Q1: Are lake and terrestrial primary productivity coherent?

Jonathan Walter, Grace Wilkinson, Rachel Fleck, Michael Pace

4/17/2019

This document organizes for openness and reproducibility analyses of the temporal coherence of interannual variation in lake primary productivity with terrestrial primary productivity in the landscape surrounding the lake.

Data import

Data produced in 'ms1_prep.Rmd' are loaded.

```
load("/Users/jonathanwalter/Box Sync/NSF EAGER Synchrony/Data/RData files/ms1_analysis_inprogress1.RData
```

```
any(sapply(analysislakes$lakedata, function(x){any(is.infinite(x))}))
```

```
## [1] FALSE
```

```
any(sapply(analysislakes$lakedata, function(x){any(is.na(x))}))
```

```
## [1] TRUE
```

```
which(sapply(analysislakes$lakedata, function(x){any(is.na(x))}))
```

```
## 7545 7595 7790 7970 8271
##   74   75   77   81   82
```

```
analysislakes$lakeinfo[which(sapply(analysislakes$lakedata, function(x){any(is.na(x))})),]
```

```
##      lagoslakeid         gnis_name  nhd_lat  nhd_long lake_area_ha
## 7445        7545        Alton Pond 41.44294 -71.71835    17.843701
## 7495        7595         Long Pond 41.41031 -71.55334    16.879950
## 7689        7790     Watchaug Pond 41.38381 -71.69161   232.391660
## 7867        7970       Yawgoo Pond 41.51113 -71.57300    60.724131
## 8165        8271 Meadow Brook Pond 41.44110 -71.69034     9.808244
##      lake_perim_meters nhd_ftype hu4_zoneid start  end
## 7445          3746.121       390     HU4_10  1989 2010
## 7495          2751.178       390     HU4_10  1993 2010
## 7689          8397.096       390     HU4_10  1989 2010
## 7867          3195.857       390     HU4_10  1989 2010
## 8165          2030.864       390     HU4_10  1989 2010
```

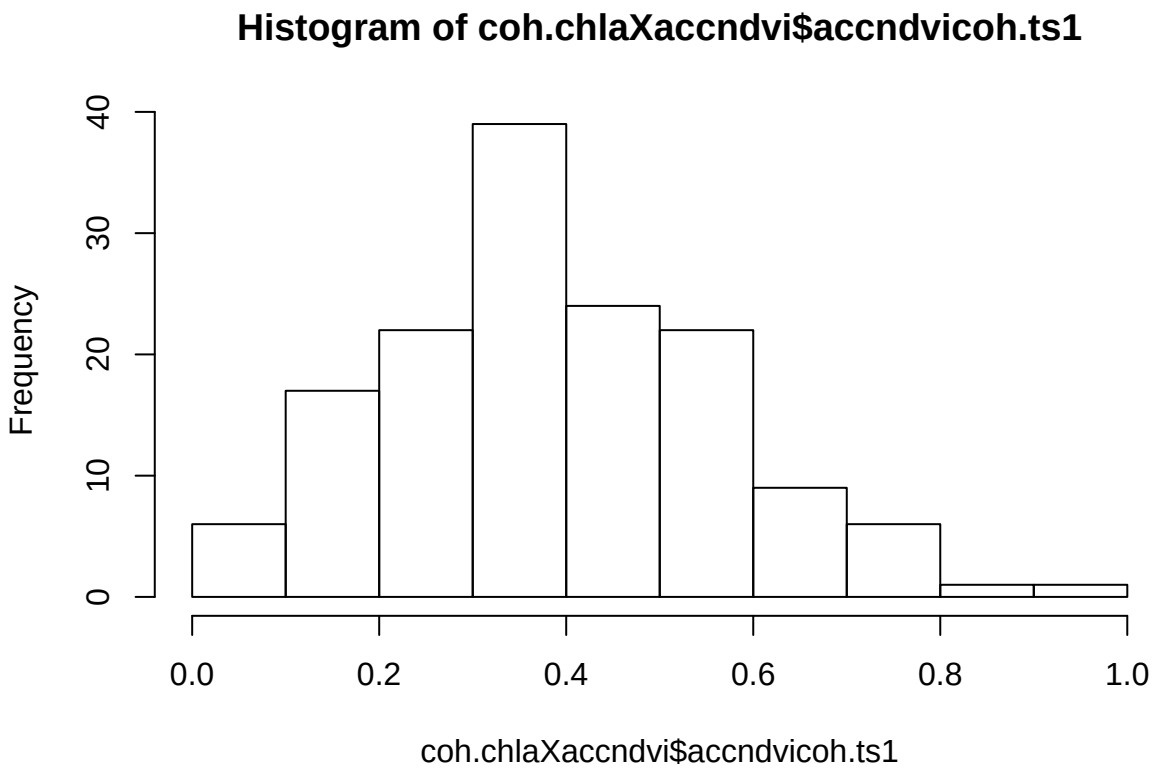
```
# image(accndvi)
# points(lakepts.prj[which(sapply(analysislakes$lakedata, function(x){any(is.na(x))})),])

dbuff[which(sapply(analysislakes$lakedata, function(x){any(is.na(x))}))]
```

```
## [1] 2500.000 2500.000 4939.589 2500.000 2500.000
```

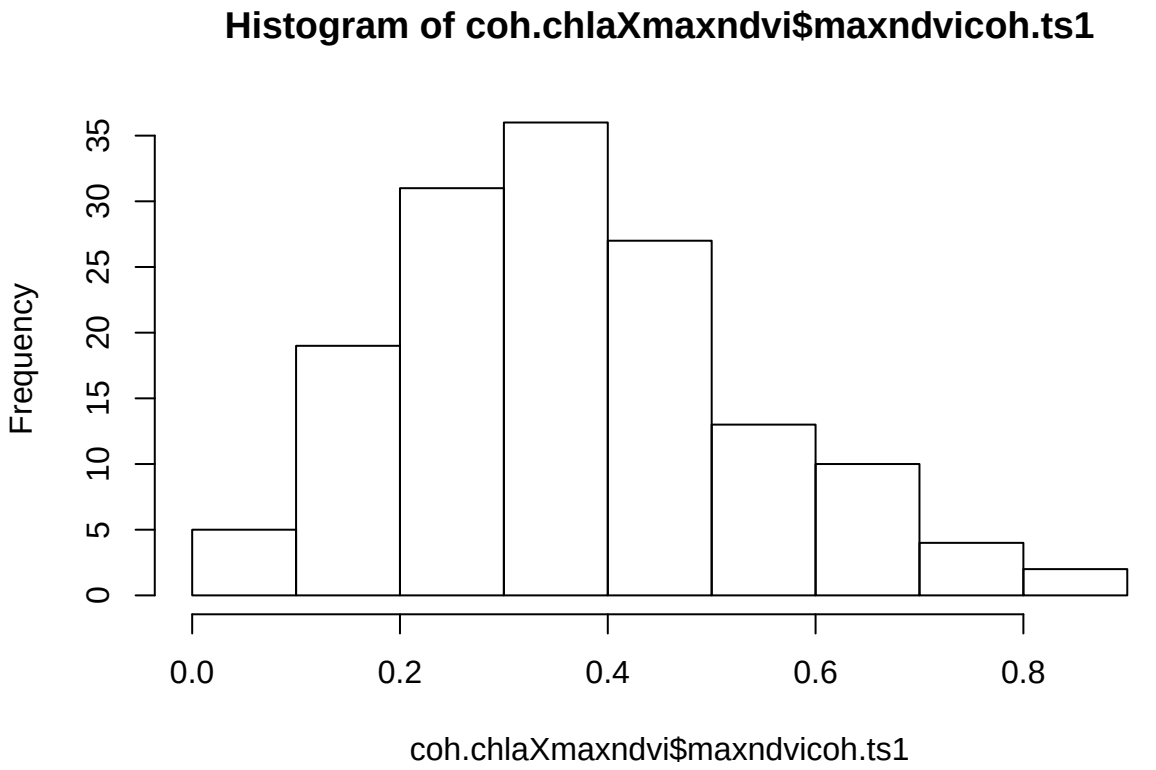
```
analysislakes$lakeinfo<-analysislakes$lakeinfo[!sapply(analysislakes$lakedata, function(x){any(is.na(x)
analysislakes$lakedata<-analysislakes$lakedata[!sapply(analysislakes$lakedata, function(x){any(is.na(x)
```

```r
source("~/GitHub/AquaTerrSynch/AnalysisCode/bandtest_coh.R")

tsranges<-rbind(c(2,4),c(4,Inf),c(2,Inf))

coh.chlaXaccndvi<-NULL
coh.chlaXmaxndvi<-NULL

for(lind in 1:length(analysislakes$lakedata)){
  lakedat.ii<-cleandat(analysislakes$lakedata[[lind]], as.numeric(colnames(analysislakes$lakedata[[lind]])), clev=1)
  chlaXaccndvi<-coh(lakedat.ii[1,], lakedat.ii[2,], as.numeric(colnames(analysislakes$lakedata[[lind]])),
