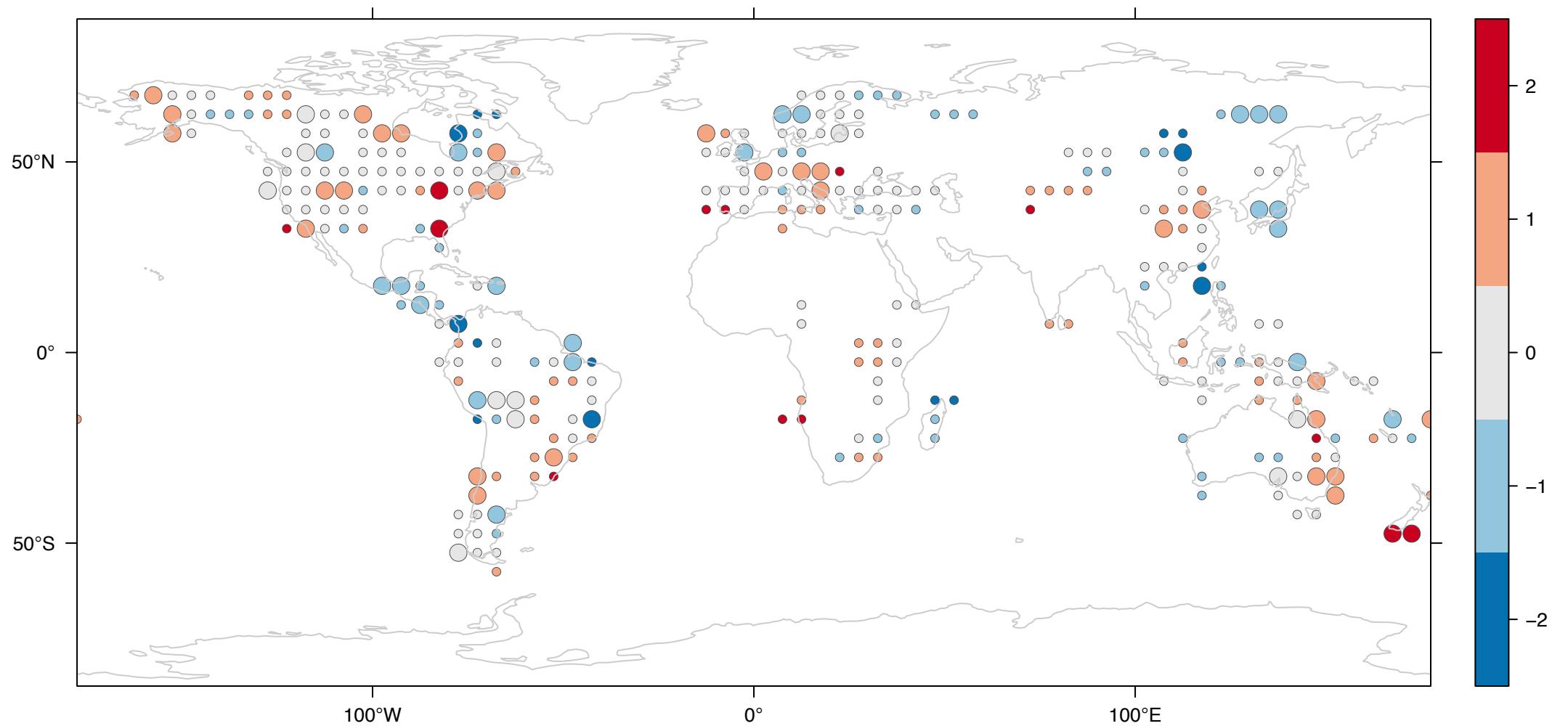
Number of sites per grid cell



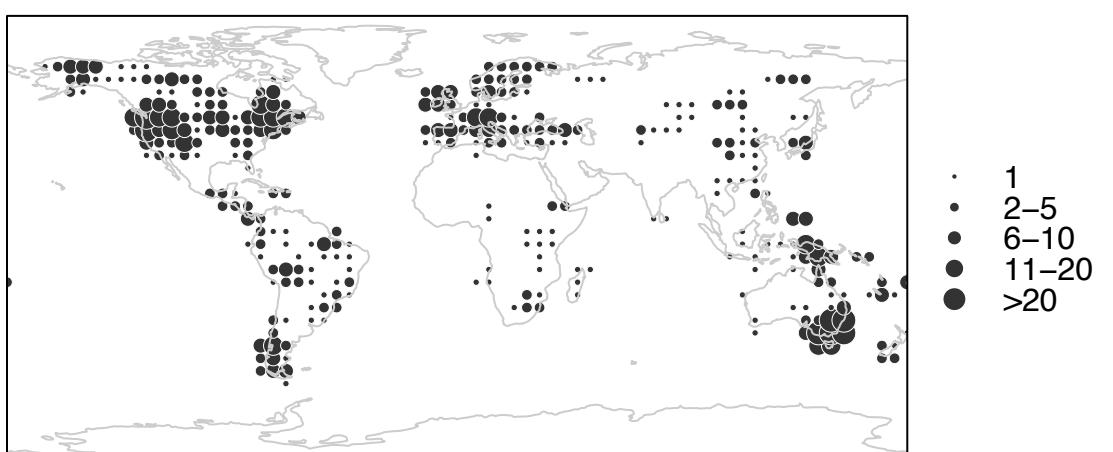
Number of grid cells influenced by each site



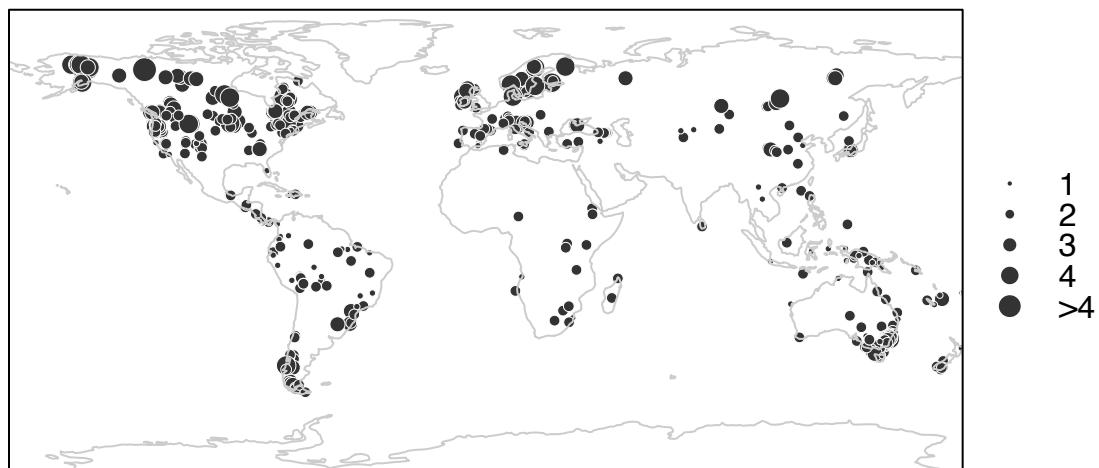
Charcoal Influx z-Scores: -60-500 BP



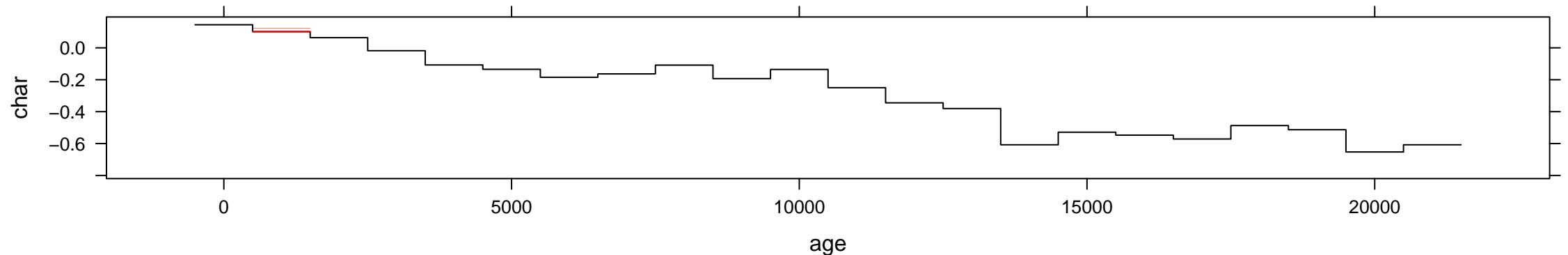
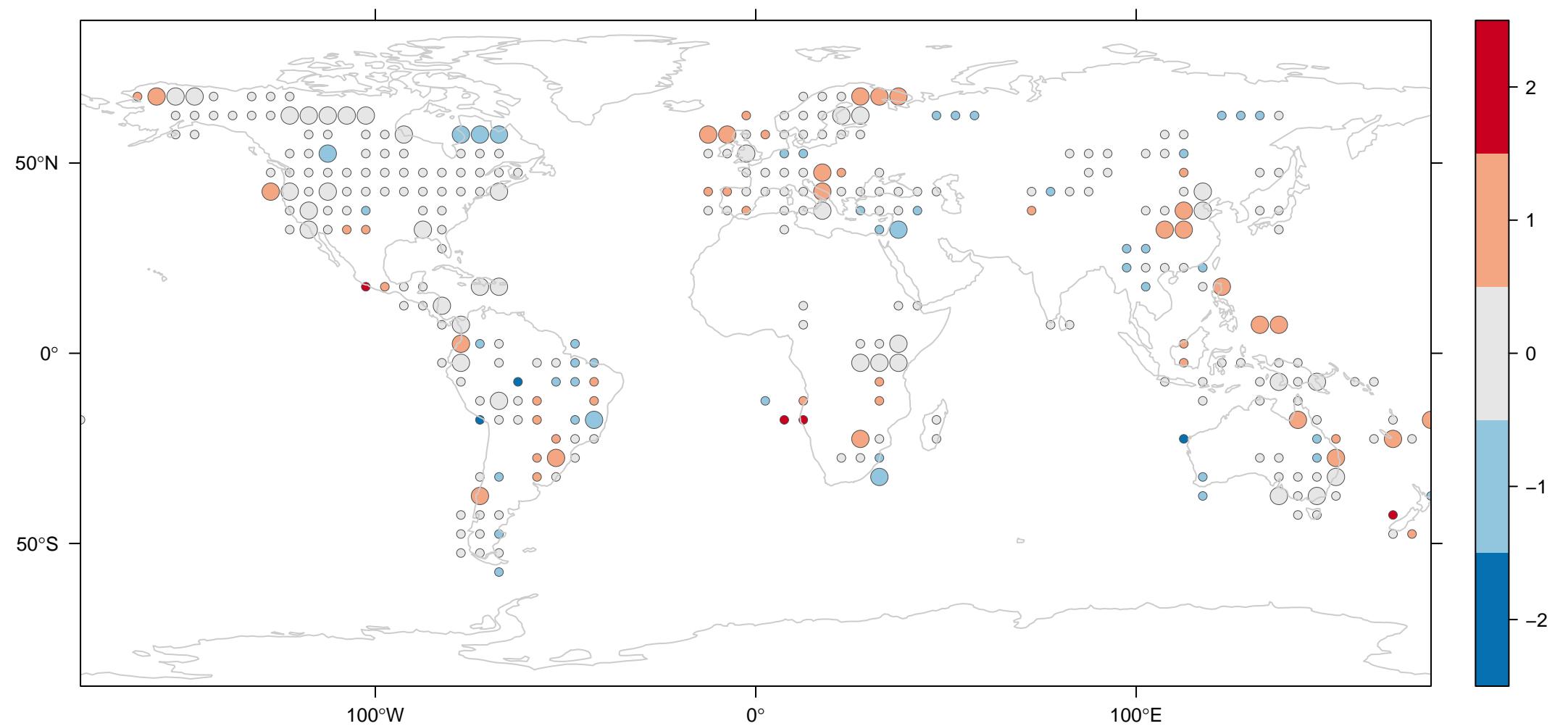
Number of sites per grid cell



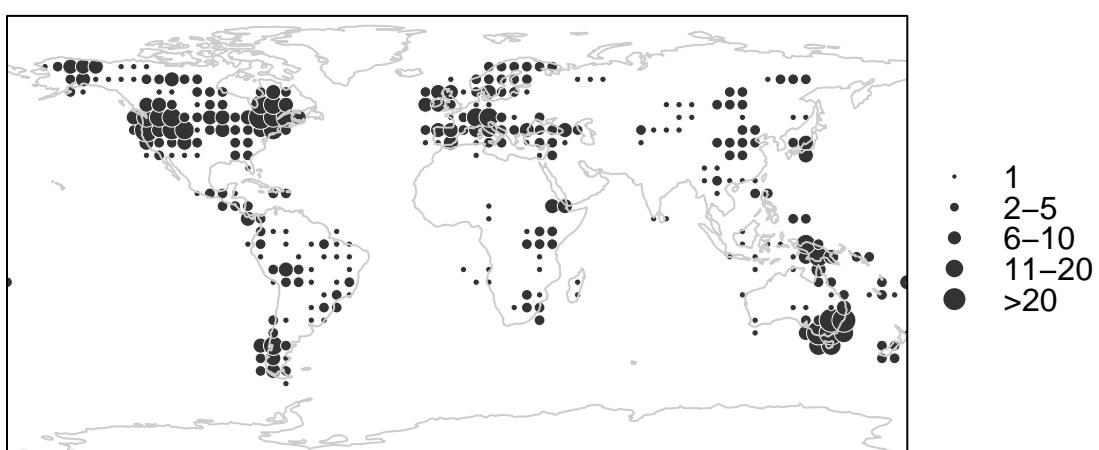
Number of grid cells influenced by each site



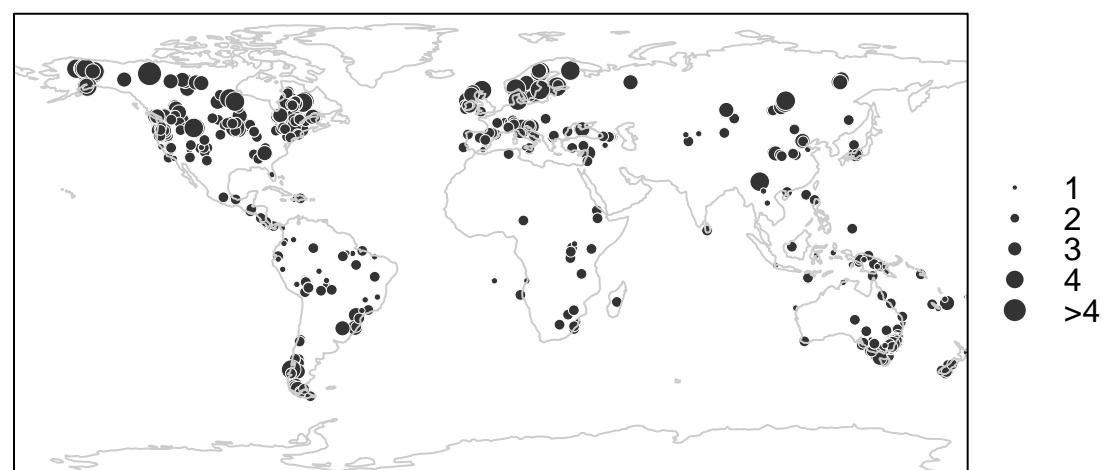
Charcoal Influx z-Scores: 500–1500 BP



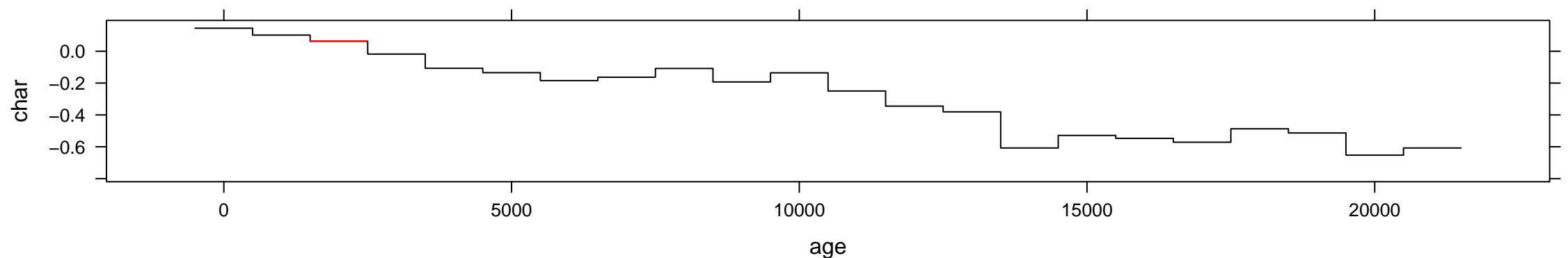
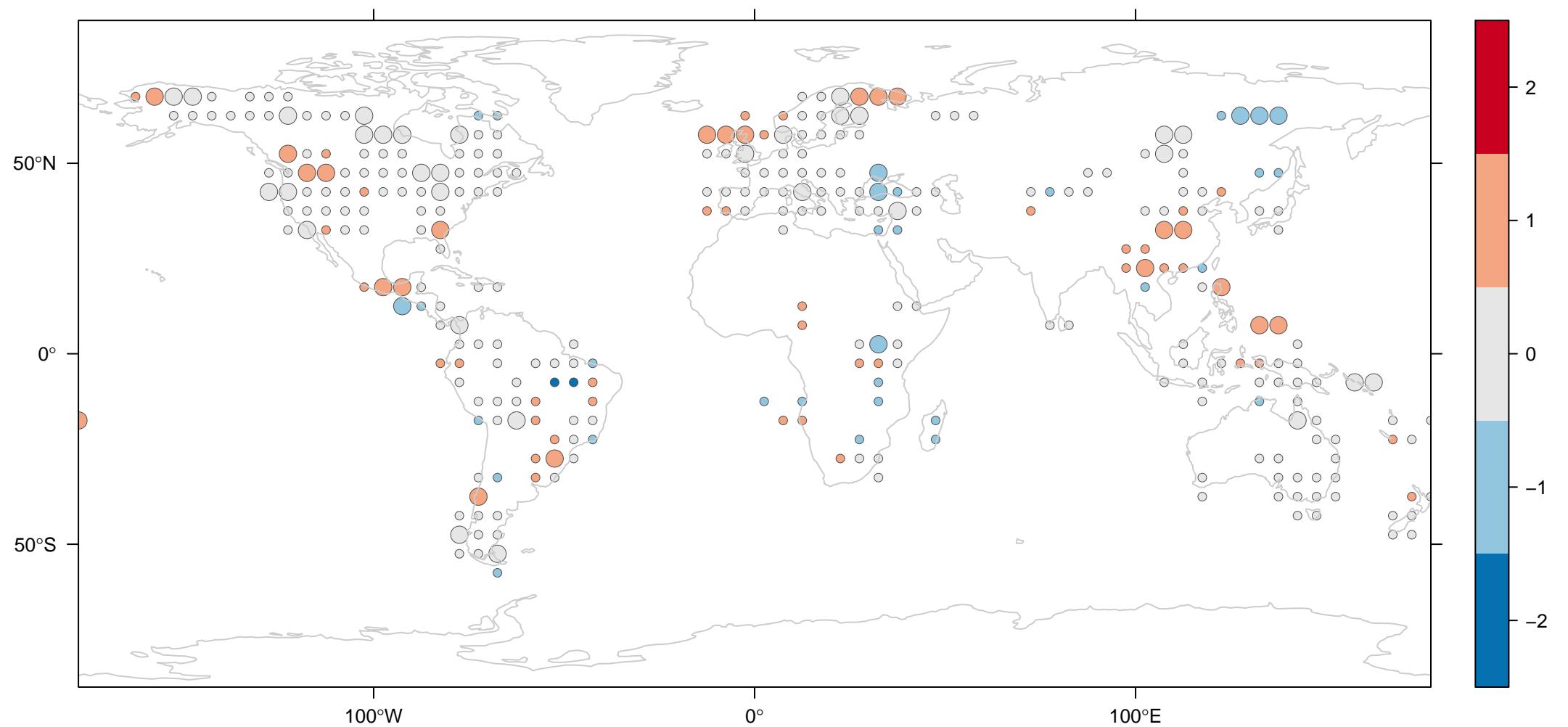
Number of sites per grid cell



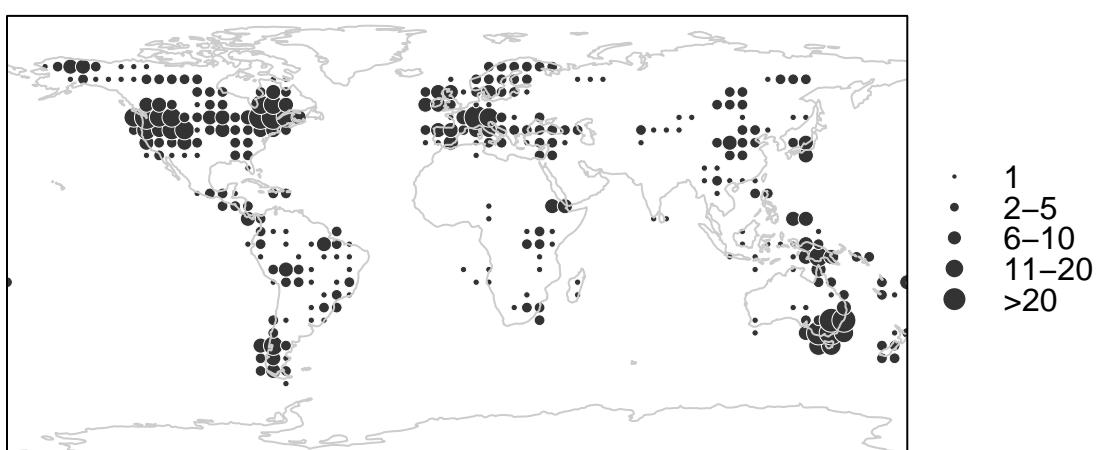
Number of grid cells influenced by each site