                    norm="powall", sigmethod="fast", nrand=10000)
  chlaXmaxndvi<-coh(lakedat.ii[1,], lakedat.ii[3,], as.numeric(colnames(analysislakes$lakedata[[lind]])),
                    norm="powall", sigmethod="fast", nrand=10000)
  for(rind in 1:nrow(tsranges)){
    chlaXaccndvi<-bandtest.coh(chlaXaccndvi, tsranges[rind,])
    chlaXmaxndvi<-bandtest.coh(chlaXmaxndvi, tsranges[rind,])
  }
  coh.chlaXaccndvi<-rbind(coh.chlaXaccndvi, c(t(as.matrix(chlaXaccndvi$bandp[,3:5]))))
  coh.chlaXmaxndvi<-rbind(coh.chlaXmaxndvi, c(t(as.matrix(chlaXmaxndvi$bandp[,3:5]))))

}

coh.chlaXaccndvi<-as.data.frame(coh.chlaXaccndvi)
coh.chlaXmaxndvi<-as.data.frame(coh.chlaXmaxndvi)

colnames(coh.chlaXaccndvi)<-paste0("accndvi",c("p.ts1","phi.ts1","coh.ts1","p.ts2","phi.ts2","coh.ts2","
colnames(coh.chlaXmaxndvi)<-paste0("maxndvi",c("p.ts1","phi.ts1","coh.ts1","p.ts2","phi.ts2","coh.ts2","

coh.chlaXaccndvi$lagoslakeid<-analysislakes$lakeinfo$lagoslakeid
coh.chlaXmaxndvi$lagoslakeid<-analysislakes$lakeinfo$lagoslakeid
```

```r
#short timescales
hist(coh.chlaXaccndvi$accndvicoh.ts1)
```




```
hist(coh.chlaXmaxndvi$maxndvicoh.ts1)
```




```
quantile(coh.chlaXaccndvi$accndvip.ts1)
```

```
##          0%         25%         50%         75%        100%
## 0.00019998 0.25027497 0.46055394 0.69833017 0.99740026
```

```r
quantile(coh.chlaXmaxndvi$maxndvip.ts1)
```

```
##          0%         25%         50%         75%        100%
## 0.00479952 0.26997300 0.52324768 0.78762124 0.97940206
```

```r
alpha=0.05
sum(coh.chlaXaccndvi$accndvip.ts1<alpha)/nrow(coh.chlaXaccndvi)
```

```
## [1] 0.06802721
```

```r
sum(coh.chlaXmaxndvi$maxndvip.ts1<alpha)/nrow(coh.chlaXmaxndvi)
```

```
## [1] 0.03401361
```

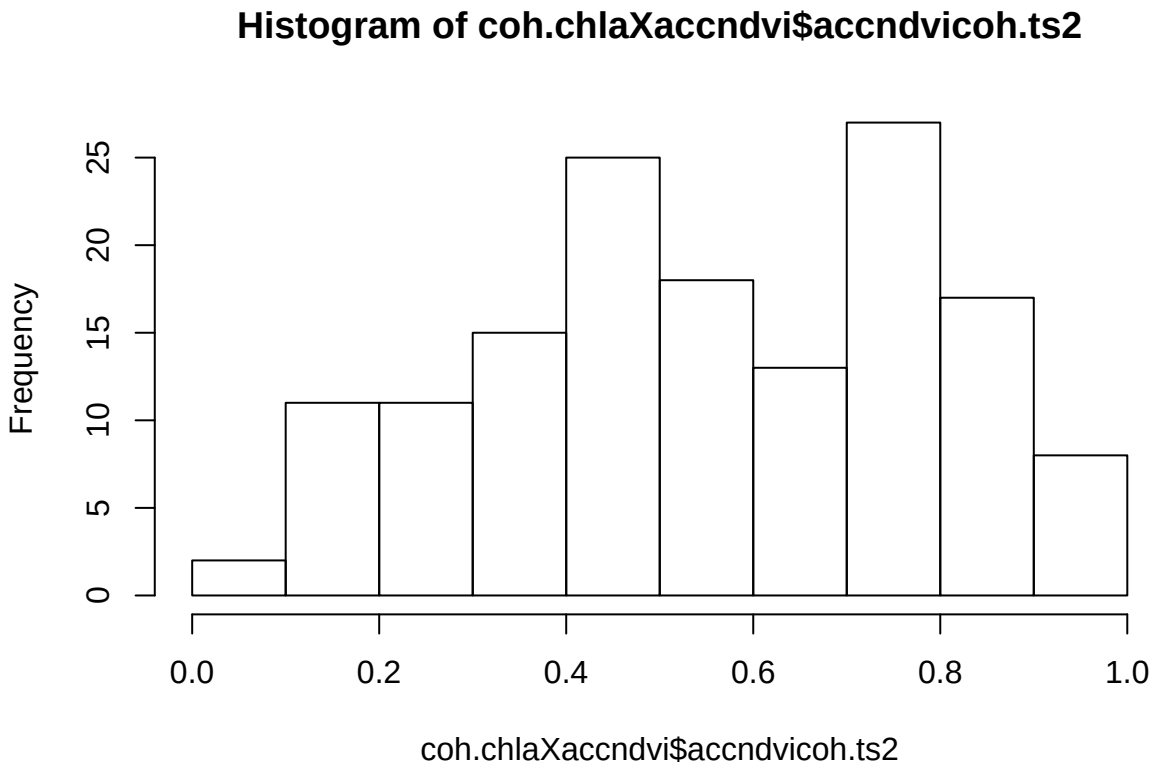
```r
print(coh.chlaXaccndvi$accndviphi.ts1[coh.chlaXaccndvi$accndvip.ts1<alpha]/pi) #only pattern is that la
```

```
##  [1] -0.69355770  0.97567765  0.84577293 -0.76068035 -0.10346014
##  [6]  0.05131054 -0.60744627 -0.56248178 -0.15437429 -0.63997328
```

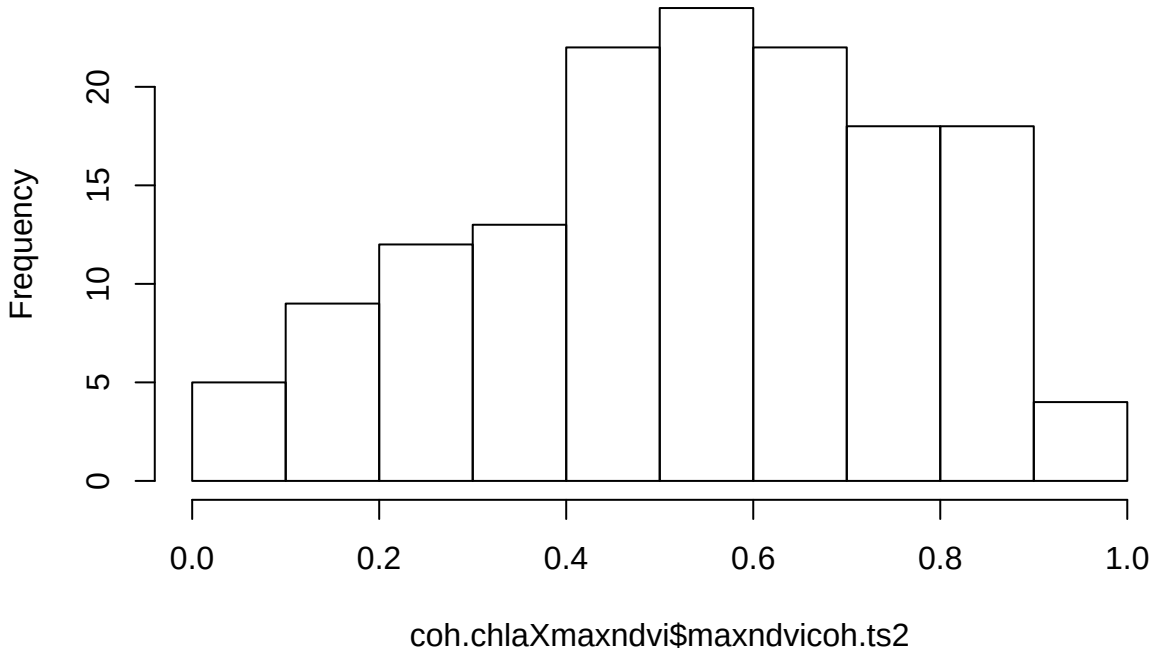
```r
print(coh.chlaXmaxndvi$maxndviphi.ts1[coh.chlaXmaxndvi$maxndvip.ts1<alpha]/pi)
```

```
## [1]  0.3030499  0.1624359 -0.9406033 -0.5034587 -0.8338166
```

```r
#long timescales
hist(coh.chlaXaccndvi$accndvicoh.ts2)
```




```r
hist(coh.chlaXmaxndvi$maxndvicoh.ts2)
```




```
quantile(coh.chlaXaccndvi$accndvip.ts2)
```

```
##         0%        25%        50%        75%       100%
## 0.00009999 0.20827917 0.48555144 0.75567443 0.97870213
```

```
quantile(coh.chlaXmaxndvi$maxndvip.ts2)
```

```
##         0%        25%        50%        75%       100%
## 0.00229977 0.17243276 0.43605639 0.76277372 0.99880012
```

```
alpha=0.05
sum(coh.chlaXaccndvi$accndvip.ts2<alpha)/nrow(coh.chlaXaccndvi)
```

```
## [1] 0.1156463
```

```
sum(coh.chlaXmaxndvi$maxndvip.ts2<alpha)/nrow(coh.chlaXmaxndvi)
```

```
## [1] 0.08843537
```

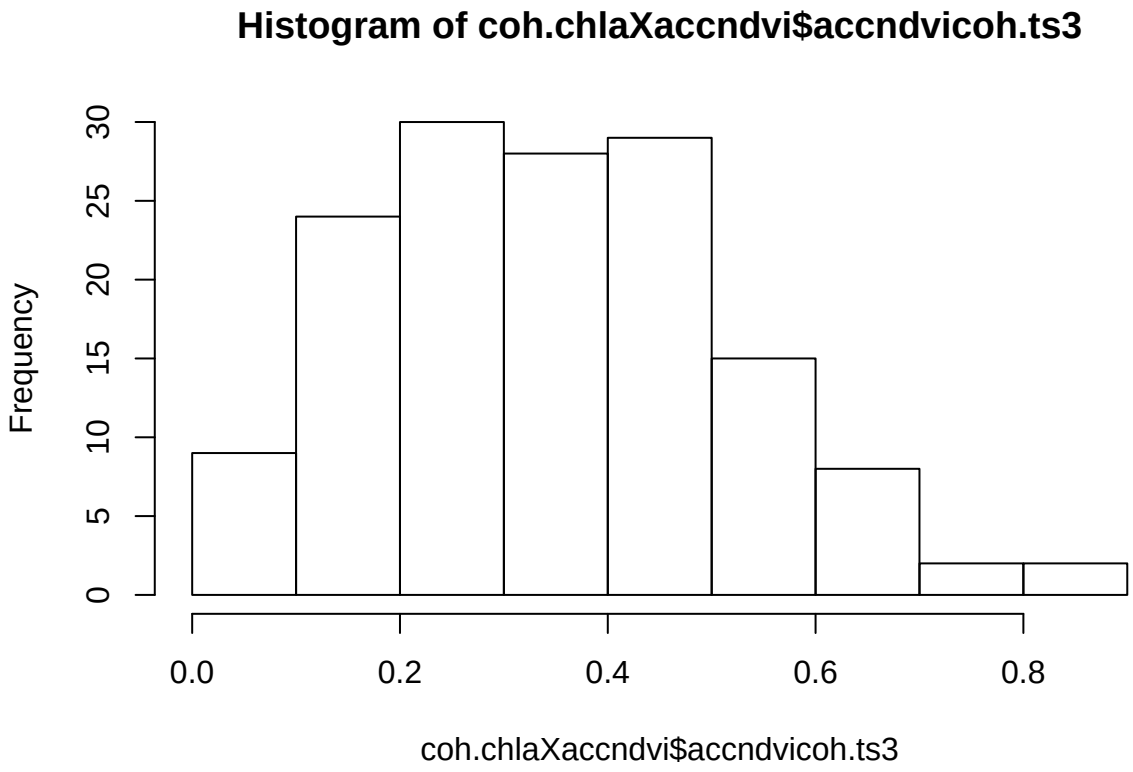
```
print(coh.chlaXaccndvi$accndviphi.ts2[coh.chlaXaccndvi$accndvip.ts2<alpha]/pi)
```

```
##  [1]  0.73992662 -0.90124264  0.53888310  0.27521830 -0.95606597
##  [6]  0.52712388  0.66512195 -0.68599147 -0.91773670 -0.29662433
## [11] -0.10820287 -0.40541240 -0.22793834 -0.04840174 -0.57269988
## [16] -0.52827164  0.88106993
```

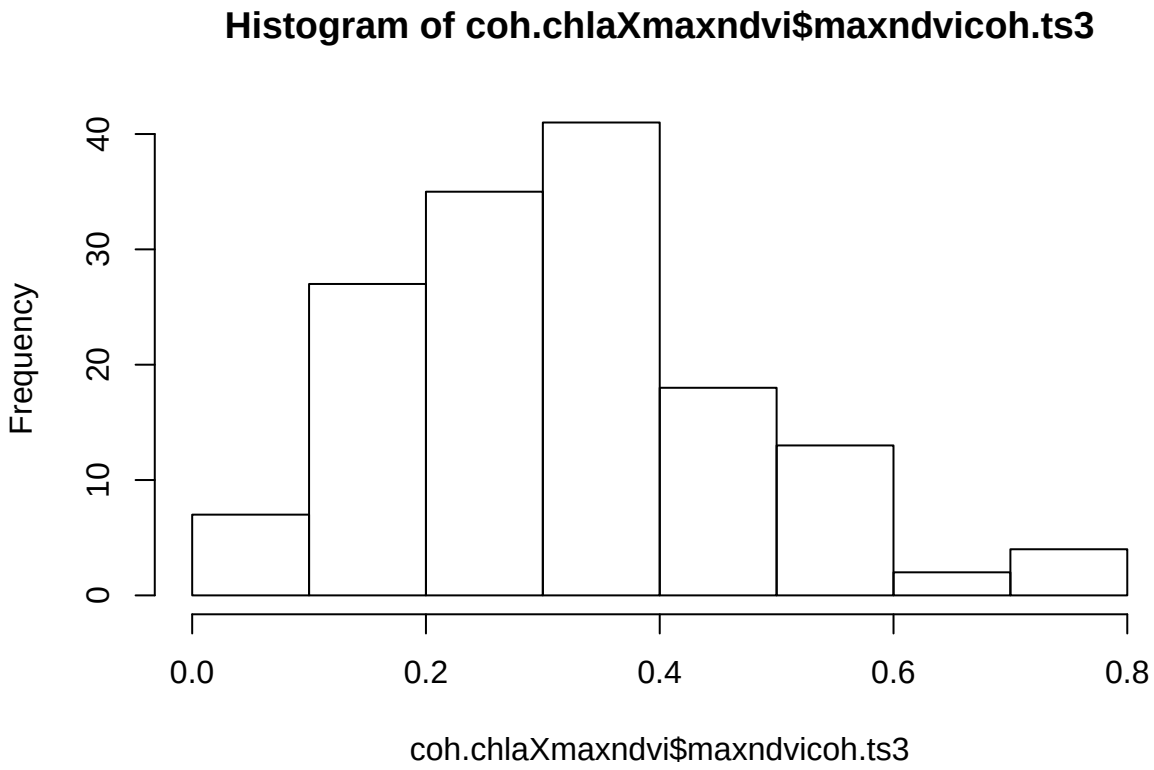
```
print(coh.chlaXmaxndvi$maxndviphi.ts2[coh.chlaXmaxndvi$maxndvip.ts2<alpha]/pi)
```

```
##  [1]  0.70551340 -0.52165283  0.31832221  0.08039247  0.71001377
##  [6] -0.31901830  0.06889035  0.75090709 -0.34232190 -0.47848554
## [11]  0.53740894  0.27725948  0.84338040
```

```
#all timescales
hist(coh.chlaXaccndvi$accndvicoh.ts3)
```




```
hist(coh.chlaXmaxndvi$maxndvicoh.ts3)
```




```
quantile(coh.chlaXaccndvi$accndvip.ts3)
```

```
##          0%         25%         50%         75%        100%
## 0.00009999 0.20057994 0.47875212 0.71967803 0.98090191
```

```r
quantile(coh.chlaXmaxndvi$maxndvip.ts3)
```

```
##          0%         25%         50%         75%        100%
## 0.00359964 0.22062794 0.47805219 0.72887711 0.99270073
```

```r
alpha=0.05
sum(coh.chlaXaccndvi$accndvip.ts3<alpha)/nrow(coh.chlaXaccndvi)
```

```
## [1] 0.06122449
```

```r
sum(coh.chlaXmaxndvi$maxndvip.ts3<alpha)/nrow(coh.chlaXmaxndvi)
```

```
## [1] 0.04761905
```

```r
print(coh.chlaXaccndvi$accndviphi.ts3[coh.chlaXaccndvi$accndvip.ts3<alpha]/pi)
```

```
## [1]  0.8639992  0.8479284  0.5604227  0.7201726 -0.3225463 -0.4610452
## [7] -0.3272096 -0.5351952 -0.2557062
```

```r
print(coh.chlaXmaxndvi$maxndviphi.ts3[coh.chlaXmaxndvi$maxndvip.ts3<alpha]/pi)
```

```
## [1]  0.5354322 -0.5225891  0.5079395  0.3106531 -0.2093039  0.5093530
## [7]  0.8755260
```

```r
#Need to add: depth, average growing season Chlorophyll-a, TSI(chla) categories, pct ag

#agriculture -- is 500m buffer best? Other options include 100m buffer (probably too small) and hu12 wa
pct.ag<-lagosne_select(table="buffer500m.lulc", vars=c("lagoslakeid","buffer500m_nlcd2001_pct_82","buff
pct.ag<-pct.ag[pct.ag$lagoslakeid %in% analysislakes$lakeinfo$lagoslakeid,]
pct.ag.avg<-data.frame(lagoslakeid=pct.ag$lagoslakeid, pct.ag=rowMeans(pct.ag[,2:4]))

#depth
depth<-lagosne_select(table="lakes_limno", vars=c("lagoslakeid","maxdepth"))
depth<-depth[depth$lagoslakeid %in% analysislakes$lakeinfo$lagoslakeid,] #use max depth because it's mo

#growing season Chlorophyll-a
chla<-lagosne_select(table="epi_nutr", vars=c("lagoslakeid","samplemonth","chla"))