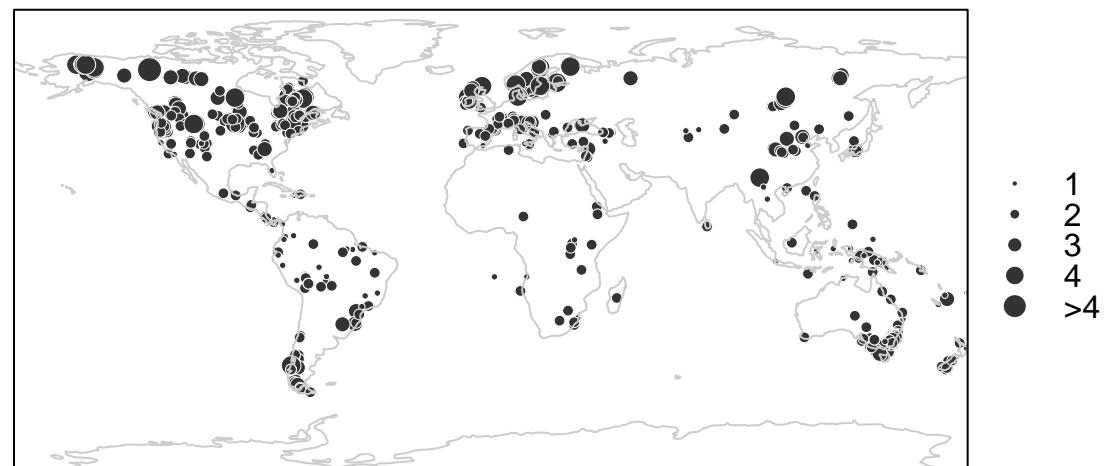
Charcoal Influx z-Scores: 1500–2500 BP



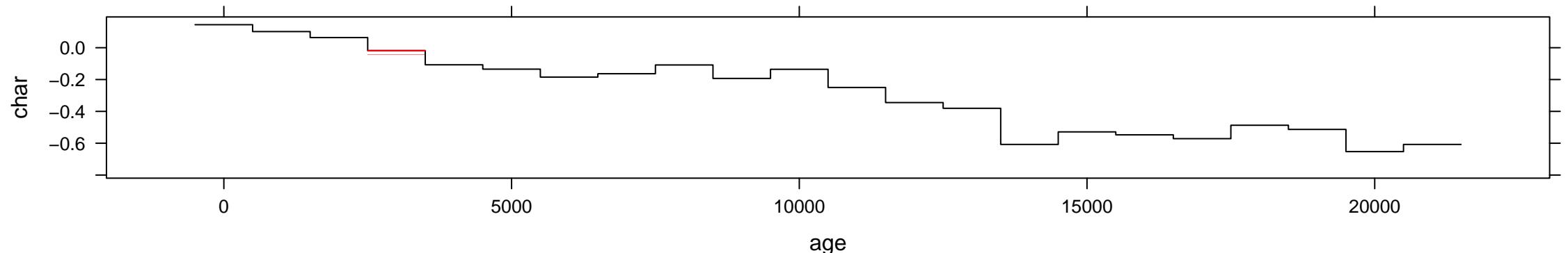
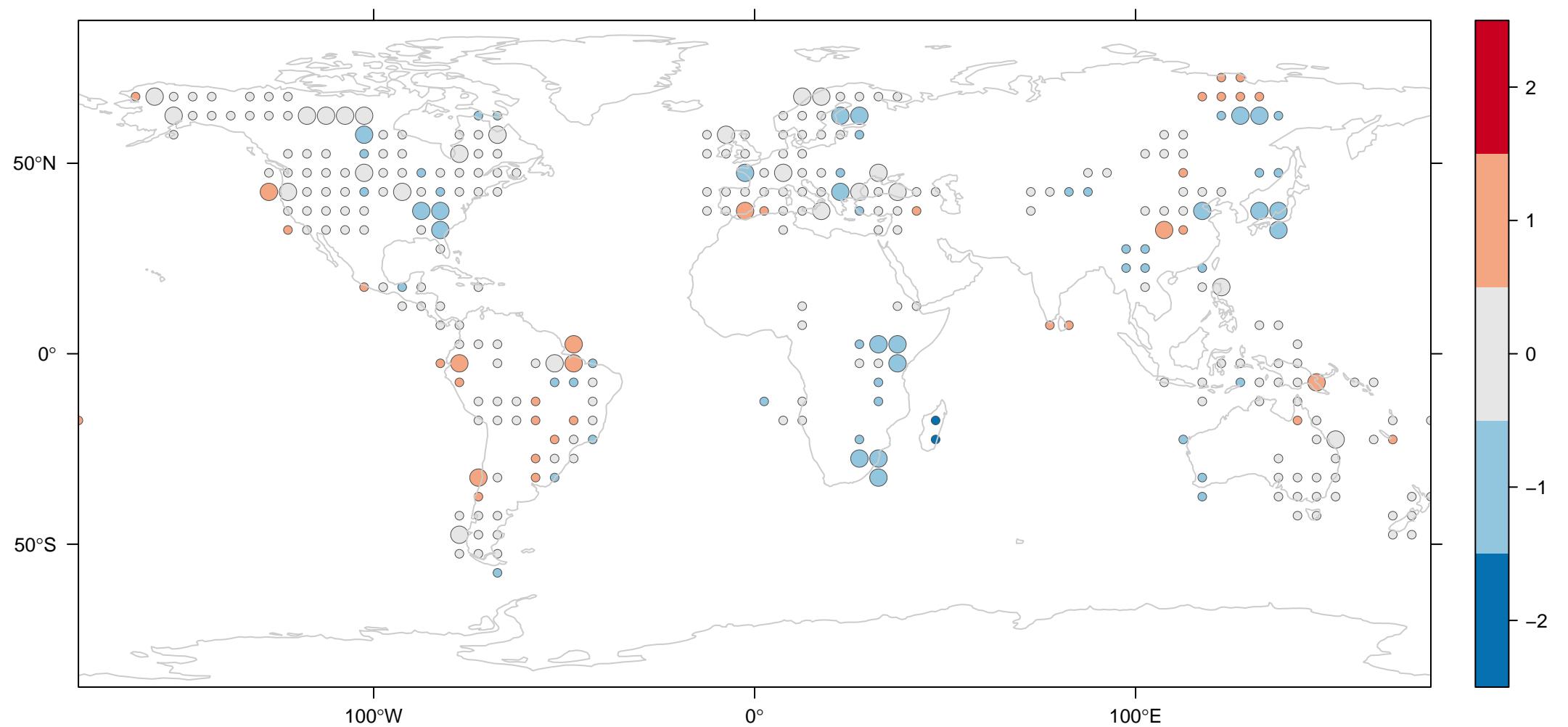
Number of sites per grid cell



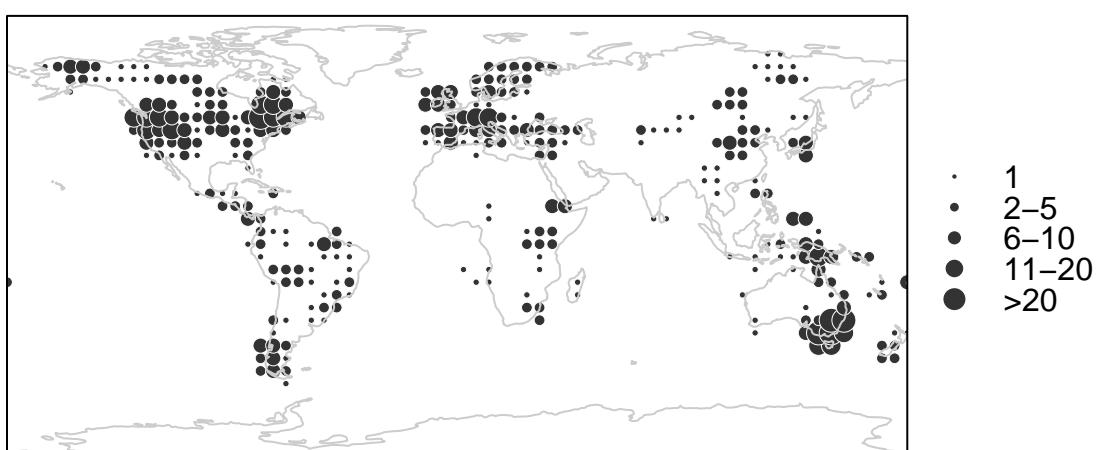
Number of grid cells influenced by each site



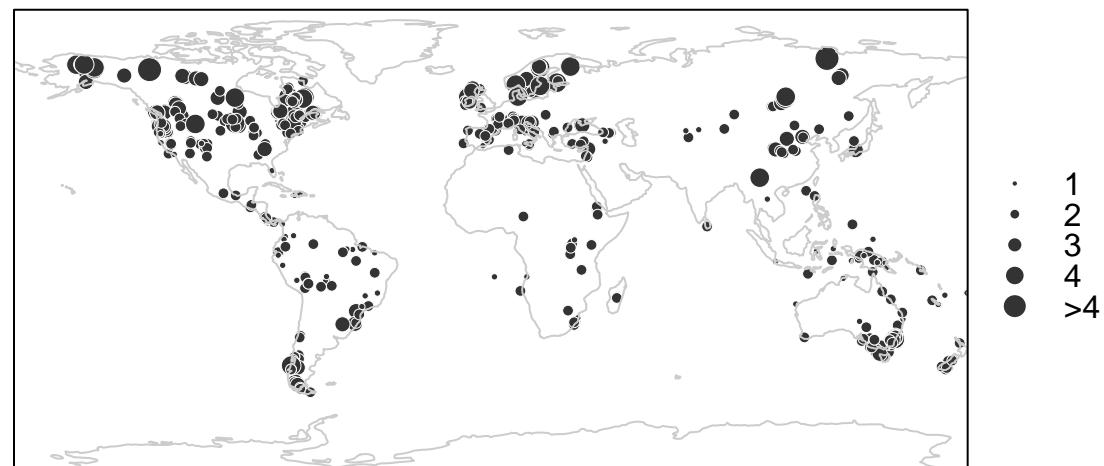
Charcoal Influx z-Scores: 2500–3500 BP



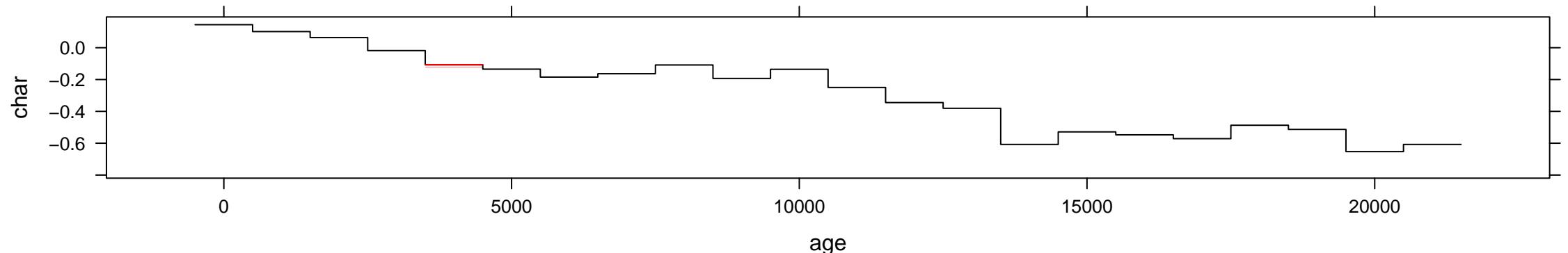
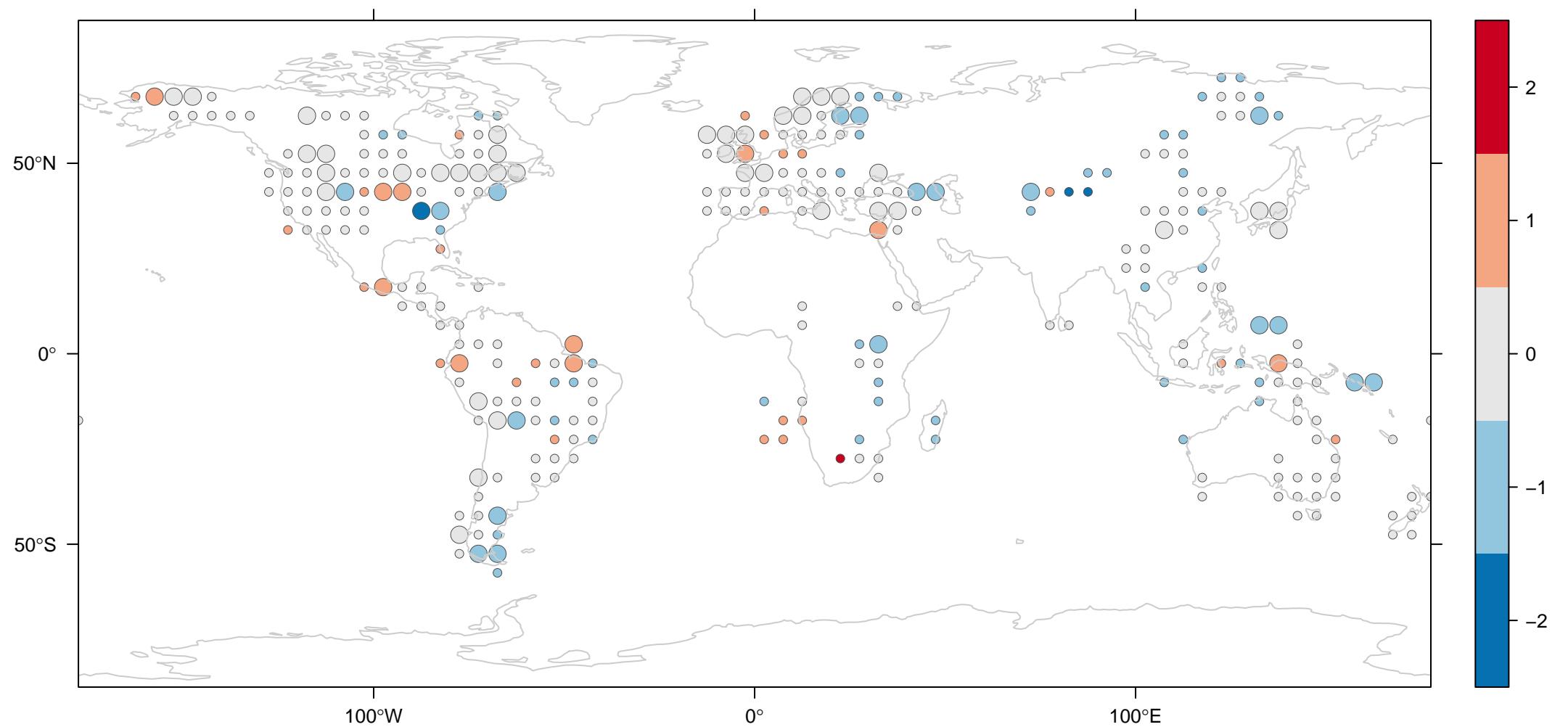
Number of sites per grid cell



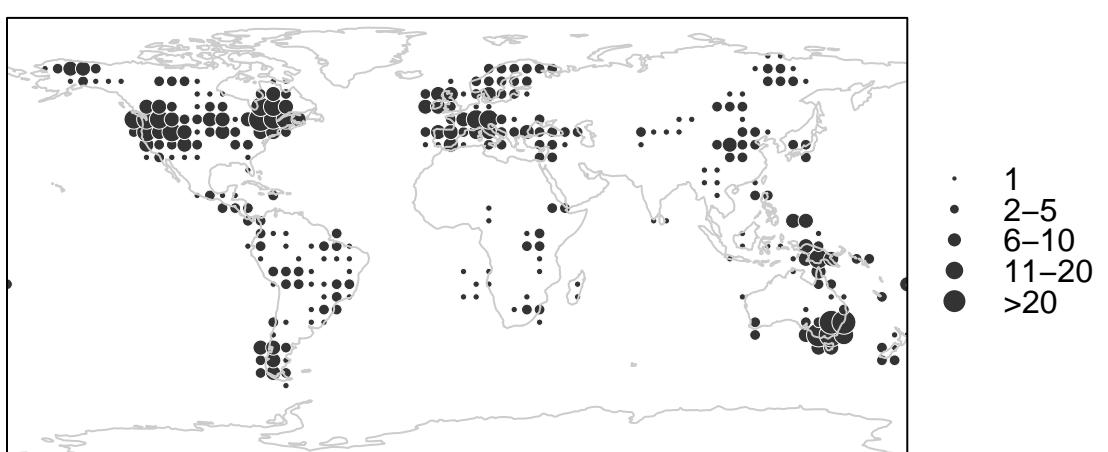
Number of grid cells influenced by each site



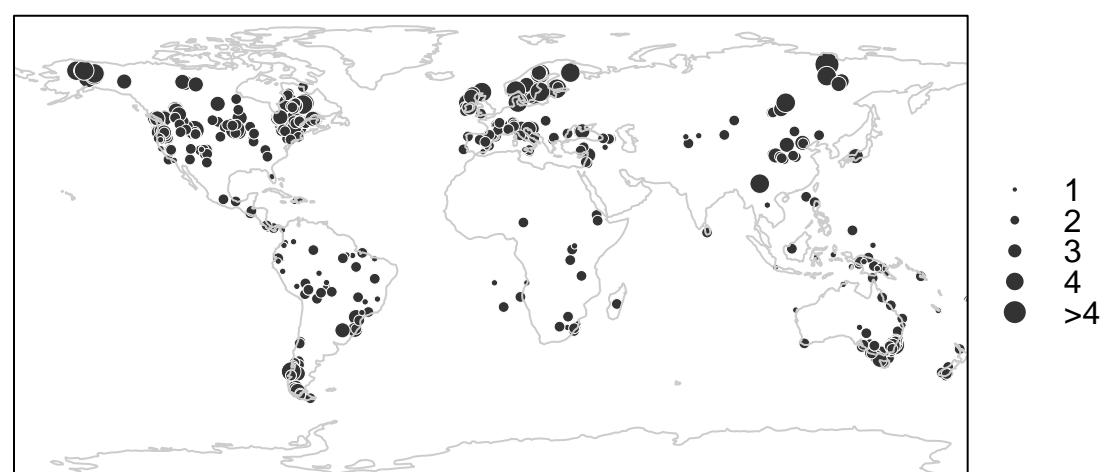
Charcoal Influx z-Scores: 3500–4500 BP



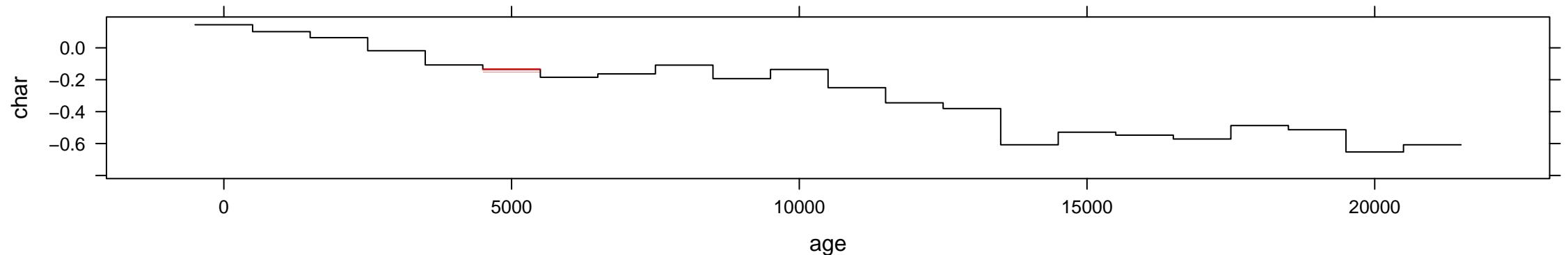
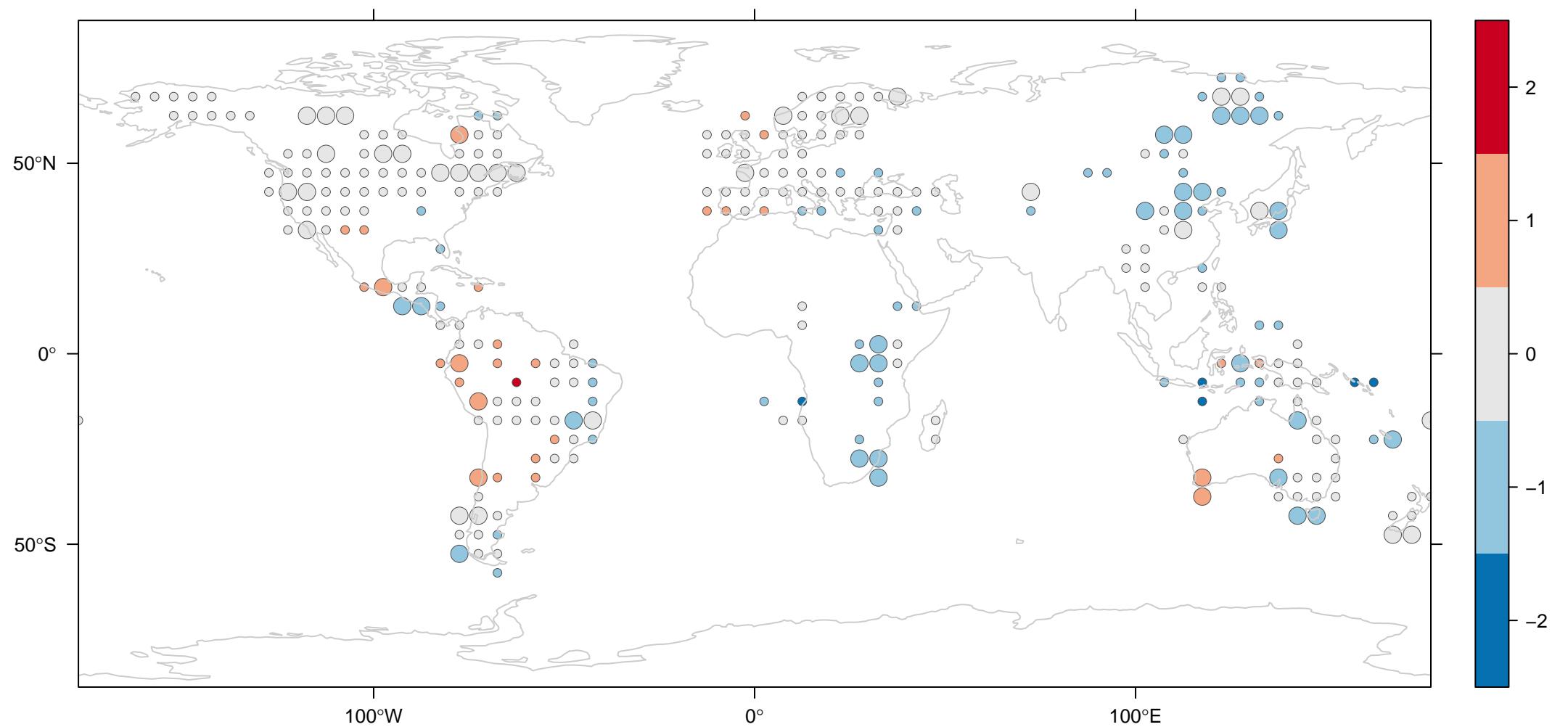
Number of sites per grid cell