chla<-chla[chla$lagoslakeid %in% analysislakes$lakeinfo$lagoslakeid,]
gs.chla<-chla[chla$samplemonth %in% 5:9,]
avg.chla<-aggregate(chla ~ lagoslakeid, data=gs.chla, FUN=mean, na.rm=T)

#Chlorophyll-a TSI class
#TSI(CHL) = 9.81 ln(CHL) + 30.6
tsi.chl<-data.frame(lagoslakeid=avg.chla$lagoslakeid, tsi=9.81 * log(avg.chla$chla) + 30.6)
tsi.chl$tsi.cat<-rep("lake",nrow(tsi.chl))

tsi.chl$tsi.cat[tsi.chl$tsi < 40]<-"oligotrophic"
tsi.chl$tsi.cat[tsi.chl$tsi >=40 & tsi.chl$tsi < 50]<-"mesotrophic"
tsi.chl$tsi.cat[tsi.chl$tsi >=50 & tsi.chl$tsi < 70]<-"eutrophic"
tsi.chl$tsi.cat[tsi.chl$tsi >= 70] <-"hypereutrophic"

#huc2 and huc4 watershed codes
huc_codes<-read.csv("/Users/jonathanwalter/GitHub/AquaTerrSynch/AnalysisCode/match_huc_codes.csv", colC

predictors<-analysislakes$lakeinfo
predictors$tslength<-predictors$end-predictors$start+1
predictors<-left_join(predictors, depth, by="lagoslakeid")
```

```
predictors<-left_join(predictors, pct.ag.avg, by="lagoslakeid")
predictors<-left_join(predictors, avg.chla, by="lagoslakeid")
predictors<-left_join(predictors, tsi.chl, by="lagoslakeid")
predictors<-left_join(predictors, huc_codes, by="hu4_zoneid")
```

```
## Warning: Column `hu4_zoneid` joining factor and character vector, coercing
## into character vector
```

```
modvars.accndvi<-left_join(predictors, coh.chlaXaccndvi, by="lagoslakeid")
modvars.accndvi$nhd_ftype<-factor(modvars.accndvi$nhd_ftype)
modvars.accndvi$tsi.cat<-factor(modvars.accndvi$tsi.cat)
modvars.accndvi$tslength<-modvars.accndvi$end-modvars.accndvi$start + 1
```

```
modvars.accndvi<-modvars.accndvi[!is.na(modvars.accndvi$maxdepth),]
modvars.accndvi<-modvars.accndvi[!is.na(modvars.accndvi$pct.ag),]

#short timescales
fm.coh.accndvi.st<-gls(accndvicoh.ts1 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.cat +
                       correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(fm.coh.accndvi.st)
```

```
## Generalized least squares fit by REML
##   Model: accndvicoh.ts1 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag +      chla + tsi.cat + huc2_
##   Data: modvars.accndvi
##        AIC     BIC   logLik
##   29.75993 80.9553 3.120035
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~nhd_lat + nhd_long
##  Parameter estimate(s):
##      range
## 0.01020709
##
## Coefficients:
##                             Value  Std.Error   t-value p-value
## (Intercept)             0.4272016 0.06975400  6.124403  0.0000
## maxdepth               -0.0007389 0.00133428 -0.553763  0.5807
## nhd_ftype436            0.0854864 0.21687431  0.394175  0.6941
## lake_area_ha           -0.0000001 0.00000189 -0.042118  0.9665
## pct.ag                 -0.0030727 0.00188636 -1.628913  0.1058
## chla                   -0.0000208 0.00299418 -0.006945  0.9945
## tsi.cathypereutrophic   0.1186269 0.21466462  0.552615  0.5815
## tsi.catmesotrophic      0.0096149 0.04944307  0.194463  0.8461
## tsi.catoligotrophic     0.0785448 0.05982687  1.312868  0.1916
## huc2_code02            -0.0802270 0.07432681 -1.079382  0.2825
## huc2_code04             0.0127429 0.05943050  0.214417  0.8306
## huc2_code07            -0.0609577 0.05423365 -1.123983  0.2631
## huc2_code08            -0.2498176 0.18847506 -1.325467  0.1874
## huc2_code09            -0.0660408 0.09570289 -0.690061  0.4914
## huc2_code10             0.0225775 0.07553533  0.298900  0.7655
## huc2_code11            -0.0780789 0.13847245 -0.563858  0.5738
##
##  Correlation:
##                        (Intr) mxdpth nh_436 lk_r_h pct.ag chla   ts.cth
## maxdepth               -0.322
```

```
## nhd_ftype436          -0.017 -0.035
## lake_area_ha           0.170 -0.573  0.019
## pct.ag                 0.133 -0.109  0.074  0.085
## chla                  -0.641  0.207  0.036 -0.113 -0.238
## tsi.cathypereutrophic  0.454 -0.101 -0.385  0.048 -0.089 -0.752
## tsi.catmesotrophic    -0.582  0.005  0.032 -0.028 -0.132  0.673 -0.458
## tsi.catoligotrophic   -0.524 -0.114  0.037  0.109 -0.097  0.642 -0.454
## huc2_code02           -0.290 -0.356  0.009  0.208  0.056 -0.156  0.101
## huc2_code04           -0.519  0.047 -0.021 -0.130 -0.213 -0.017  0.066
## huc2_code07           -0.527 -0.031 -0.011  0.022 -0.053 -0.118  0.062
## huc2_code08           -0.058 -0.055 -0.008  0.013  0.044 -0.224  0.180
## huc2_code09           -0.308 -0.031 -0.017  0.028 -0.199 -0.014  0.060
## huc2_code10           -0.272 -0.206 -0.012  0.065 -0.005 -0.307  0.267
## huc2_code11           -0.207 -0.212  0.009  0.061  0.037 -0.047  0.033
##                       ts.ctm ts.ctl hc2_02 hc2_04 hc2_07 hc2_08 hc2_09
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic    0.703
## huc2_code02           -0.083  0.048
## huc2_code04           -0.065 -0.137  0.498
## huc2_code07           -0.097 -0.088  0.596  0.741
## huc2_code08           -0.083 -0.084  0.206  0.204  0.252
## huc2_code09           -0.099  0.008  0.352  0.447  0.469  0.127
## huc2_code10           -0.050 -0.032  0.516  0.515  0.606  0.257  0.334
## huc2_code11            0.089  0.099  0.304  0.262  0.311  0.116  0.168
##                       hc2_10
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02
## huc2_code04
## huc2_code07
## huc2_code08
## huc2_code09
## huc2_code10
## huc2_code11            0.299
##
## Standardized residuals:
##           Min            Q1           Med            Q3           Max
## -1.875885e+00 -6.542012e-01 -1.890345e-15  6.077325e-01  2.829310e+00
##
## Residual standard error: 0.1761937
## Degrees of freedom: 143 total; 127 residual
```

```
dredge.coh.accndvi.st<-dredge(fm.coh.accndvi.st, beta="sd") #intercept only is best model. Disappointin
```

```
## Warning in dredge(fm.coh.accndvi.st, beta = "sd"): comparing models fitted
## by REML
```

```
## Warning in dredge(fm.coh.accndvi.st, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored
```

```
## Fixed term is "(Intercept)"
```

```
print(head(dredge.coh.accndvi.st))
```

```
## Global model call: gls(model = accndvicoh.ts1 ~ maxdepth + nhd_ftype + lake_area_ha +
##     pct.ag + chla + tsi.cat + huc2_code, data = modvars.accndvi,
##     correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##     (Int)        chl        mxd nhd_fty    pct.ag tsi.cat df logLik  AICc
## 1  0.3886                                                  3 42.097 -78.0
## 17 0.3879                              +                   4 41.425 -74.6
## 33 0.3976                                -0.001869         4 37.268 -66.2
## 65 0.3686                                                +  6 38.748 -64.9
## 2  0.3980 -0.0008757                                       4 36.539 -64.8
## 9  0.4009           -0.0006435                             4 36.296 -64.3
##    delta weight
## 1   0.00  0.845
## 17  3.46  0.150
## 33 11.77  0.002
## 65 13.14  0.001
## 2  13.23  0.001
## 9  13.72  0.001
## Models ranked by AICc(x)
```

```
fm.p.accndvi.st<-gls(accndvip.ts1 ~ tslength + maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + ts
                     correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(fm.p.accndvi.st)
```

```
## Generalized least squares fit by REML
##   Model: accndvip.ts1 ~ tslength + maxdepth + nhd_ftype + lake_area_ha +      pct.ag + chla + tsi.ca
##   Data: modvars.accndvi
##        AIC      BIC    logLik
##   162.5399 216.4293 -62.26995
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~nhd_lat + nhd_long
##  Parameter estimate(s):
##       range
## 0.008615349
##
## Coefficients:
##                            Value Std.Error    t-value p-value
## (Intercept)            0.1269522 0.3023176  0.4199299  0.6753
## tslength               0.0128091 0.0131020  0.9776387  0.3301
## maxdepth               0.0009036 0.0021961  0.4114461  0.6814
## nhd_ftype436           0.3911038 0.3570238  1.0954558  0.2754
## lake_area_ha          -0.0000013 0.0000031 -0.4057159  0.6856
```

```