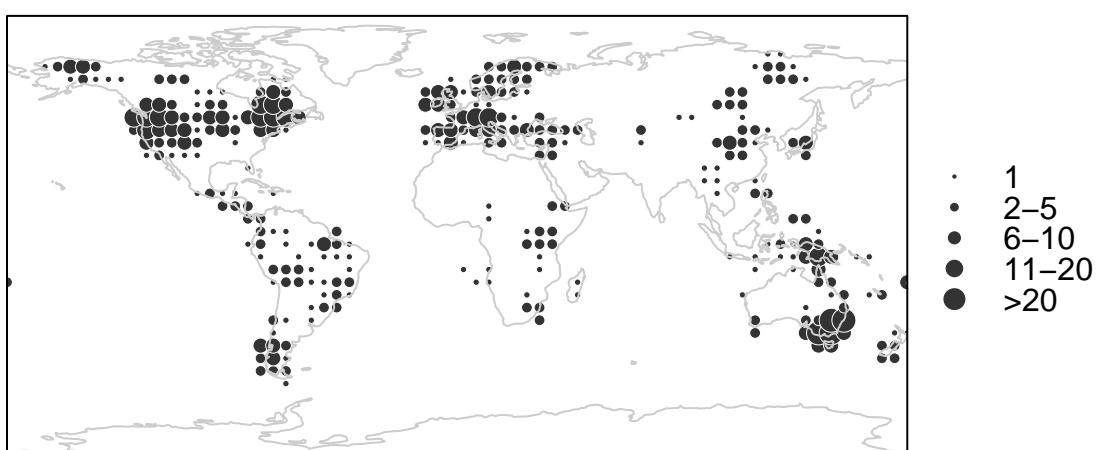
Number of grid cells influenced by each site



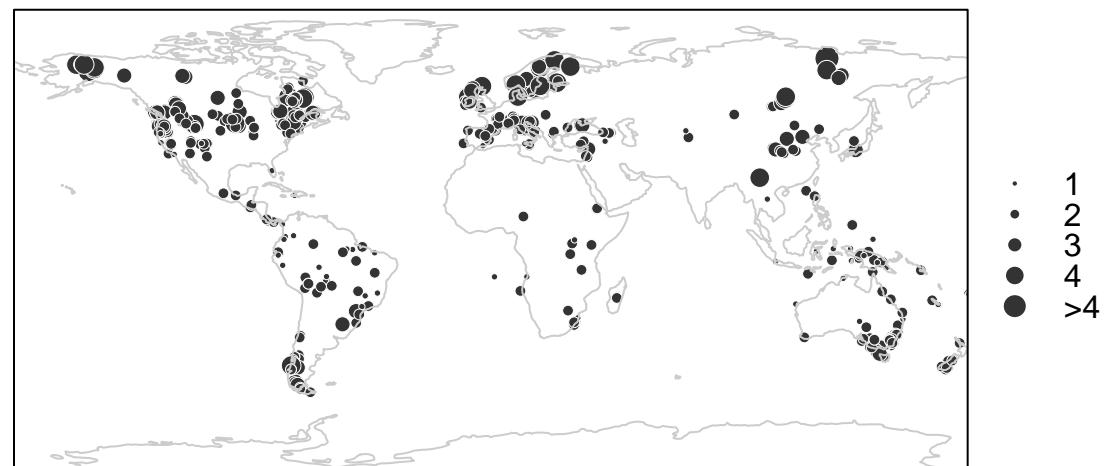
Charcoal Influx z-Scores: 4500–5500 BP



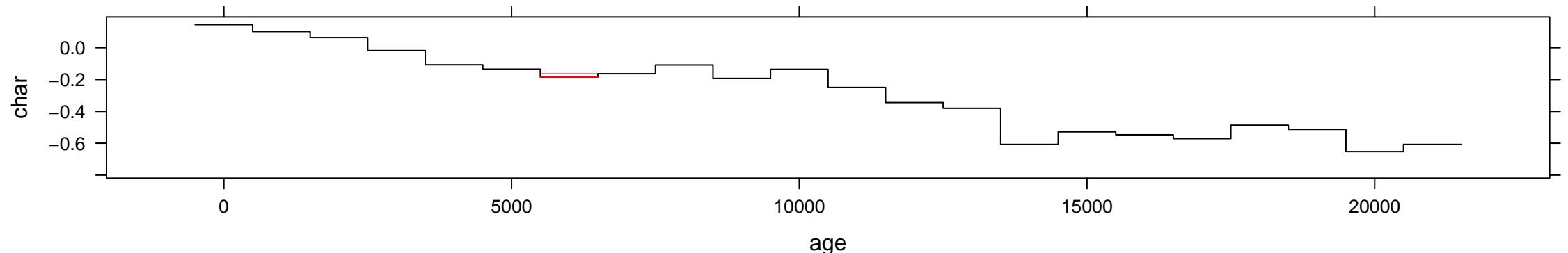
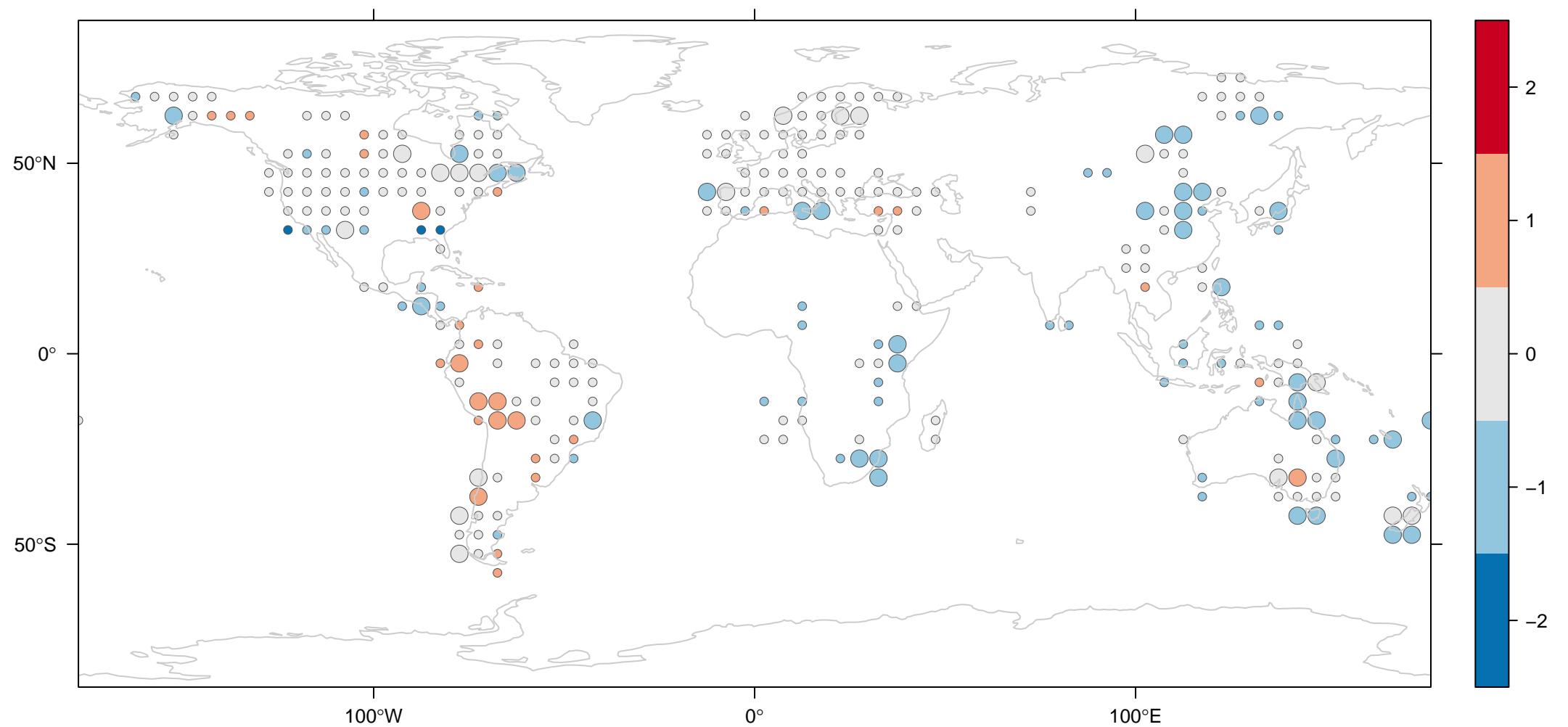
Number of sites per grid cell



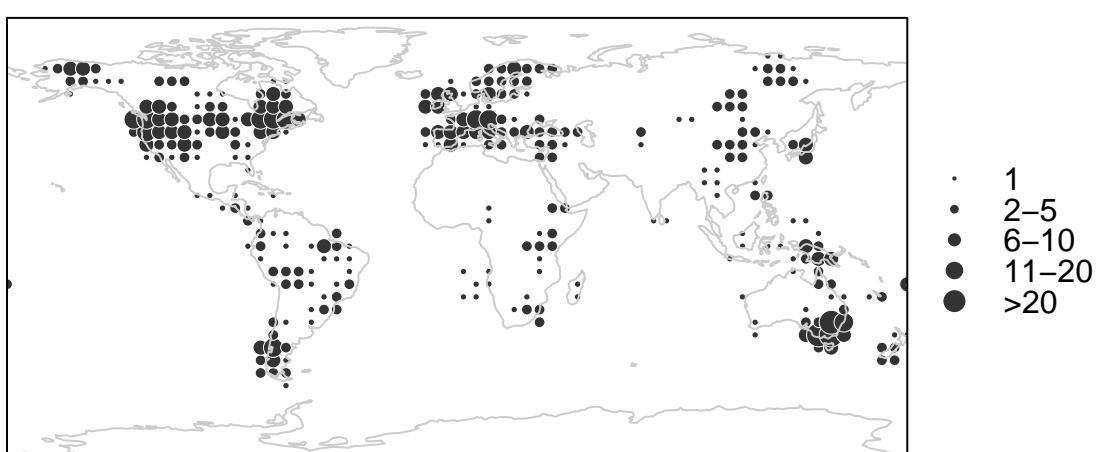
Number of grid cells influenced by each site



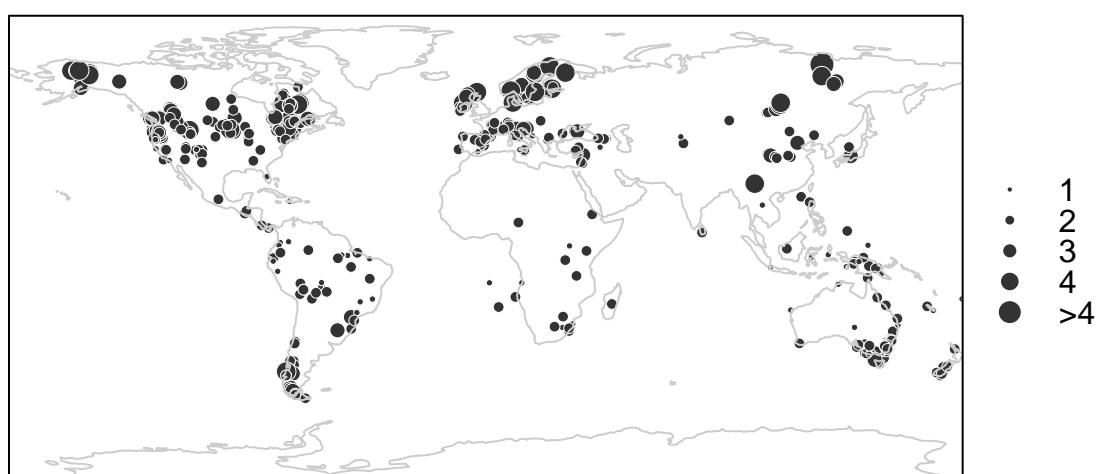
Charcoal Influx z-Scores: 5500–6500 BP



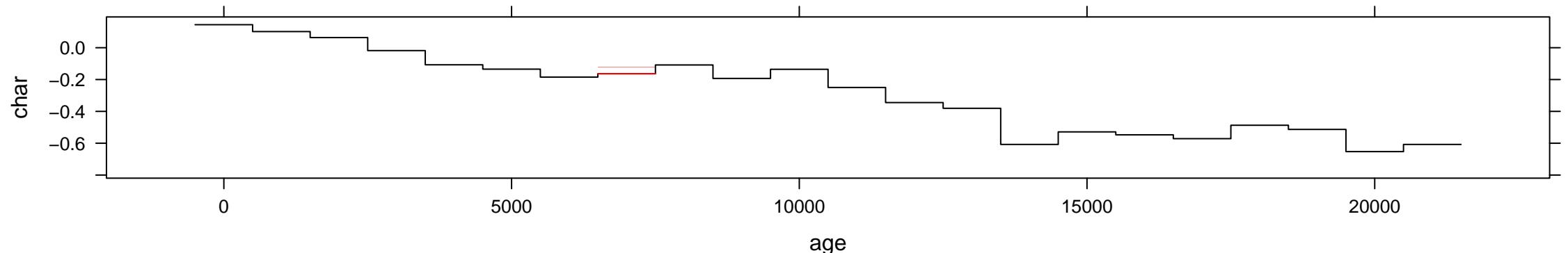
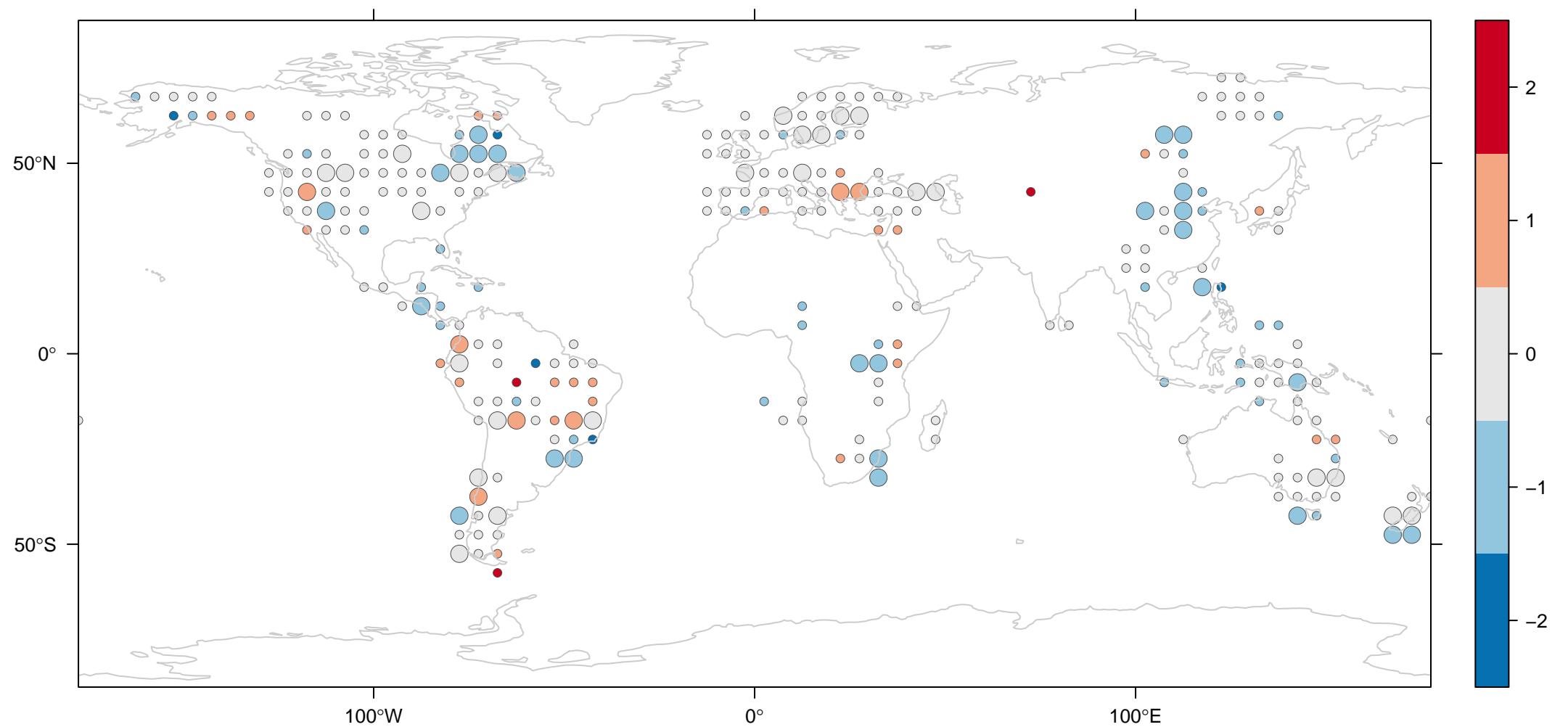
Number of sites per grid cell



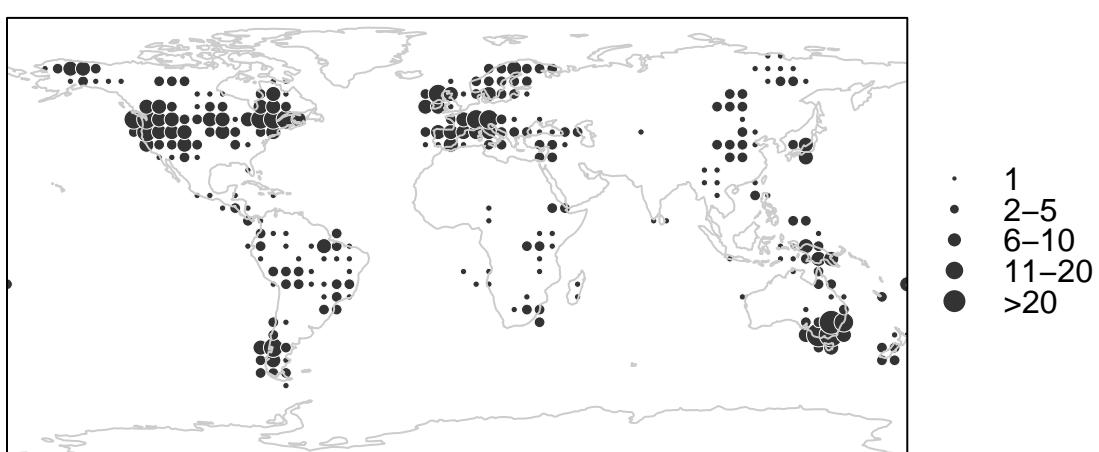
Number of grid cells influenced by each site



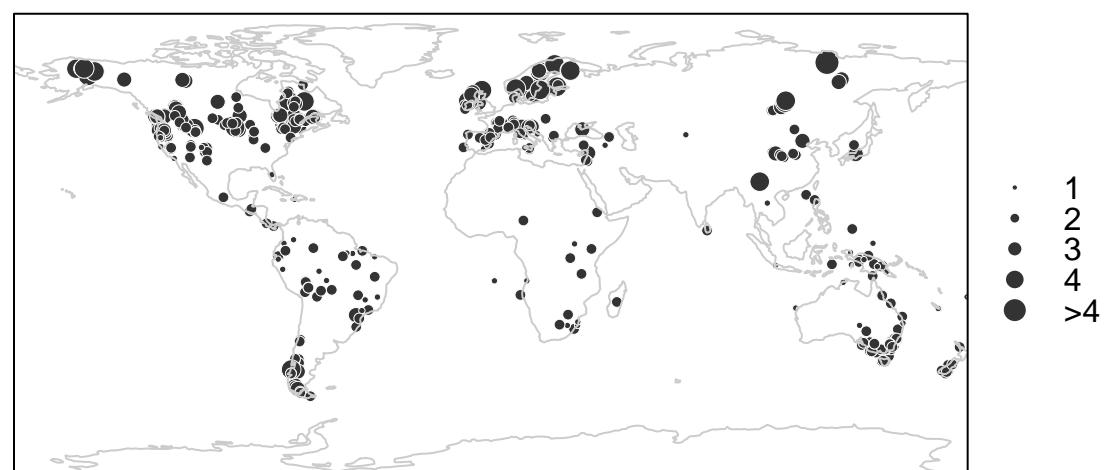
Charcoal Influx z-Scores: 6500–7500 BP



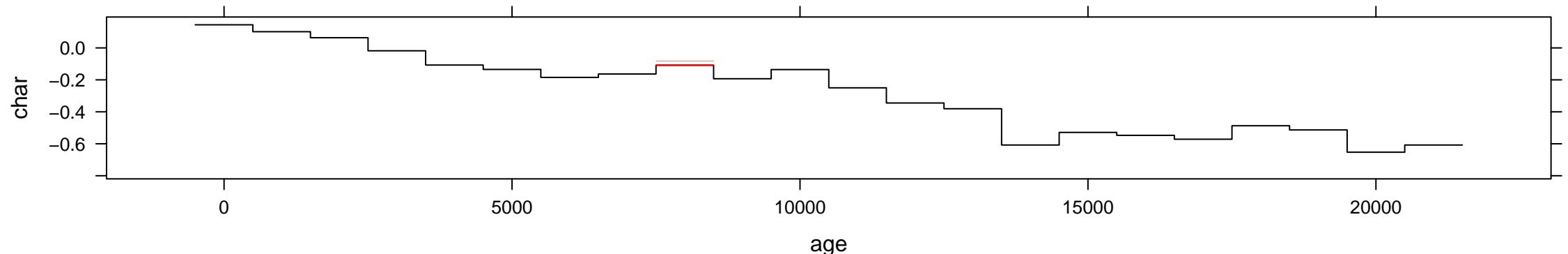
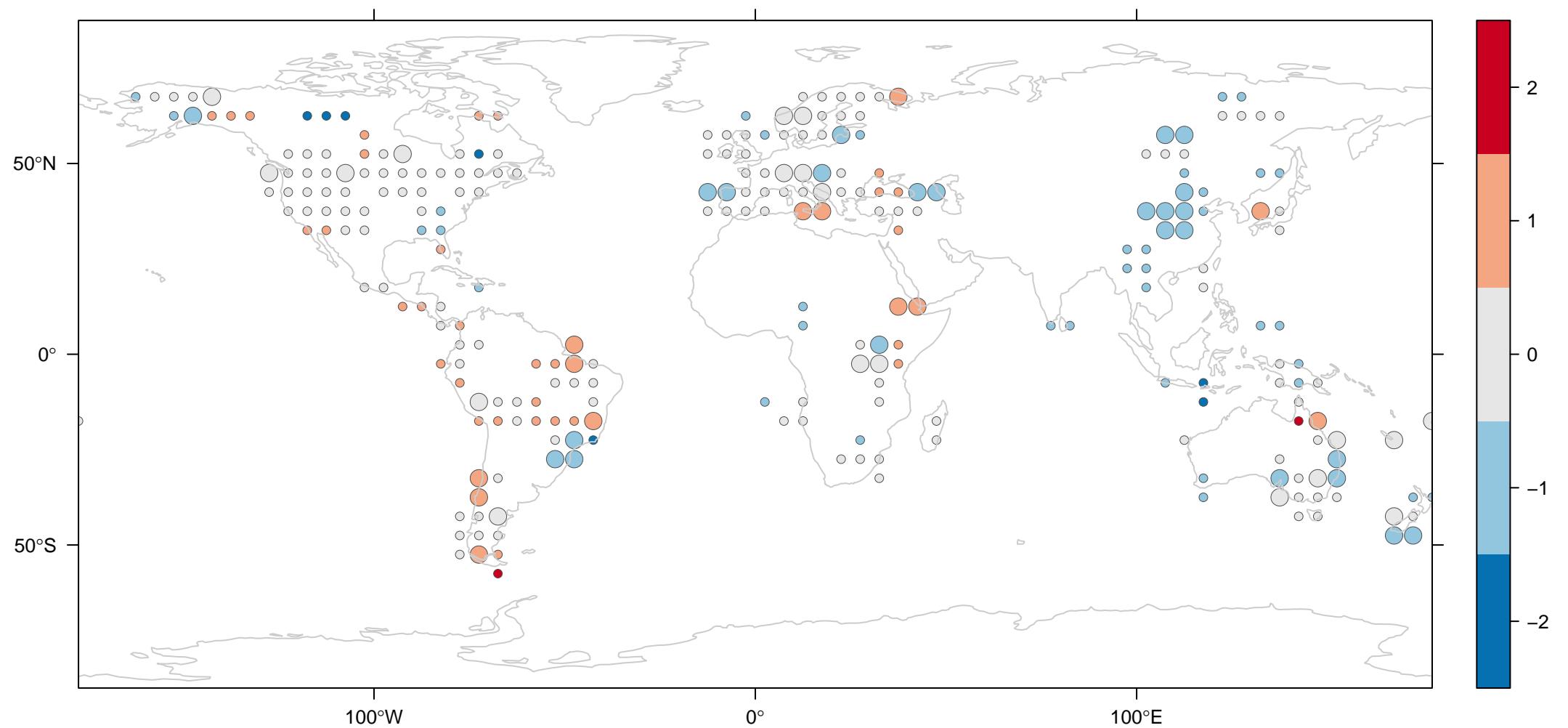
Number of sites per grid cell