## pct.ag                 0.0060254 0.0031045  1.9408788  0.0545
## chla                   0.0032723 0.0049026  0.6674558  0.5057
## tsi.cathypereutrophic -0.5327321 0.3515321 -1.5154581  0.1322
## tsi.catmesotrophic     0.0946554 0.0809872  1.1687701  0.2447
## tsi.catoligotrophic    0.0666966 0.0977252  0.6824910  0.4962
## huc2_code02            0.0367639 0.1213500  0.3029576  0.7624
## huc2_code04           -0.0915190 0.0971452 -0.9420843  0.3480
## huc2_code07           -0.0137036 0.0883488 -0.1551082  0.8770
## huc2_code08            0.1379913 0.3100448  0.4450687  0.6570
## huc2_code09            0.0123327 0.1567862  0.0786597  0.9374
## huc2_code10           -0.1720022 0.1244802 -1.3817628  0.1695
## huc2_code11            0.0214742 0.2287625  0.0938711  0.9254
##
##  Correlation:
##                       (Intr) tslngt mxdpth nh_436 lk_r_h pct.ag chla
## tslength              -0.926
## maxdepth              -0.007 -0.122
## nhd_ftype436          -0.119  0.121 -0.049
## lake_area_ha           0.016  0.052 -0.574  0.025
## pct.ag                -0.062  0.120 -0.122  0.088  0.090
## chla                  -0.182 -0.064  0.214  0.027 -0.116 -0.244
## tsi.cathypereutrophic  0.234 -0.069 -0.093 -0.390  0.044 -0.096 -0.744
## tsi.catmesotrophic    -0.204 -0.017  0.009  0.029 -0.030 -0.133  0.672
## tsi.catoligotrophic   -0.202  0.005 -0.112  0.037  0.108 -0.095  0.641
## huc2_code02           -0.115  0.008 -0.355  0.009  0.209  0.057 -0.157
## huc2_code04           -0.257  0.068  0.037 -0.012 -0.125 -0.202 -0.022
## huc2_code07           -0.213  0.017 -0.034 -0.009  0.024 -0.050 -0.120
## huc2_code08            0.086 -0.116 -0.041 -0.022  0.007  0.030 -0.214
## huc2_code09           -0.040 -0.080 -0.022 -0.026  0.025 -0.207 -0.009
## huc2_code10            0.026 -0.137 -0.187 -0.028  0.057 -0.021 -0.295
## huc2_code11            0.061 -0.149 -0.190 -0.010  0.053  0.018 -0.037
##                       ts.cth ts.ctm ts.ctl hc2_02 hc2_04 hc2_07 hc2_08
## tslength
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic    -0.455
## tsi.catoligotrophic   -0.453  0.703
## huc2_code02            0.101 -0.084  0.047
## huc2_code04            0.061 -0.066 -0.138  0.496
## huc2_code07            0.061 -0.098 -0.090  0.596  0.740
## huc2_code08            0.186 -0.081 -0.084  0.203  0.193  0.248
## huc2_code09            0.065 -0.099  0.007  0.349  0.438  0.465  0.134
## huc2_code10            0.274 -0.047 -0.033  0.509  0.499  0.597  0.268
## huc2_code11            0.043  0.090  0.097  0.299  0.248  0.304  0.131
##                       hc2_09 hc2_10
## tslength
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
```

```
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02
## huc2_code04
## huc2_code07
## huc2_code08
## huc2_code09
## huc2_code10            0.339
## huc2_code11            0.176  0.313
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -1.94107750 -0.68067740 -0.01990797  0.84916917  1.74873566