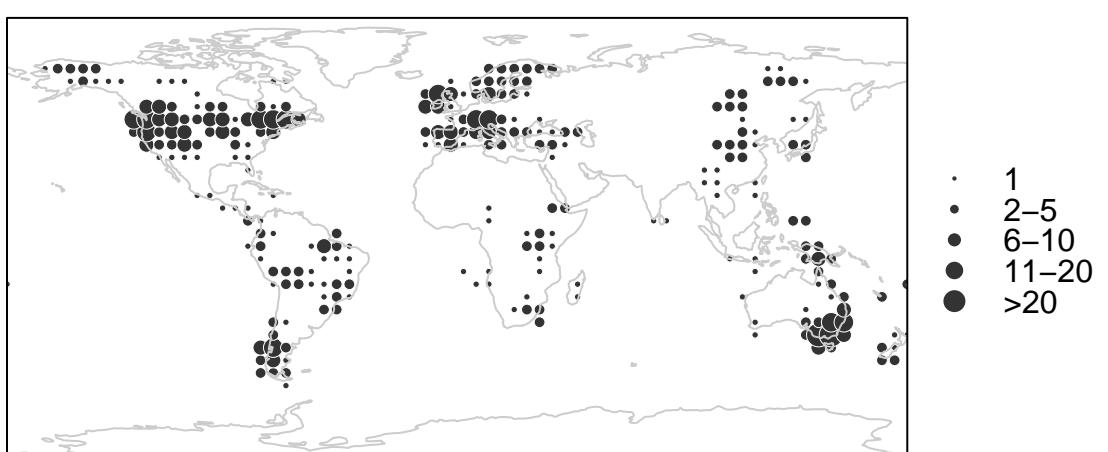
Number of grid cells influenced by each site



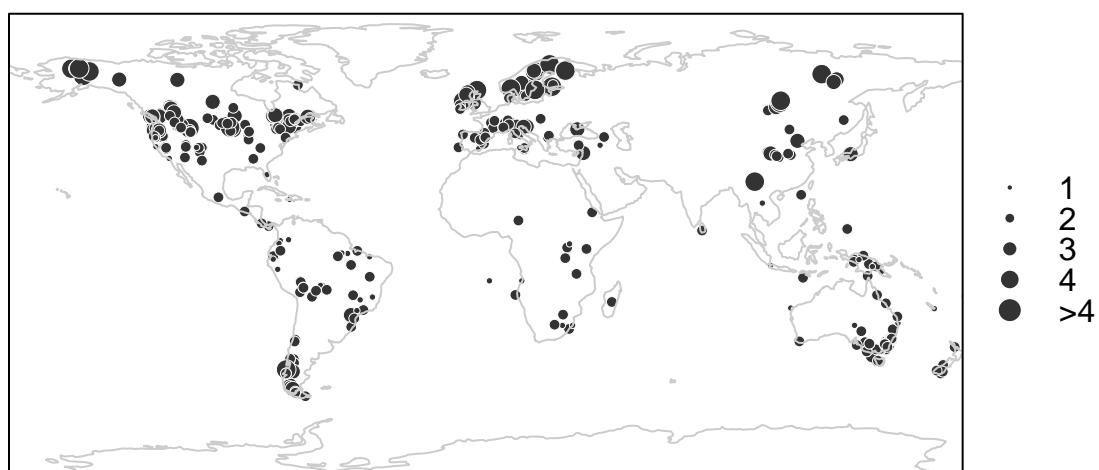
Charcoal Influx z-Scores: 7500–8500 BP



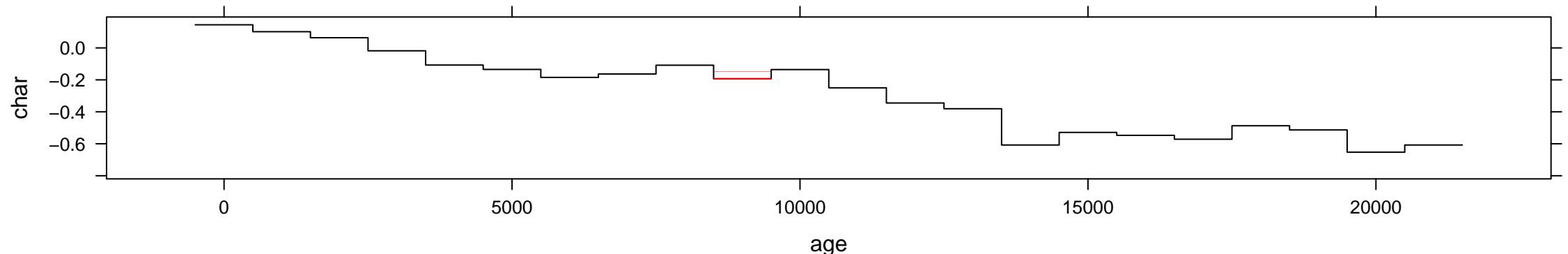
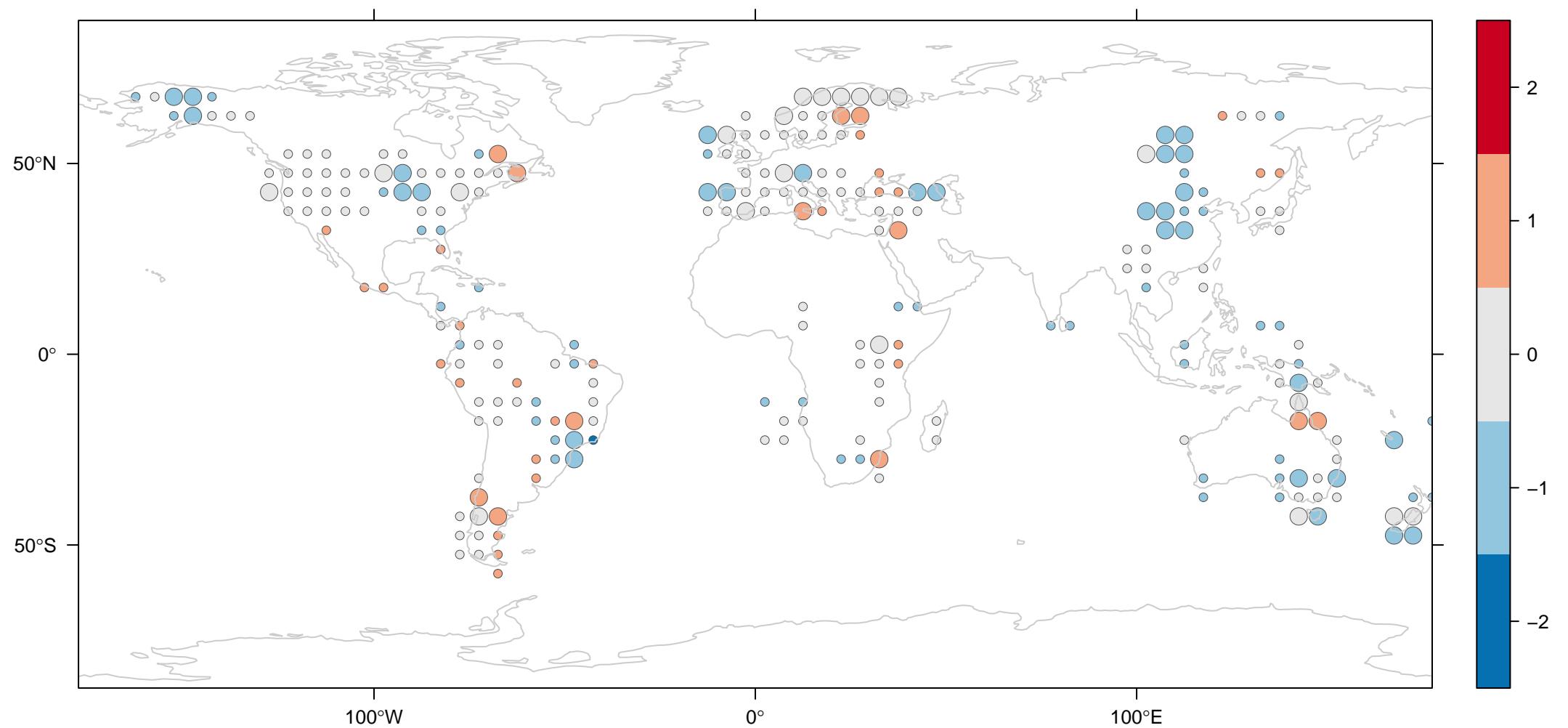
Number of sites per grid cell



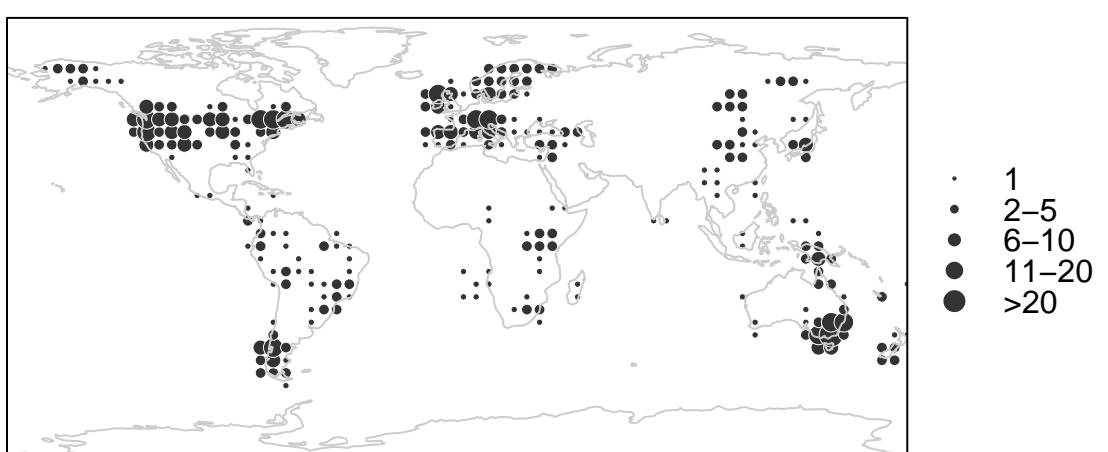
Number of grid cells influenced by each site



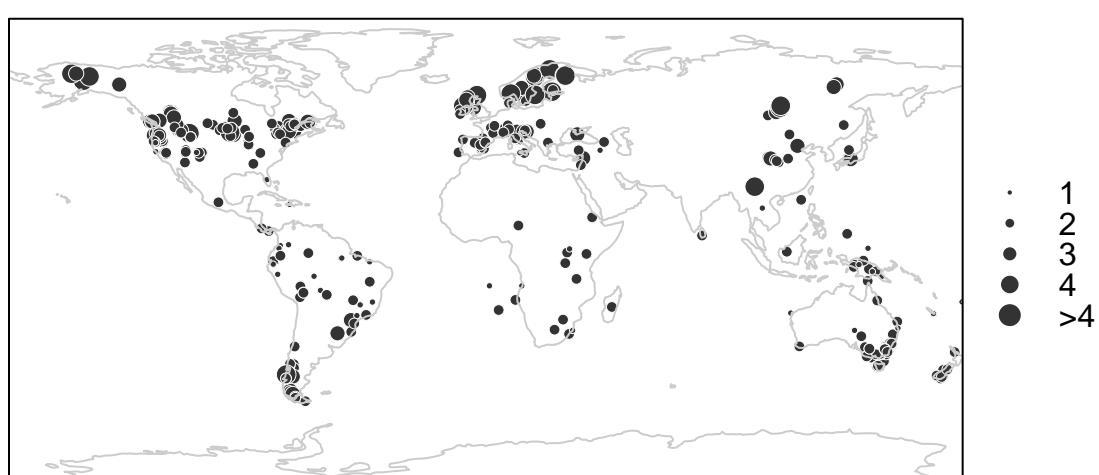
Charcoal Influx z-Scores: 8500–9500 BP



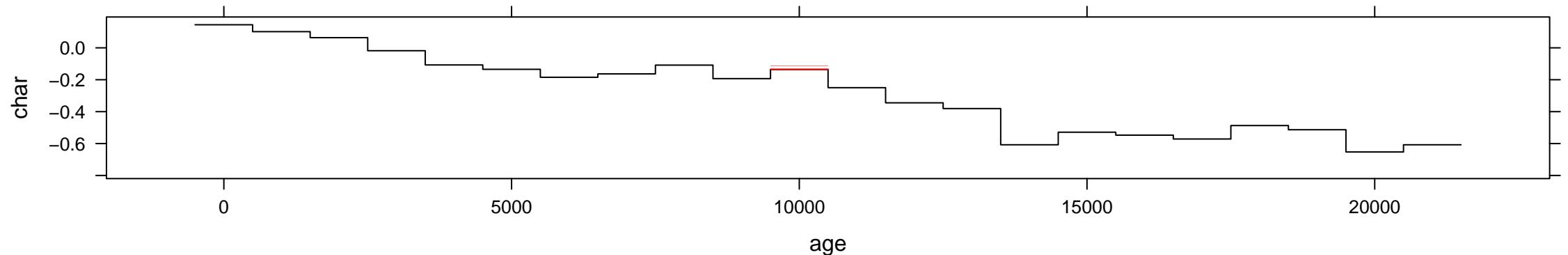
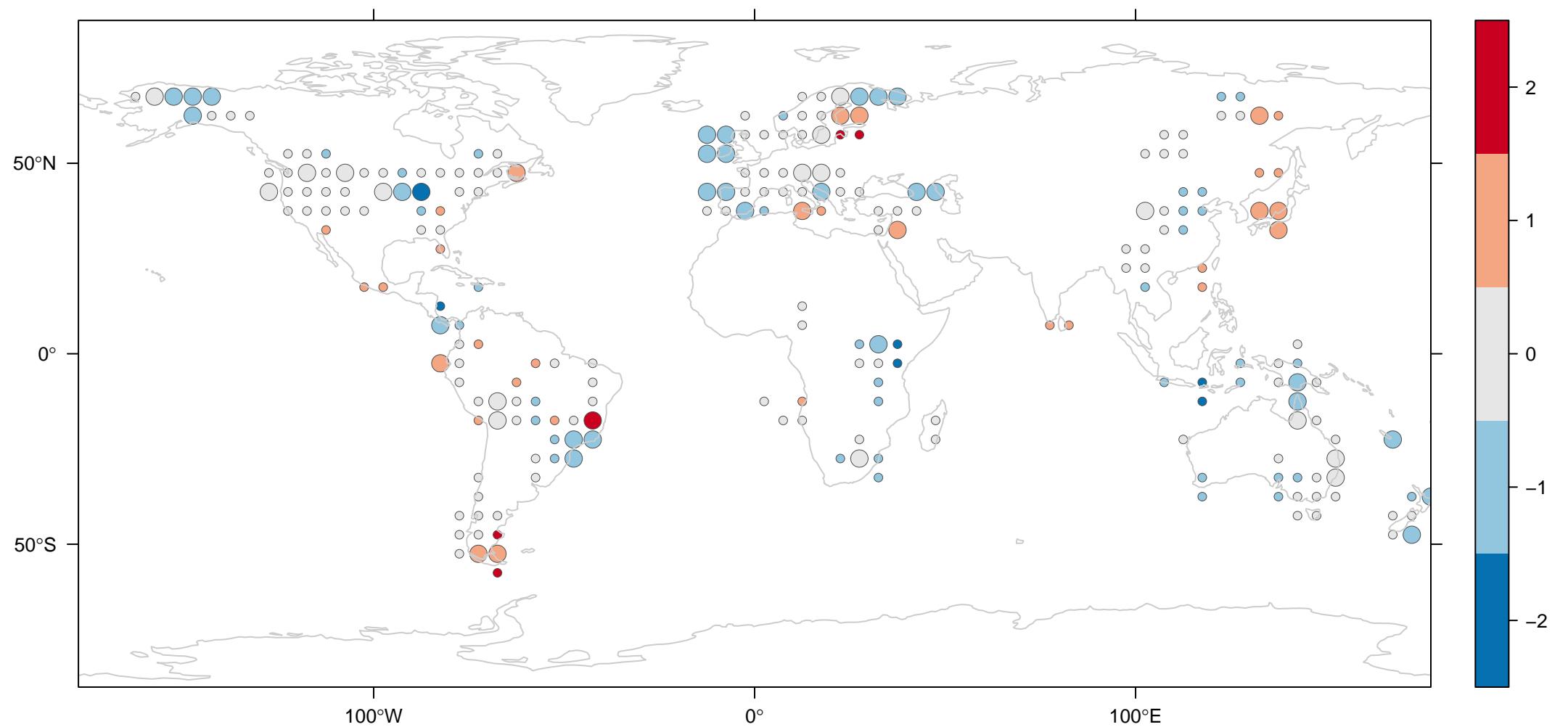
Number of sites per grid cell



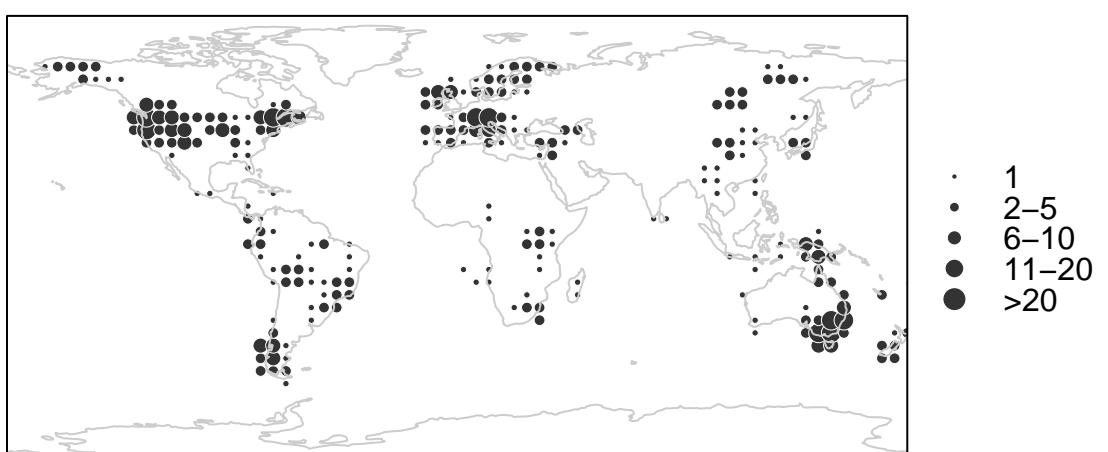
Number of grid cells influenced by each site



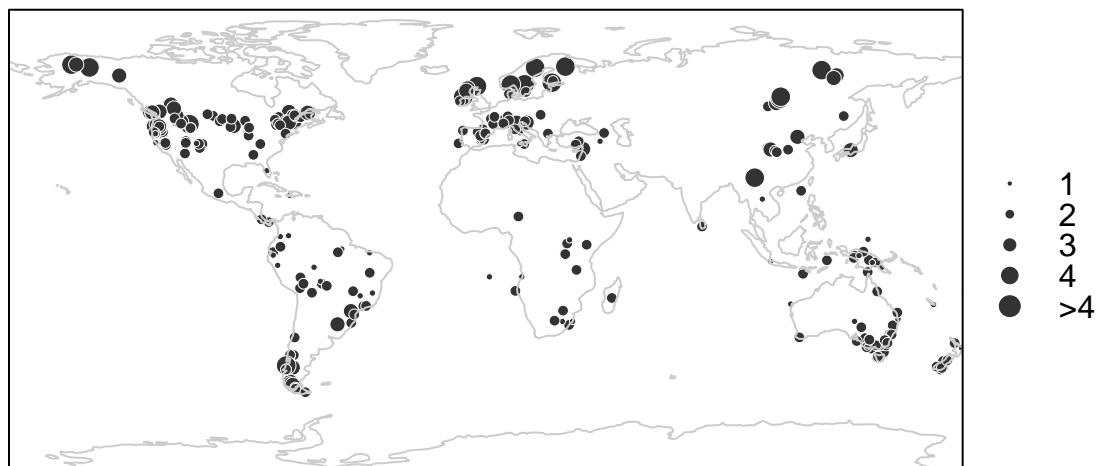
Charcoal Influx z-Scores: 9500–10500 BP



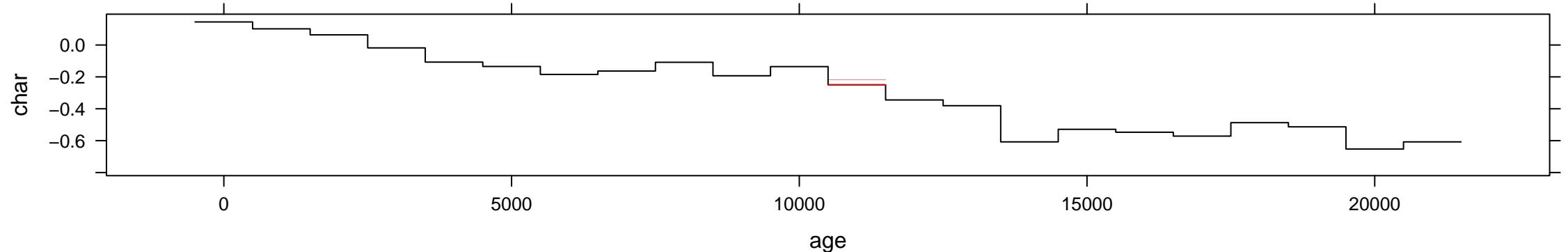
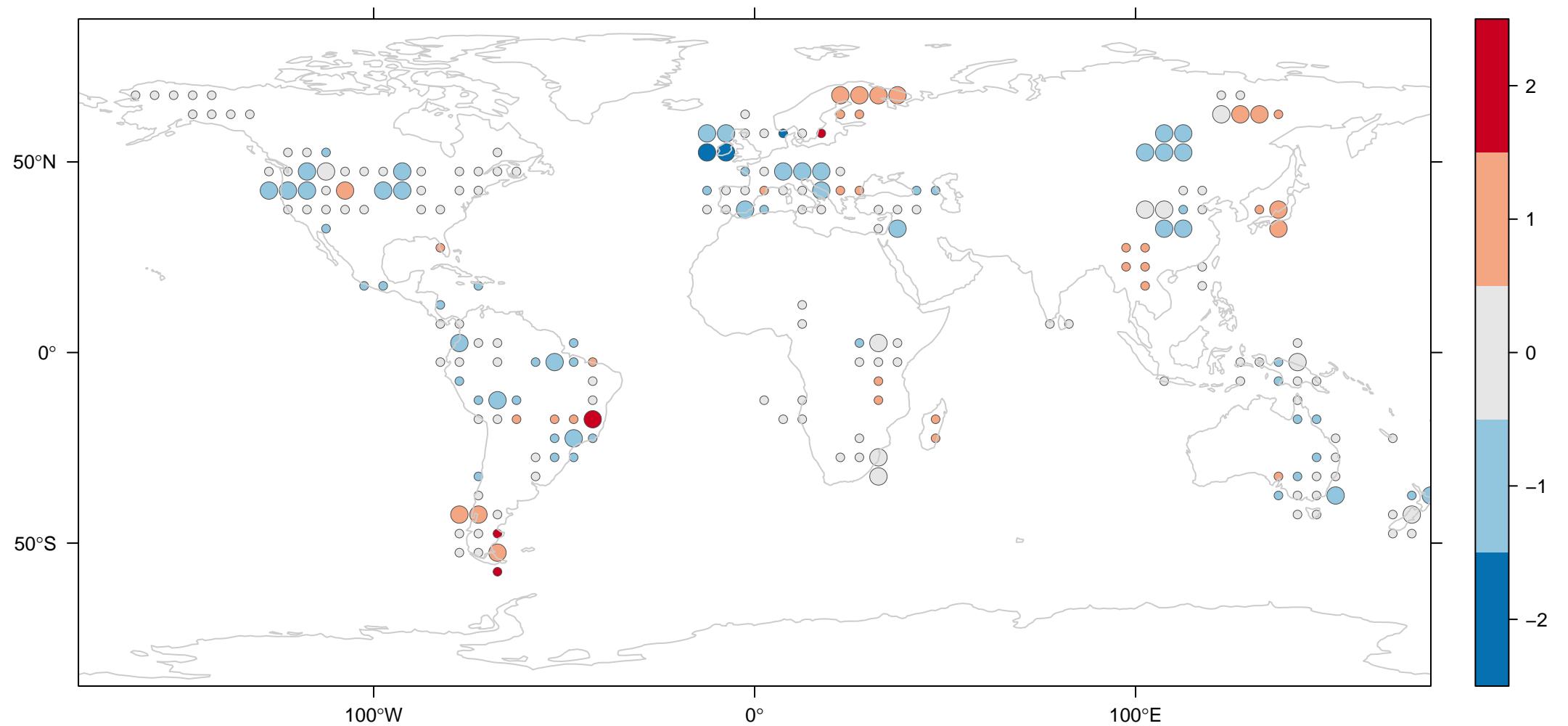
Number of sites per grid cell



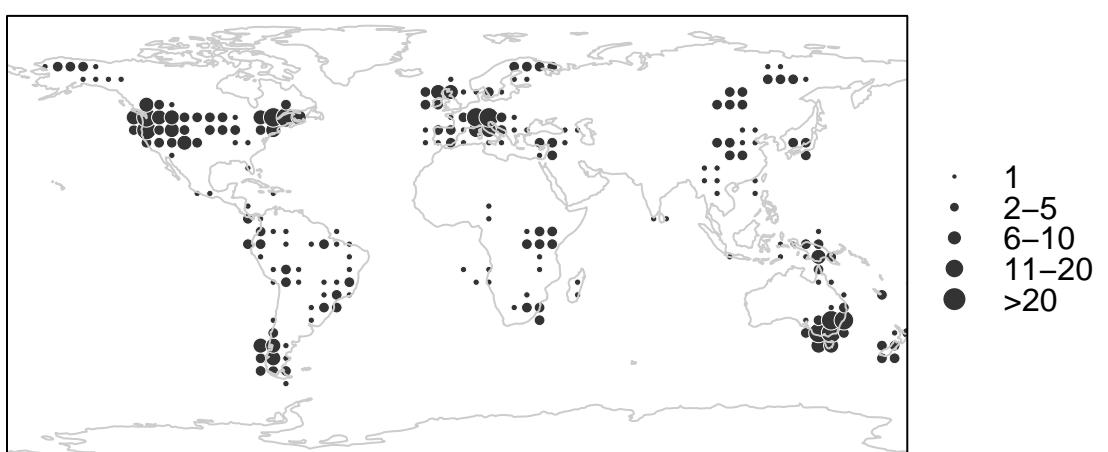
Number of grid cells influenced by each site



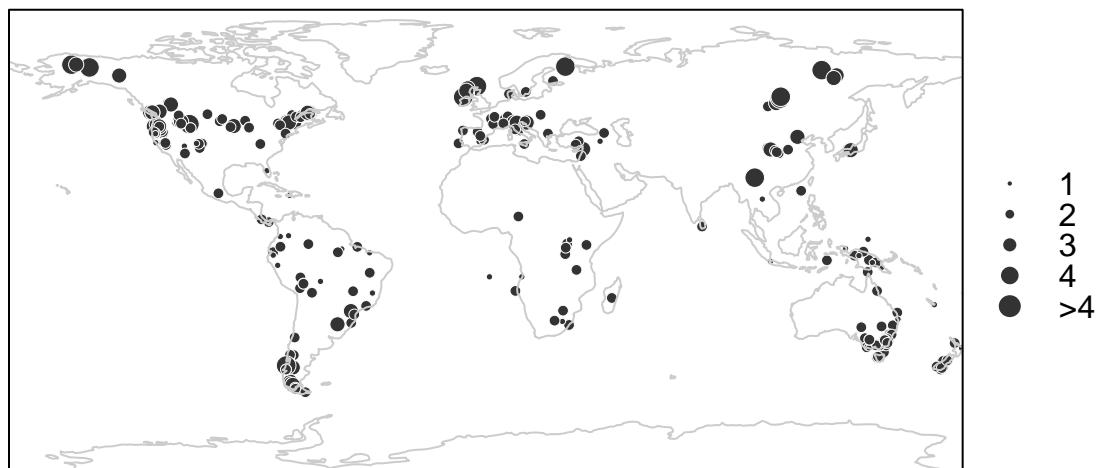
Charcoal Influx z-Scores: 10500–11500 BP



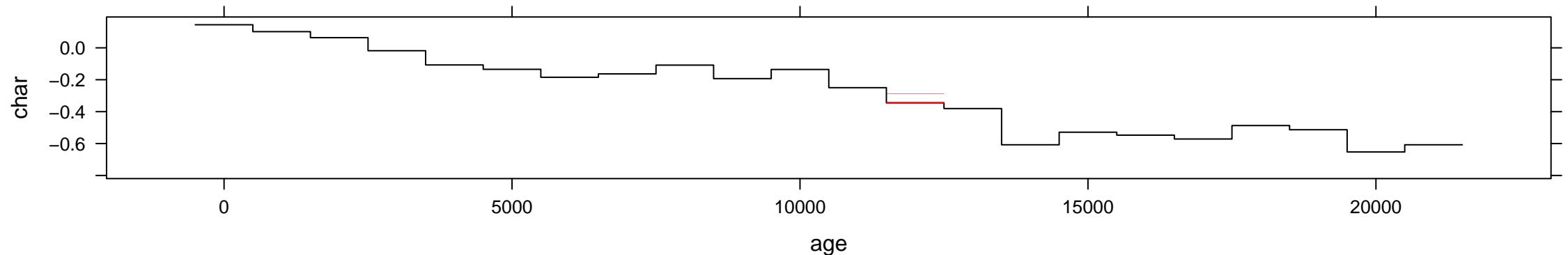
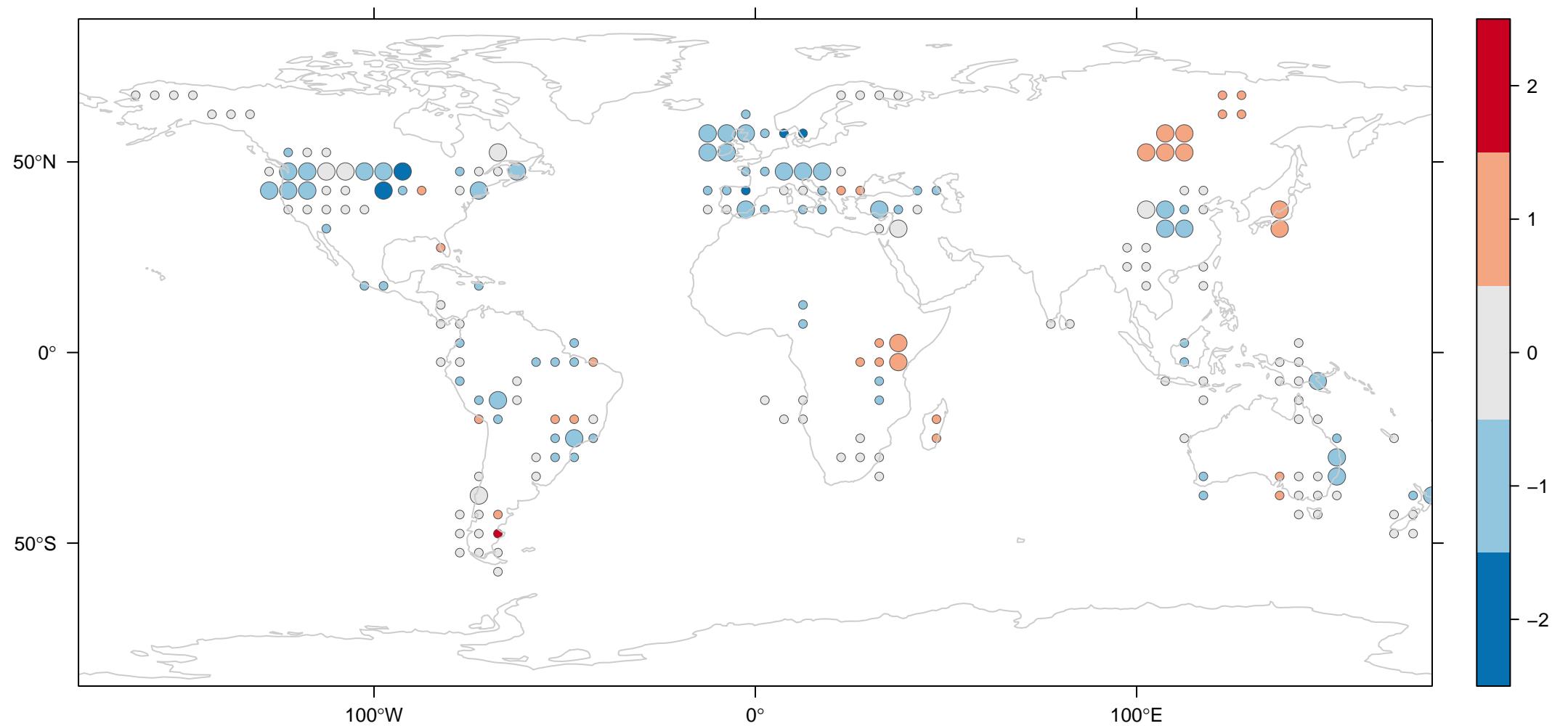
Number of sites per grid cell



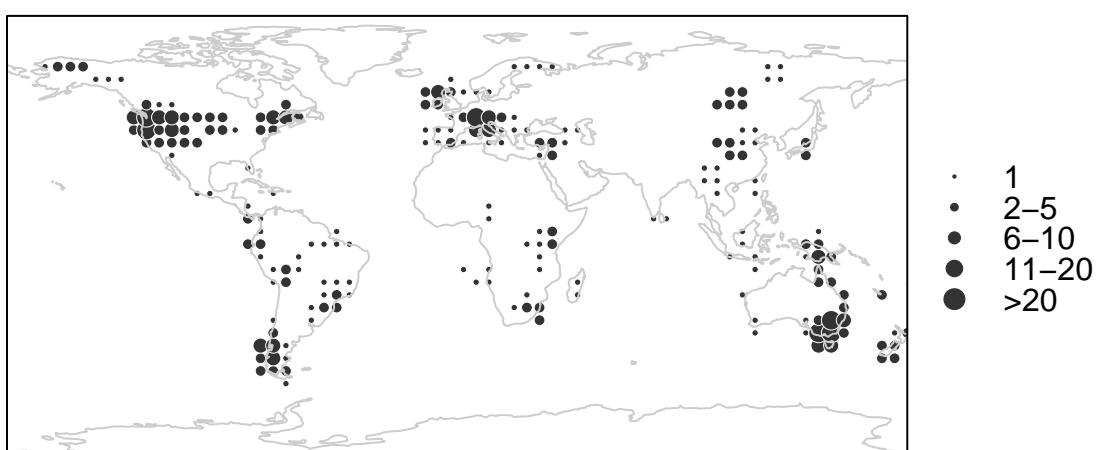
Number of grid cells influenced by each site



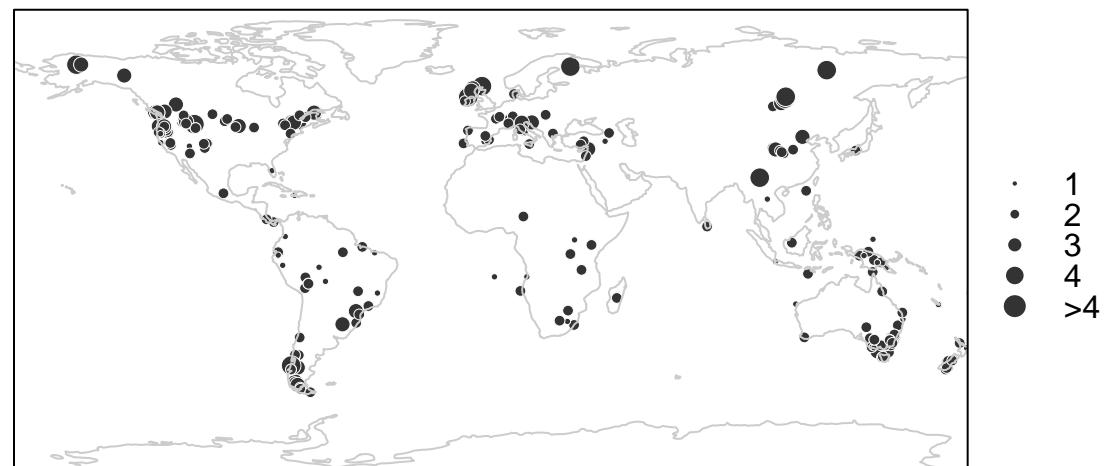
Charcoal Influx z-Scores: 11500–12500 BP



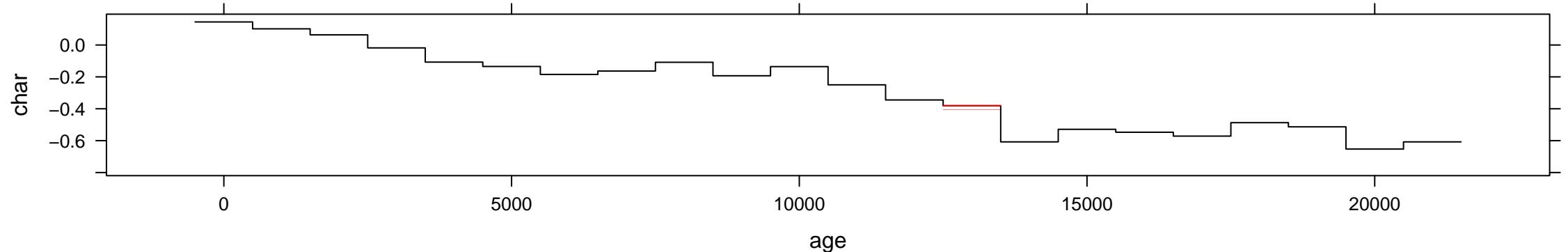
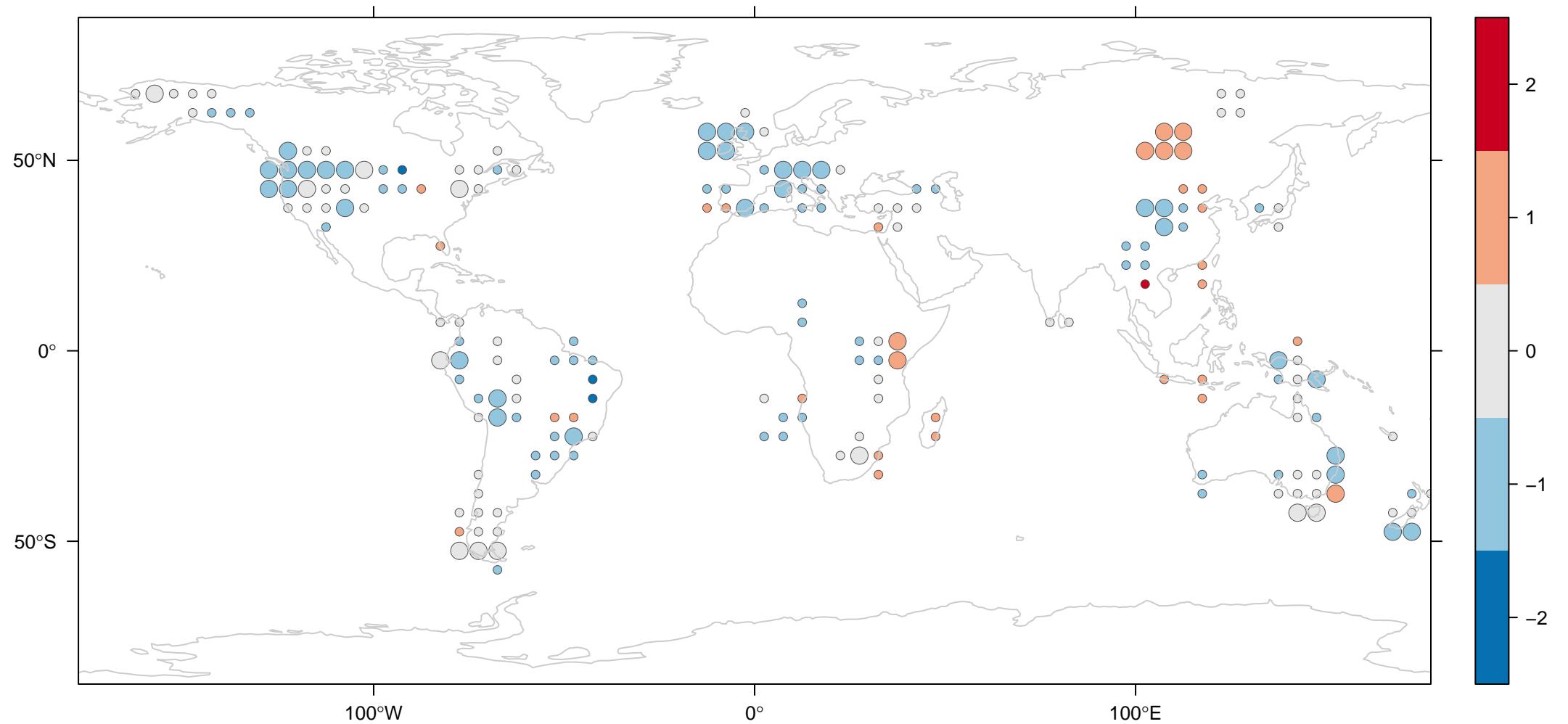
Number of sites per grid cell



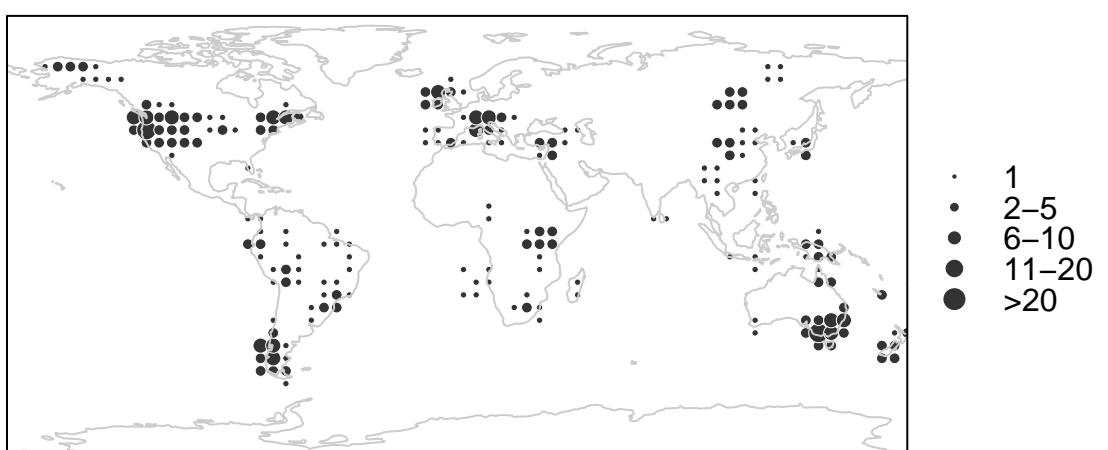
Number of grid cells influenced by each site



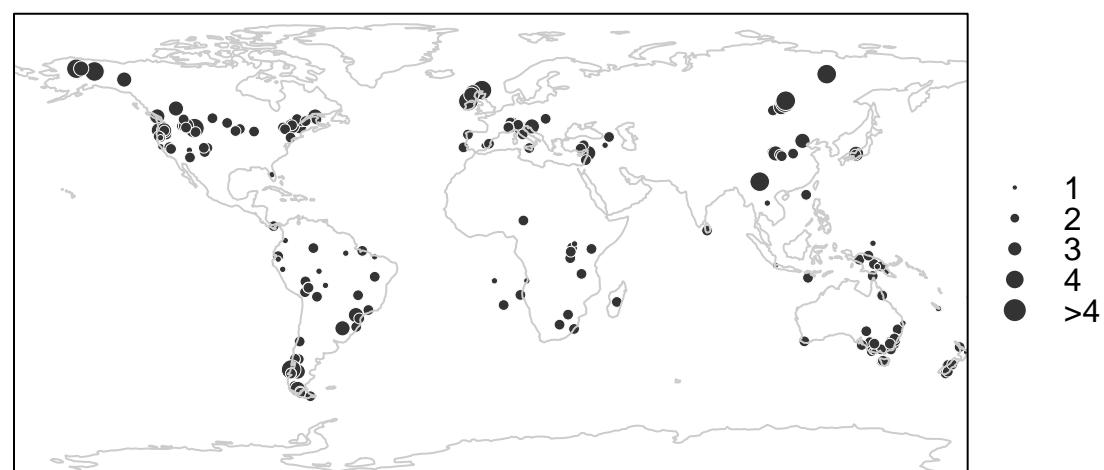
Charcoal Influx z-Scores: 12500–13500 BP



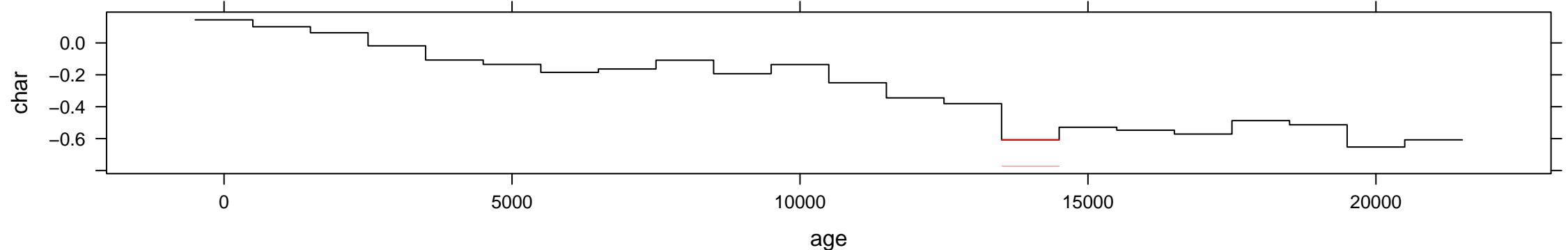
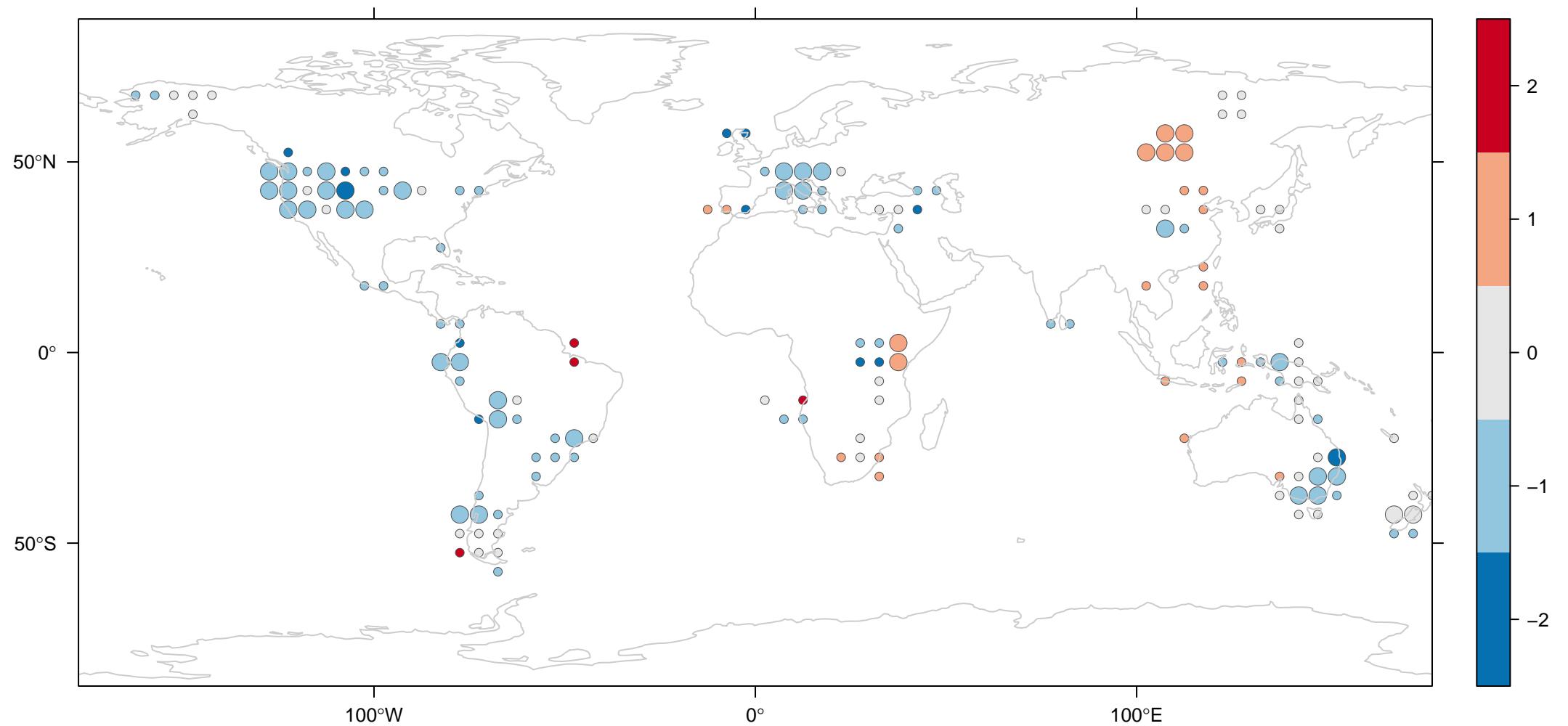
Number of sites per grid cell



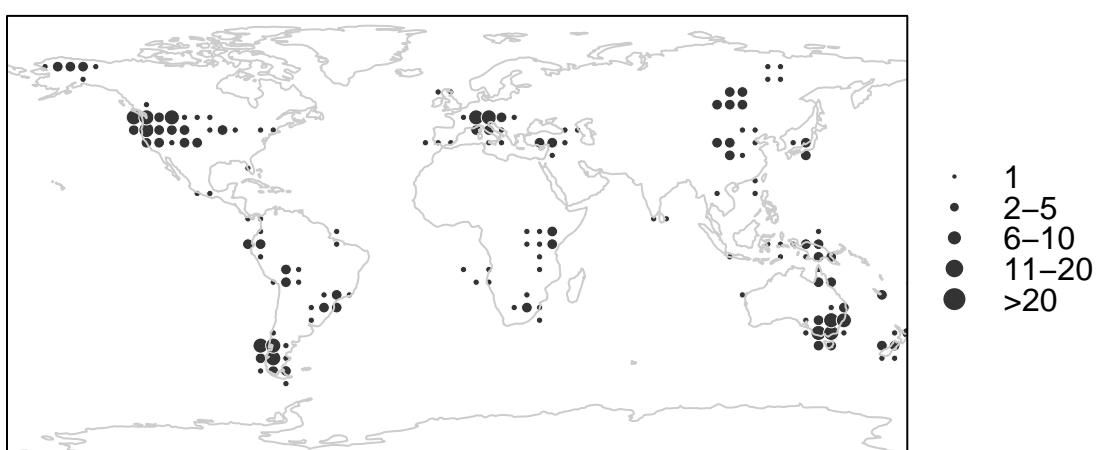
Number of grid cells influenced by each site



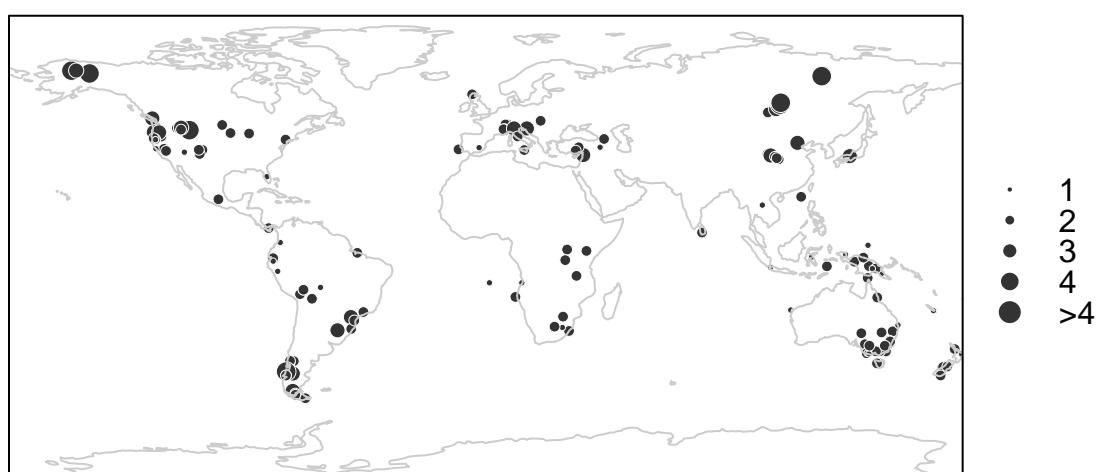
Charcoal Influx z-Scores: 13500–14500 BP



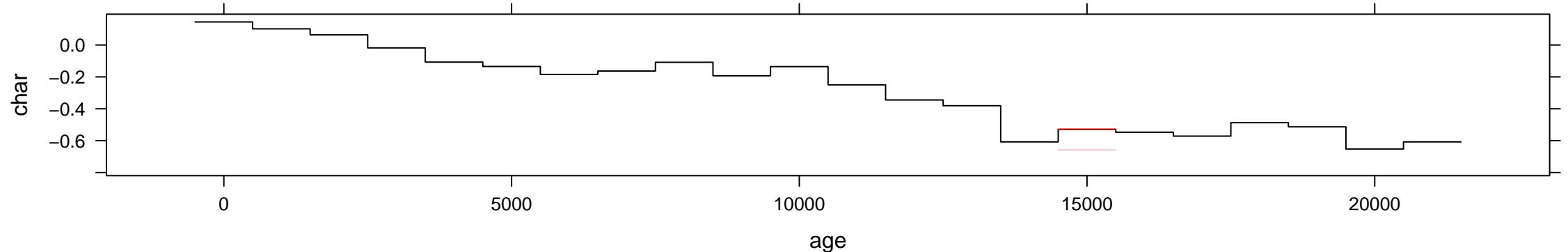
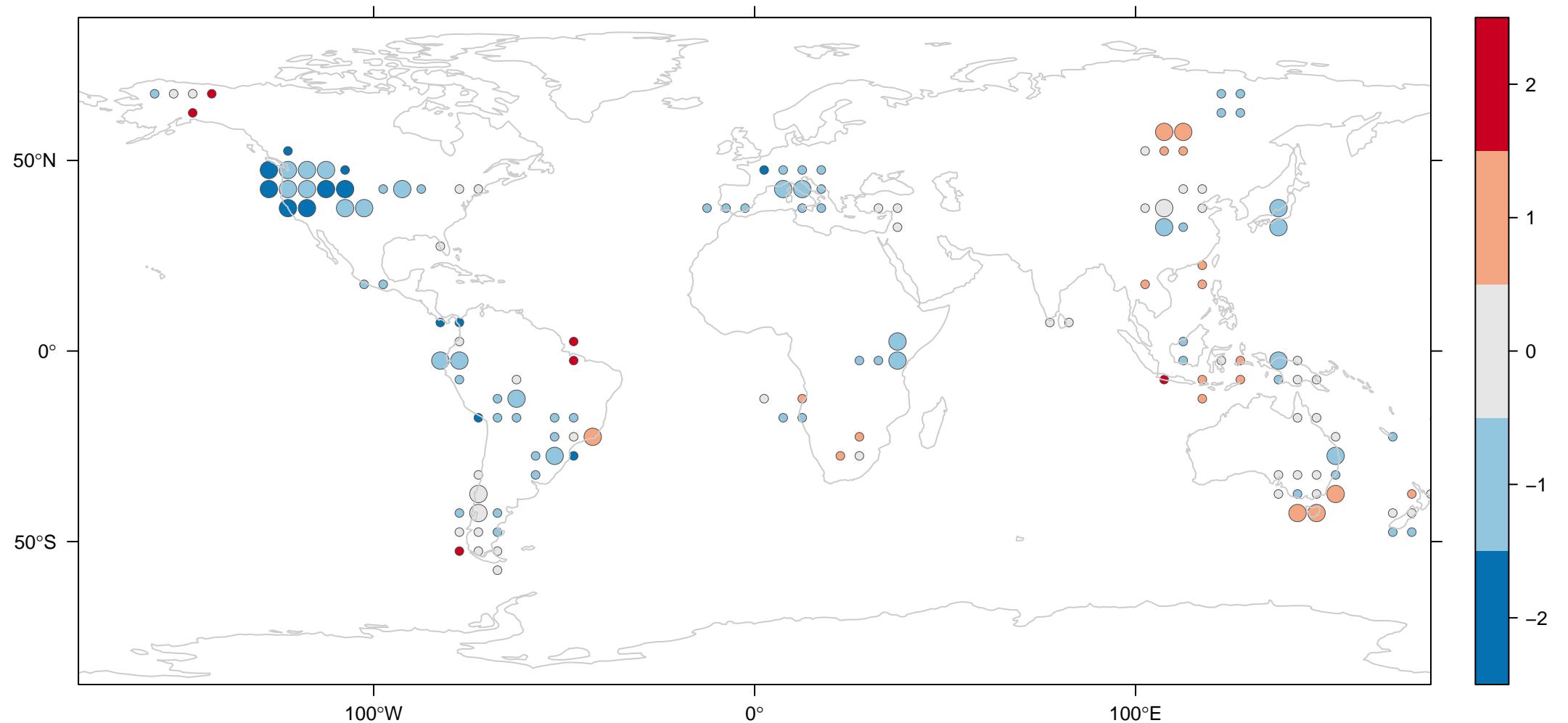
Number of sites per grid cell



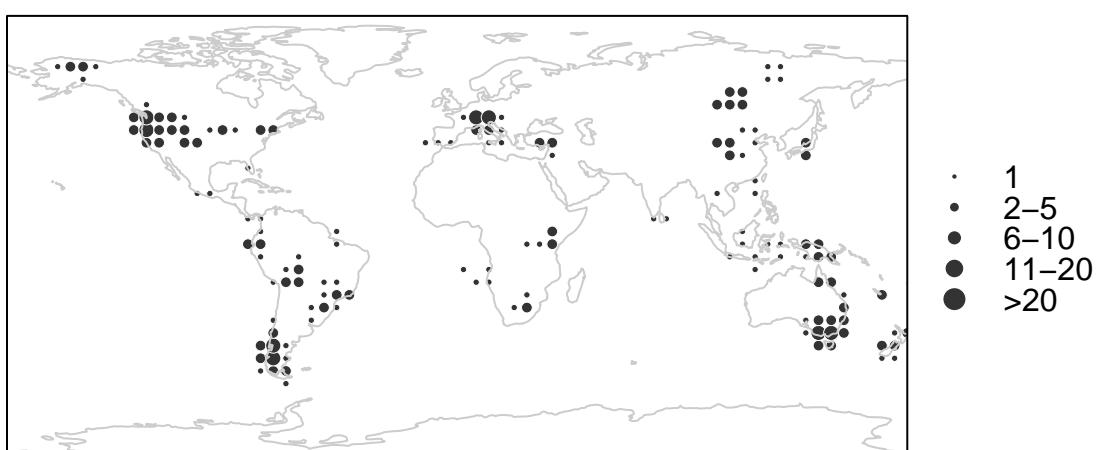
Number of grid cells influenced by each site



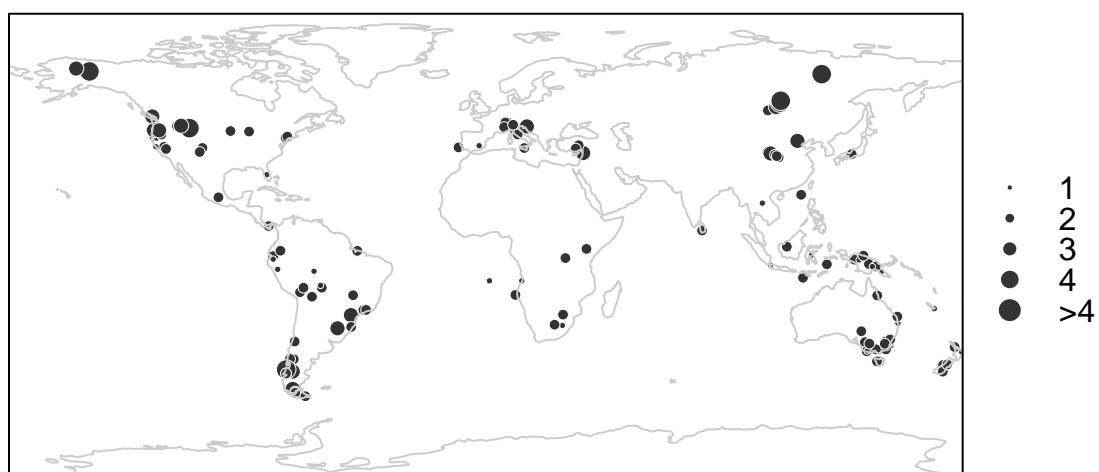
Charcoal Influx z-Scores: 14500–15500 BP



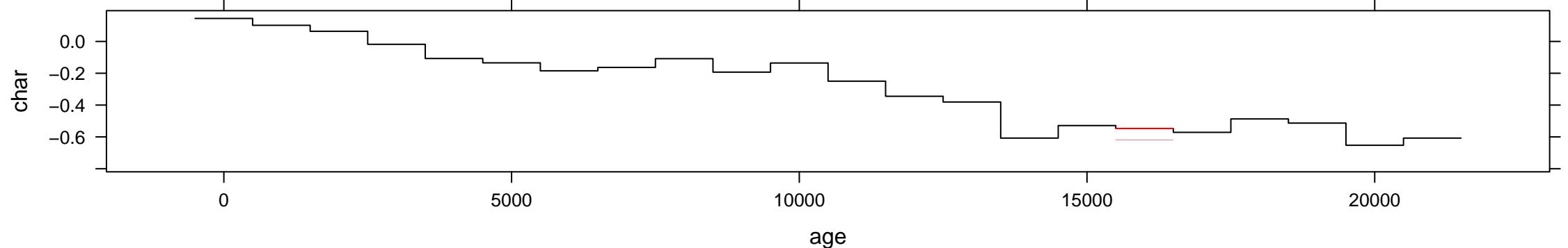
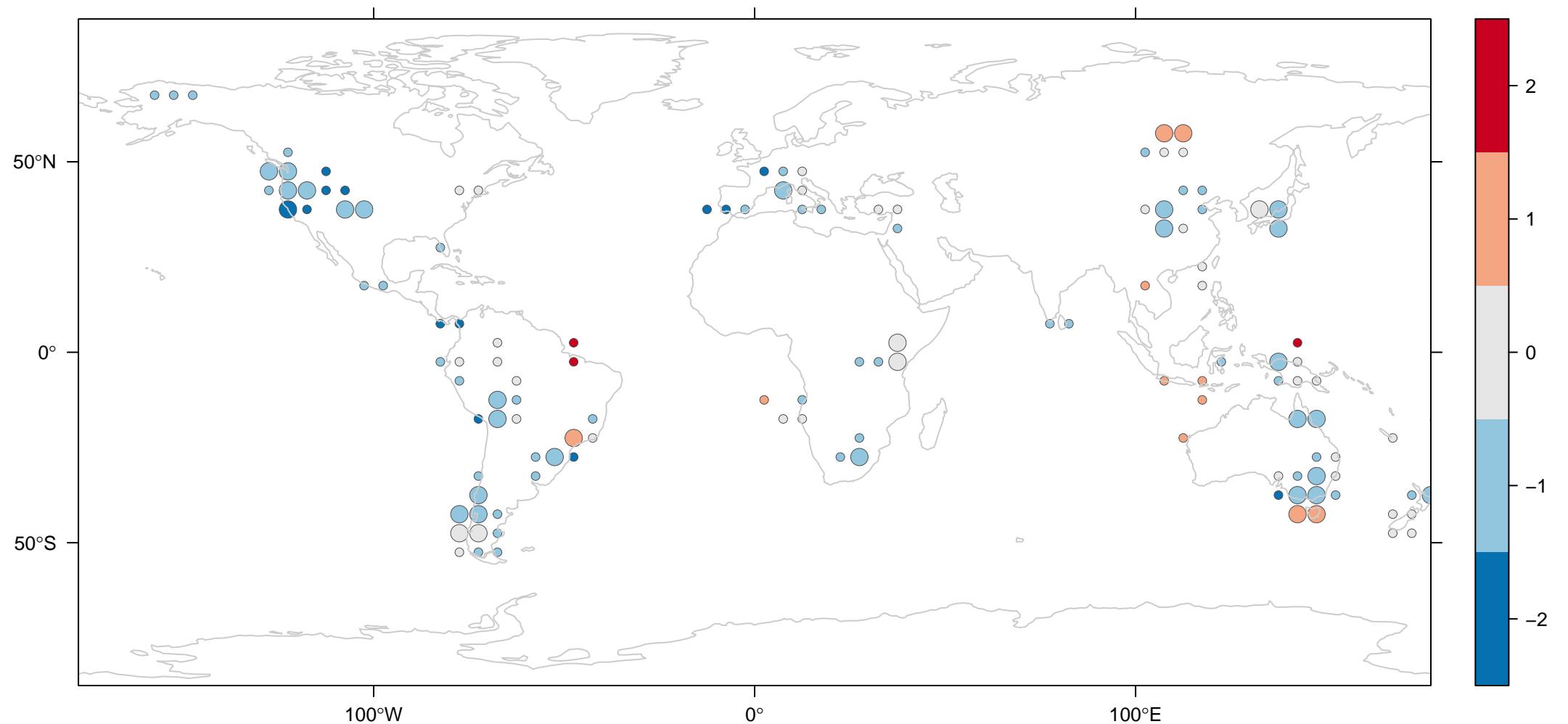
Number of sites per grid cell



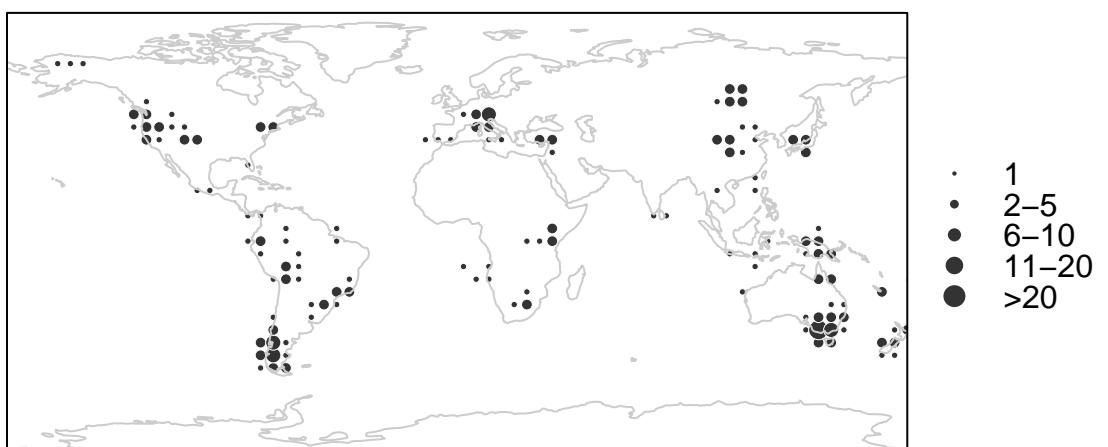
Number of grid cells influenced by each site



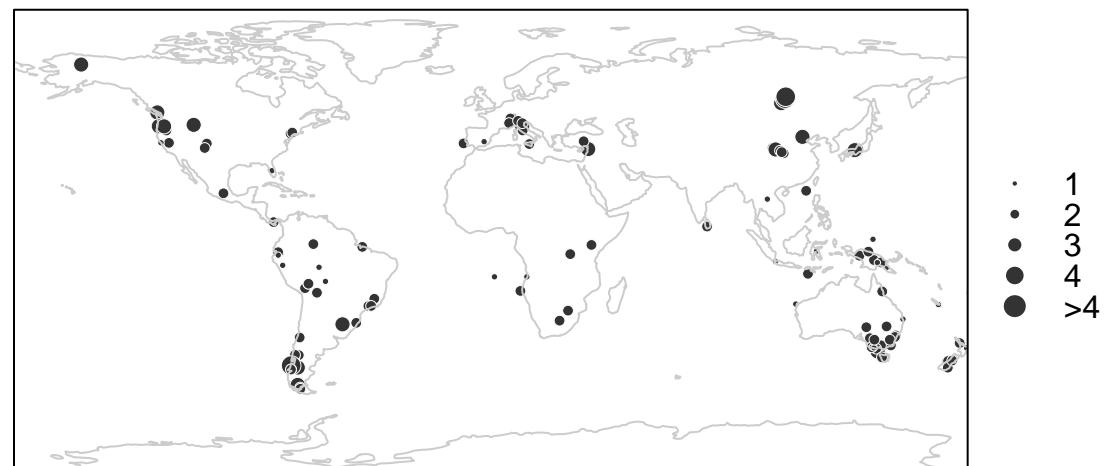
Charcoal Influx z-Scores: 15500–16500 BP



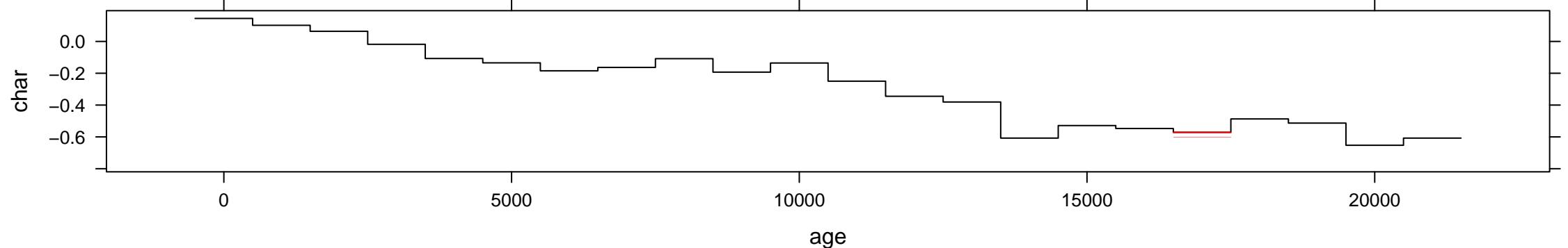
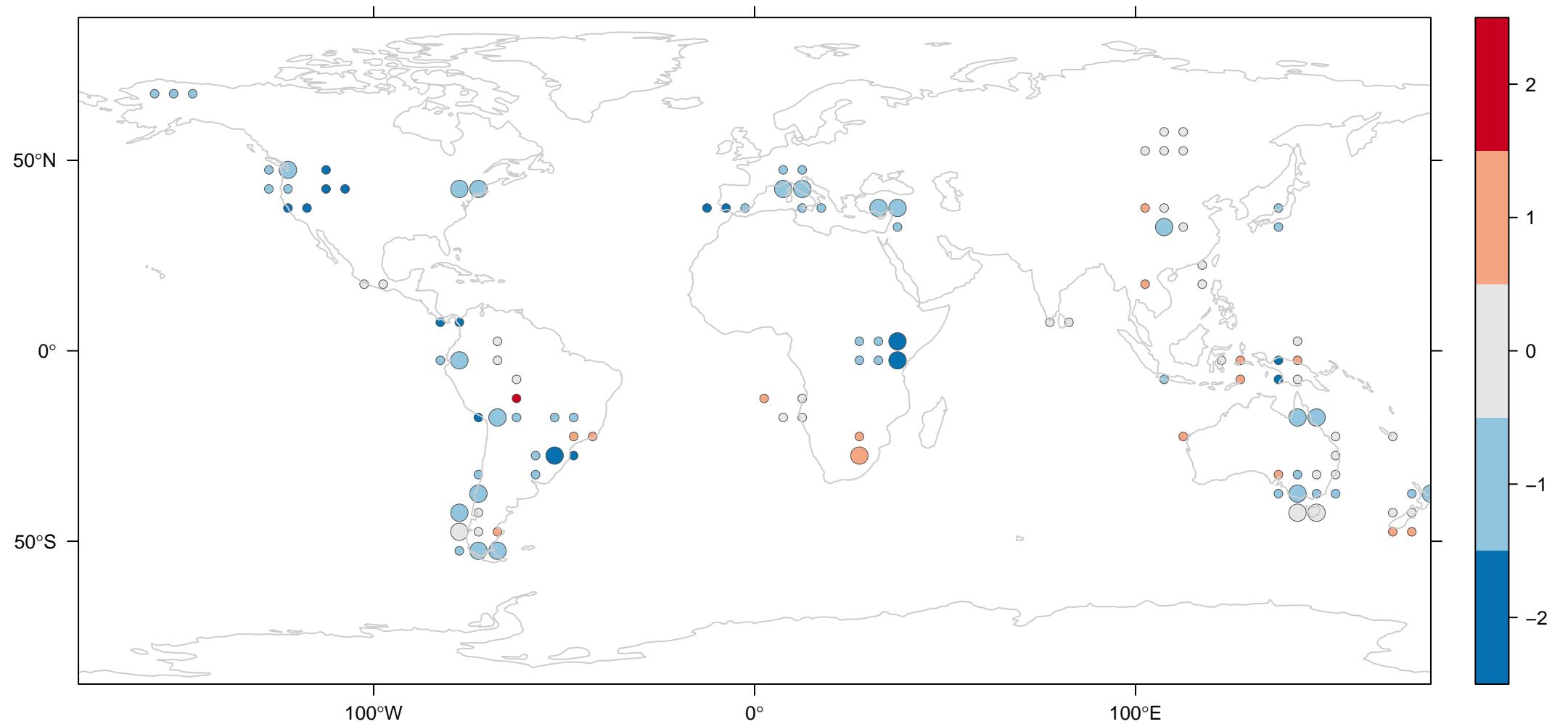
Number of sites per grid cell



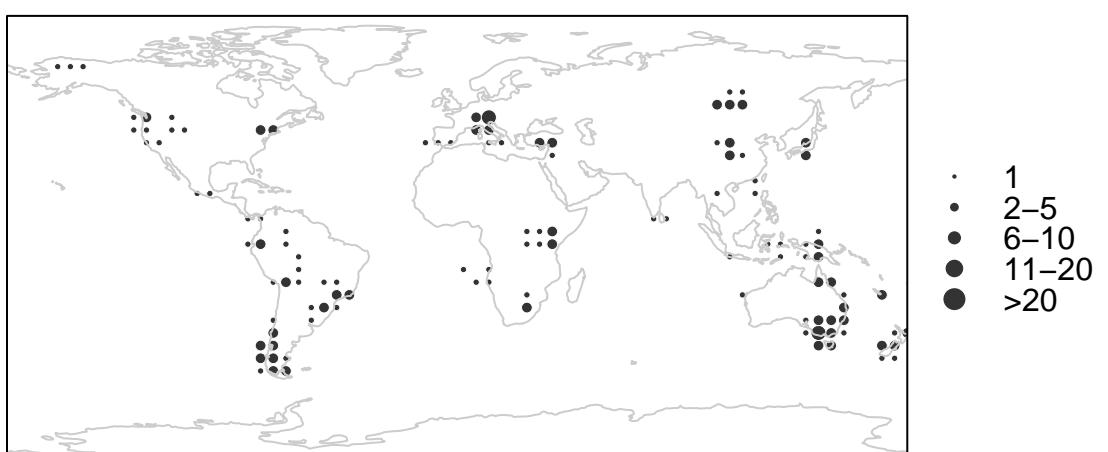
Number of grid cells influenced by each site



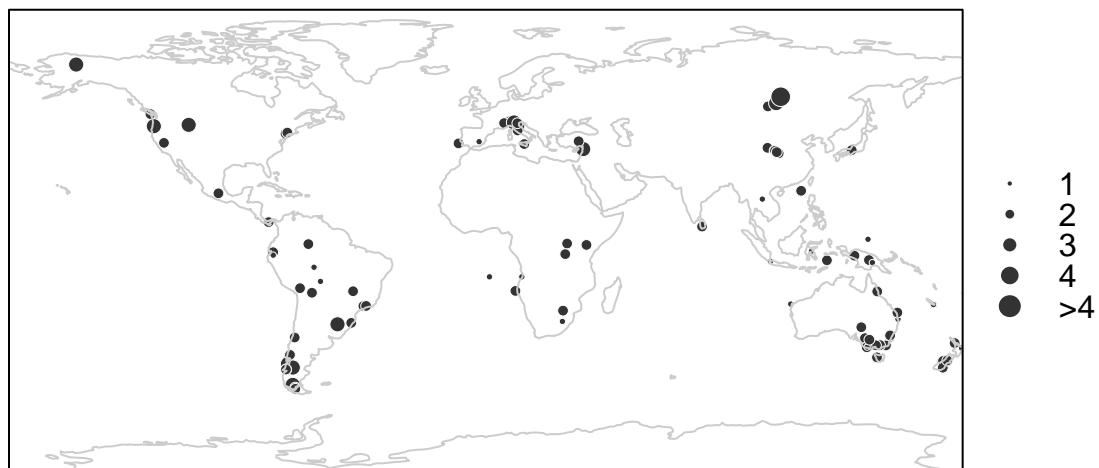
Charcoal Influx z-Scores: 16500–17500 BP



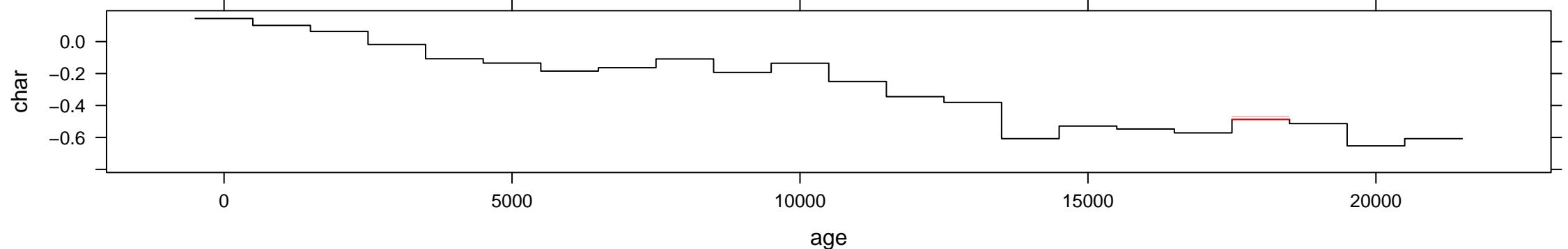
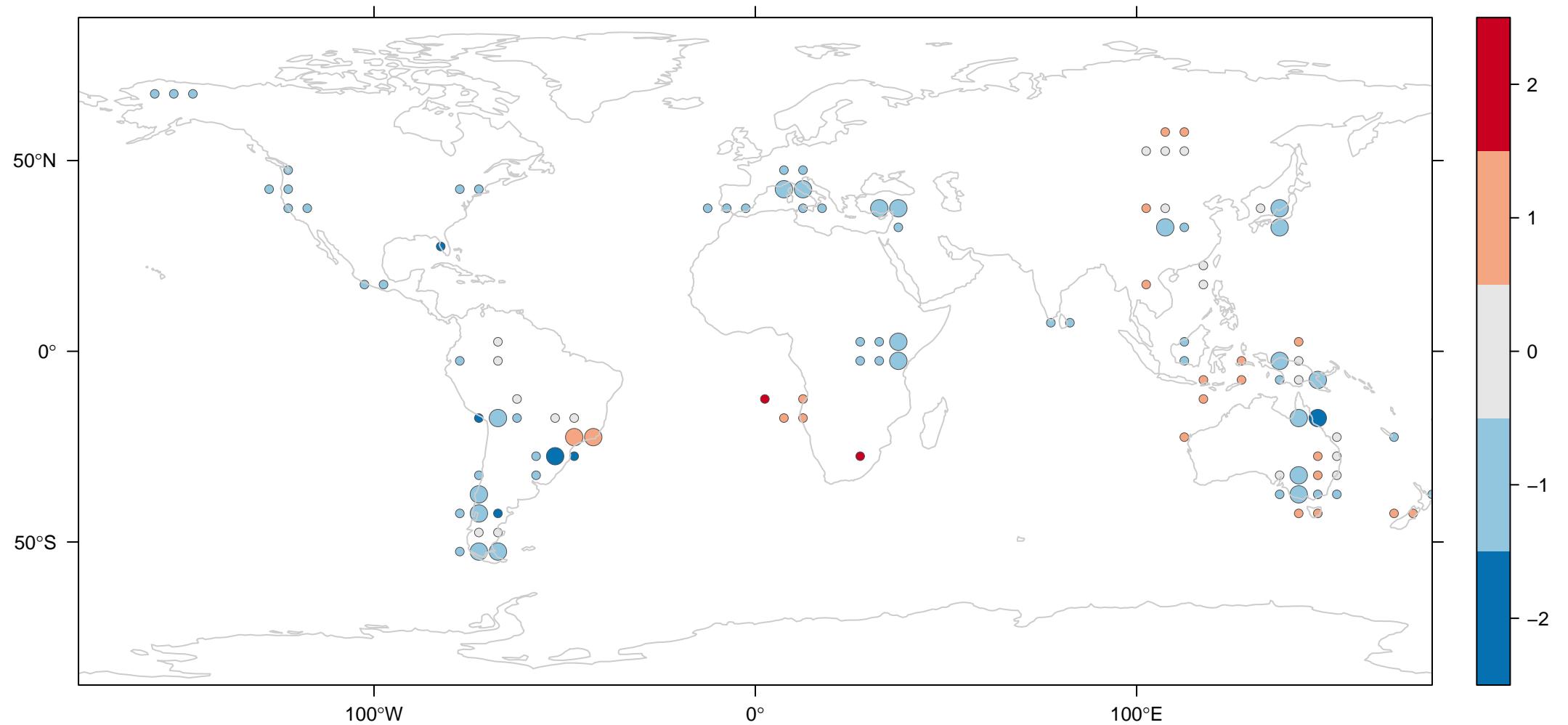
Number of sites per grid cell



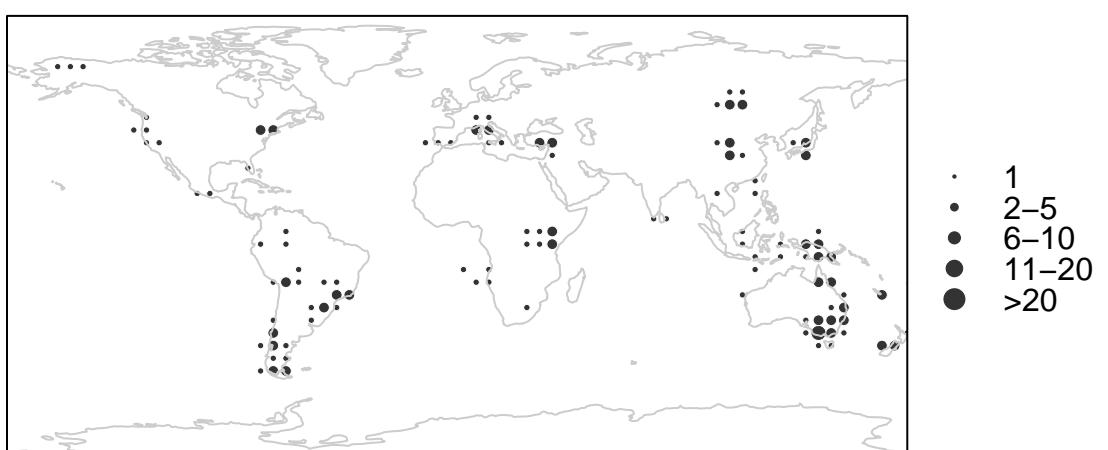
Number of grid cells influenced by each site



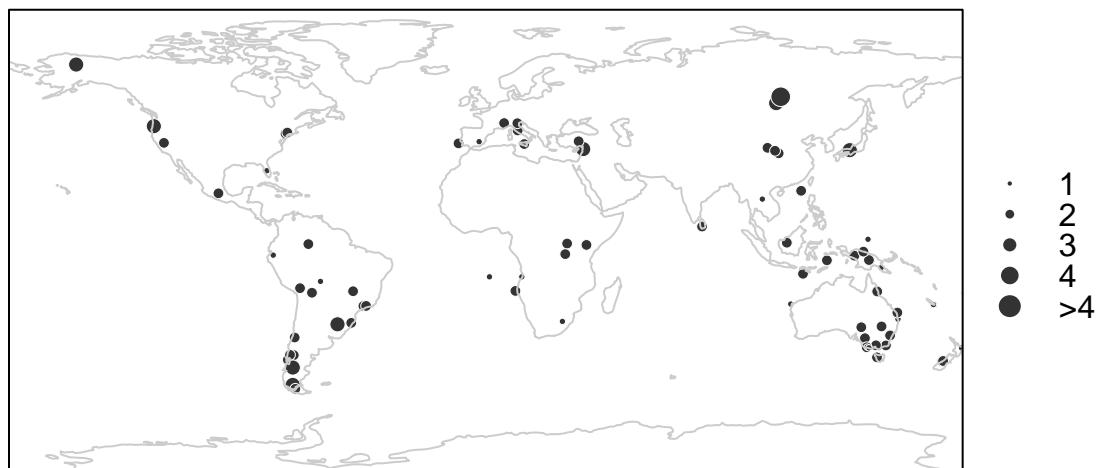
Charcoal Influx z-Scores: 17500–18500 BP



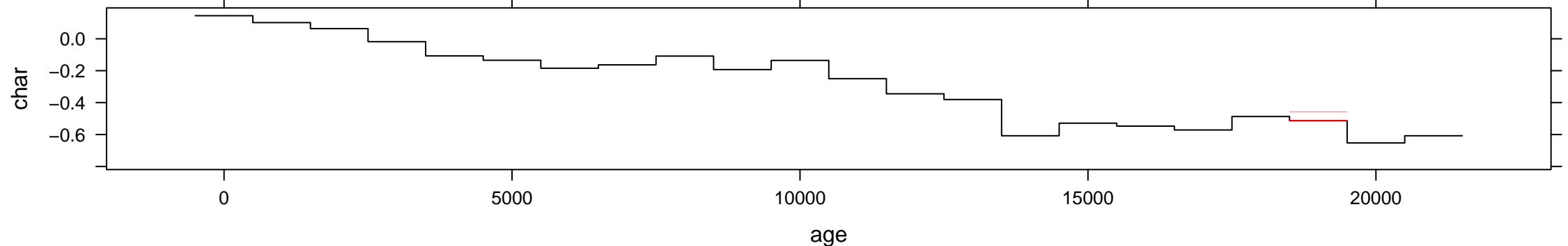
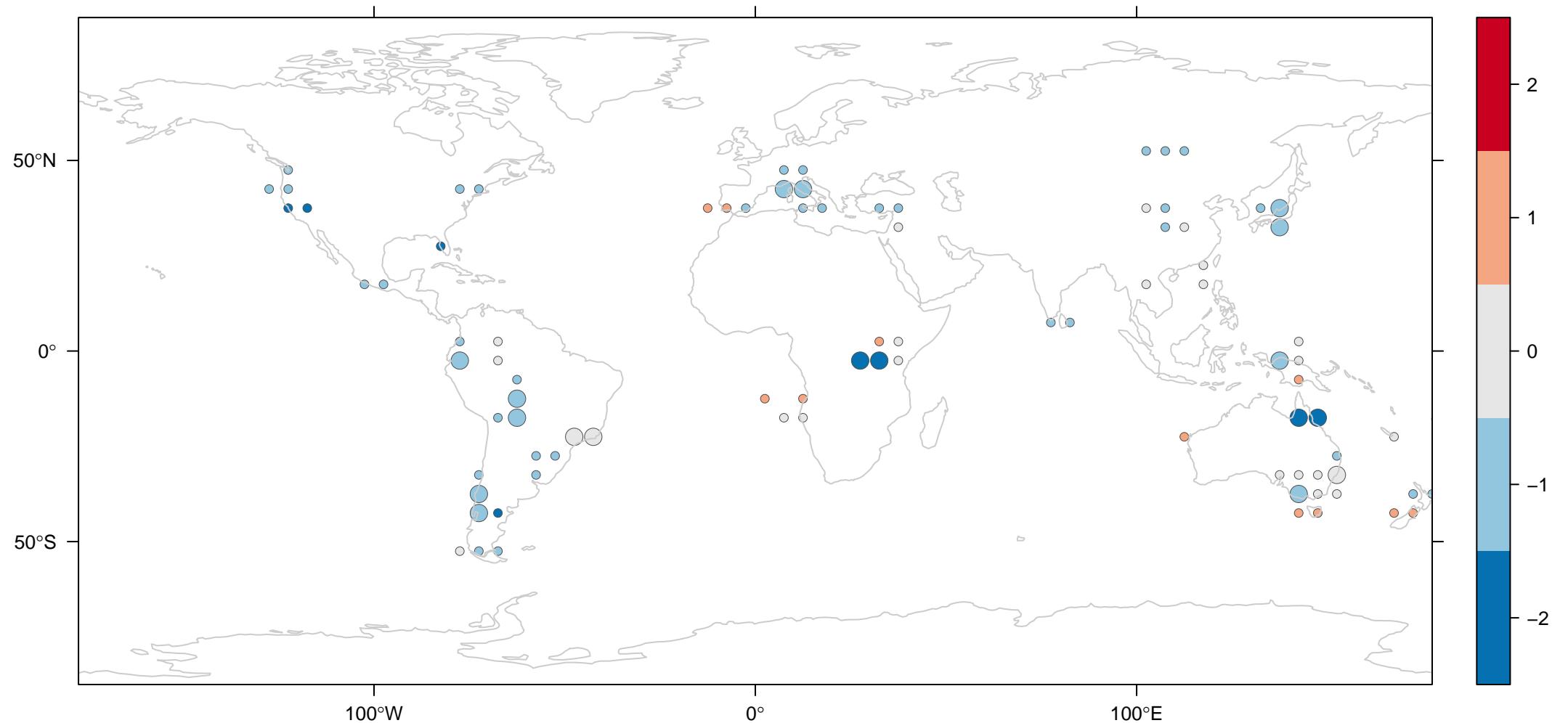
Number of sites per grid cell



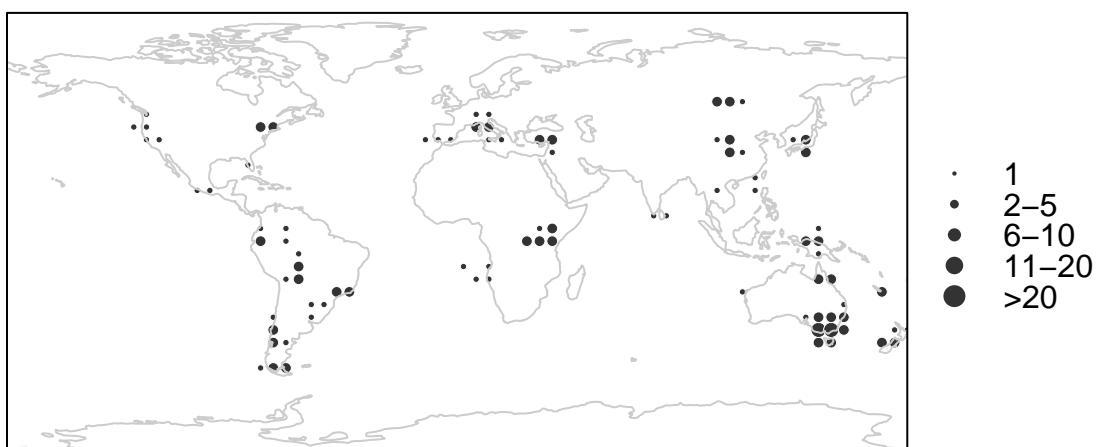
Number of grid cells influenced by each site



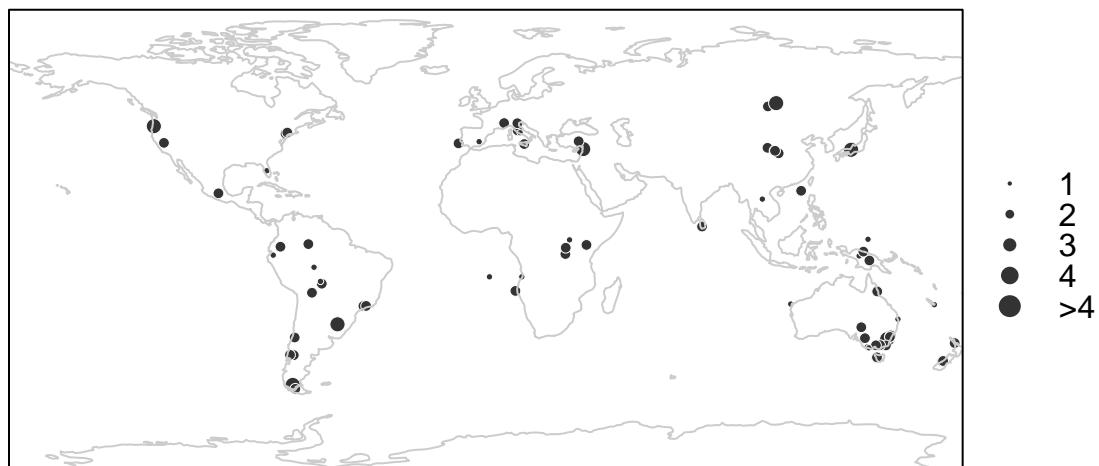
Charcoal Influx z-Scores: 18500–19500 BP



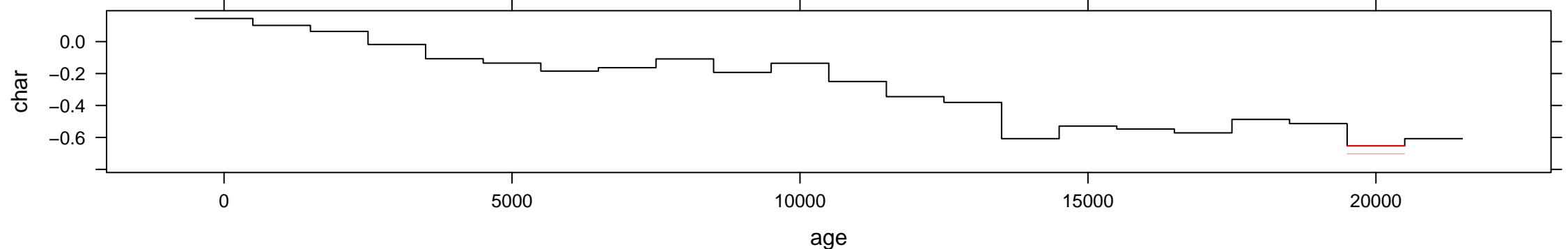
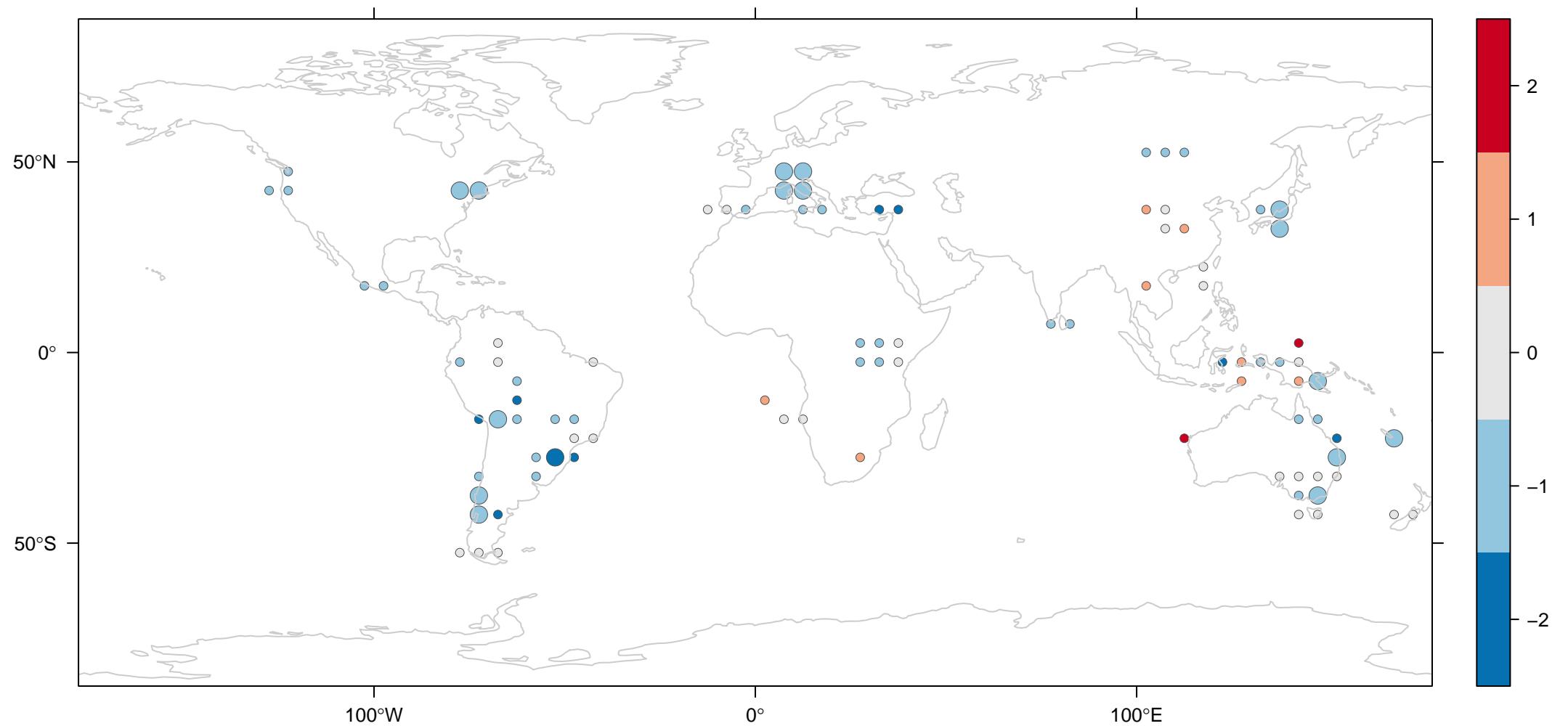
Number of sites per grid cell



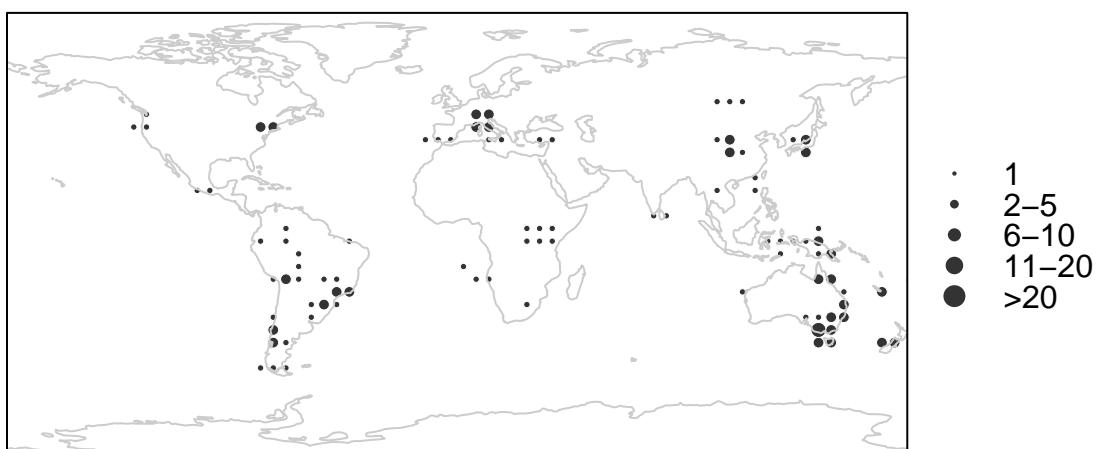
Number of grid cells influenced by each site



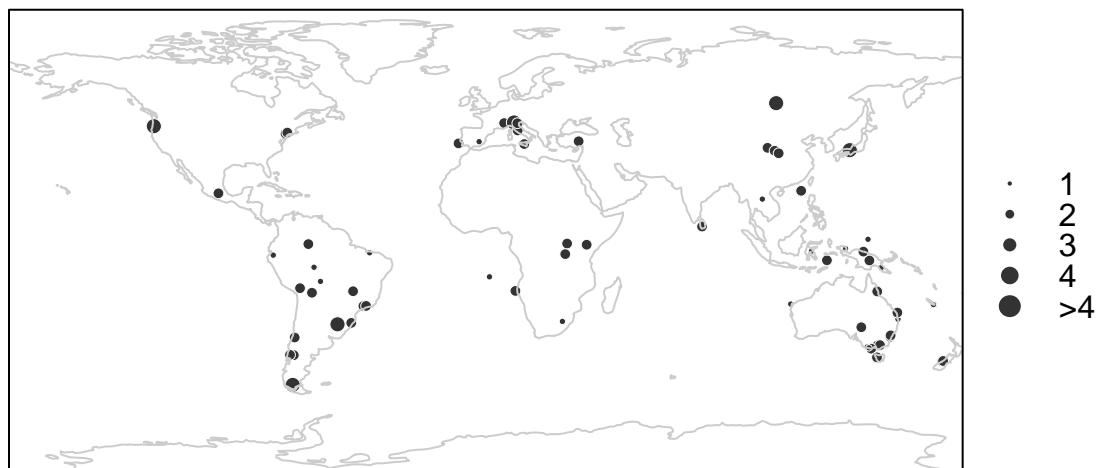
Charcoal Influx z-Scores: 19500–20500 BP



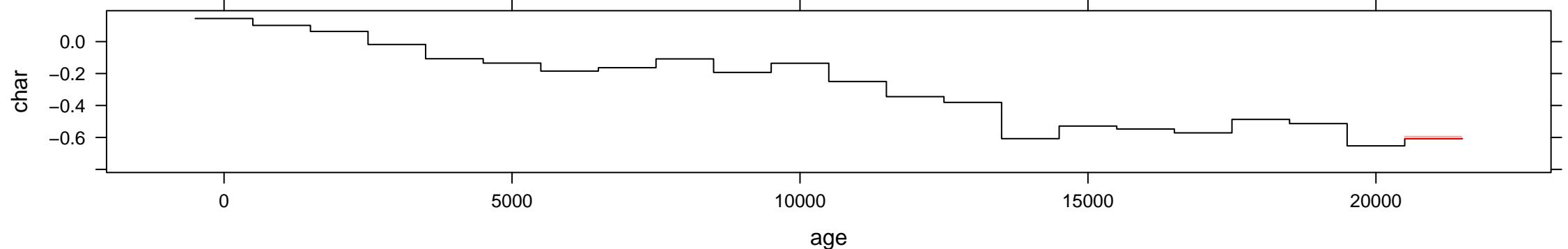
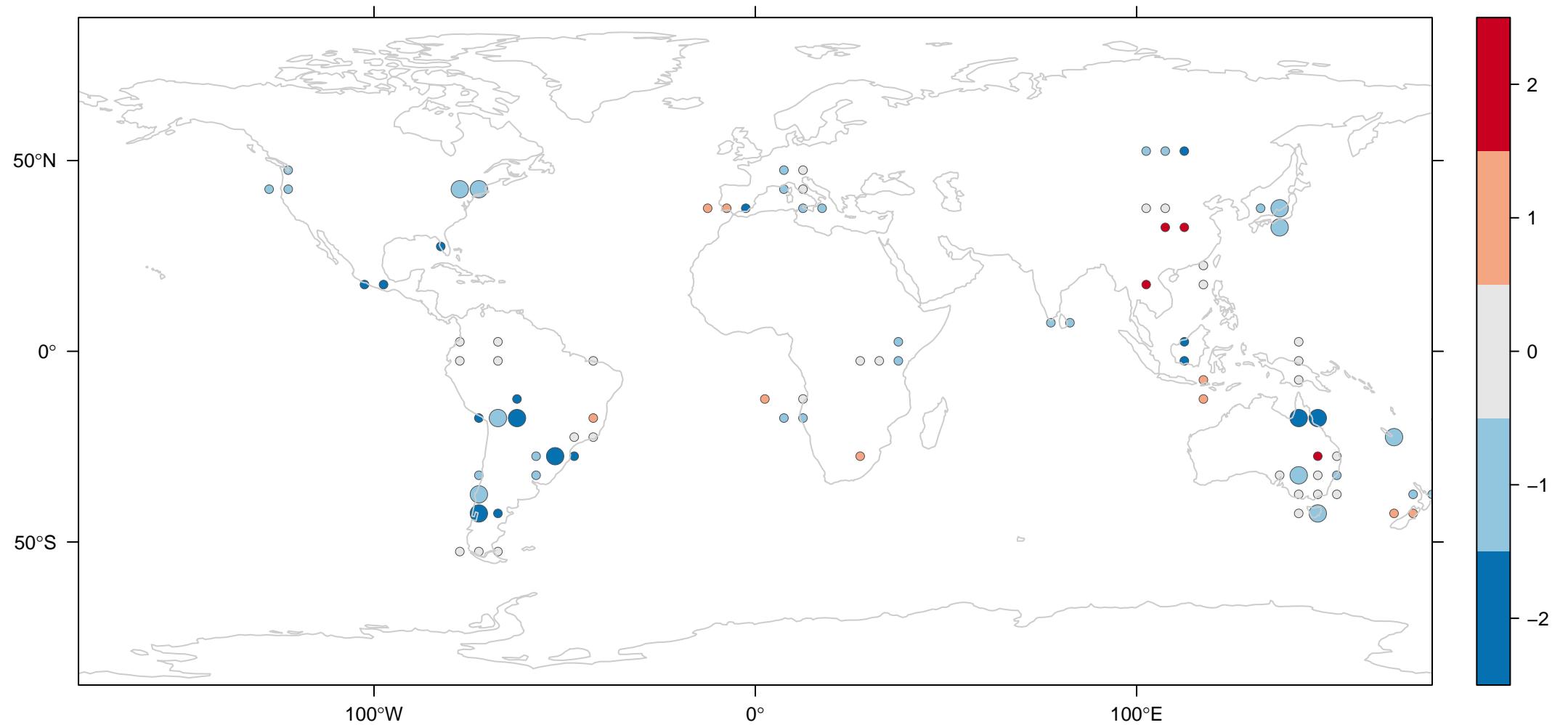
Number of sites per grid cell



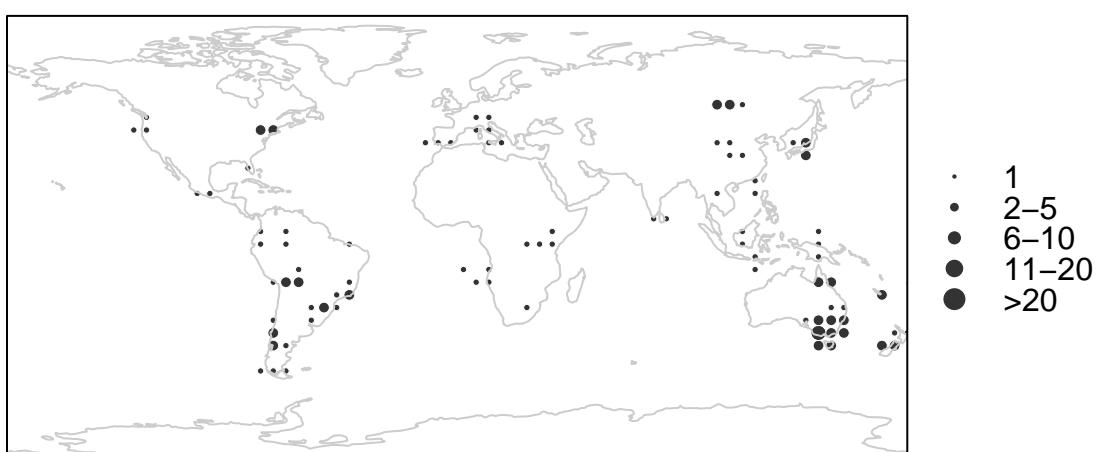
Number of grid cells influenced by each site



Charcoal Influx z-Scores: 20500–21500 BP



Number of sites per grid cell



Number of grid cells influenced by each site