##
## Residual standard error: 0.2879222
## Degrees of freedom: 143 total; 126 residual
```

```
dredge.p.accndvi.st<-dredge(fm.p.accndvi.st, beta="sd") #intercept only is best model. Disappointing.
```

```
## Warning in dredge(fm.p.accndvi.st, beta = "sd"): comparing models fitted by
## REML
```

```
## Warning in dredge(fm.p.accndvi.st, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored
```

```
## Fixed term is "(Intercept)"
```

```
print(head(dredge.p.accndvi.st))
```

```
## Global model call: gls(model = accndvip.ts1 ~ tslength + maxdepth + nhd_ftype +
##     lake_area_ha + pct.ag + chla + tsi.cat + huc2_code, data = modvars.accndvi,
##     correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##      (Int)    chl nhd_fty   pct.ag      tsl df  logLik AICc delta weight
## 1   0.4872                                  3 -25.632 57.4  0.00  0.762
## 17  0.4862              +                   4 -25.820 59.9  2.49  0.219
## 129 0.2987                          0.008592  4 -28.890 66.1  8.63  0.010
## 33  0.4698                0.003608          4 -29.671 67.6 10.20  0.005
## 145 0.2919              +           0.008850  5 -29.060 68.6 11.12  0.003
## 2   0.4926 -5e-04                           4 -30.961 70.2 12.78  0.001
## Models ranked by AICc(x)
```

```
fm.phi.accndvi.st<-gls(cos(accndviphi.ts1) ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.
                       correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(fm.phi.accndvi.st)
```

```
## Generalized least squares fit by REML
##   Model: cos(accndviphi.ts1) ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag +      chla + tsi.cat + h
##   Data: modvars.accndvi
##        AIC      BIC    logLik
##   379.8733 431.0687 -171.9367
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~nhd_lat + nhd_long
```

```
##  Parameter estimate(s):
##       range
## 0.0005117253
##
## Coefficients:
##                            Value Std.Error    t-value p-value
## (Intercept)            0.0643578 0.2725684  0.2361163  0.8137
## maxdepth              -0.0063600 0.0052668 -1.2075571  0.2295
## nhd_ftype436          -1.1010917 0.8585645 -1.2824800  0.2020
## lake_area_ha           0.0000108 0.0000075  1.4430122  0.1515
## pct.ag                -0.0045016 0.0074632 -0.6031789  0.5475
## chla                   0.0232531 0.0118538  1.9616640  0.0520
## tsi.cathypereutrophic -0.9112866 0.8494063 -1.0728513  0.2854
## tsi.catmesotrophic     0.3067180 0.1974672  1.5532608  0.1228
## tsi.catoligotrophic    0.2490623 0.2362416  1.0542696  0.2938
## huc2_code02           -0.4354037 0.2921736 -1.4902225  0.1386
## huc2_code04           -0.4482296 0.2318423 -1.9333387  0.0554
## huc2_code07           -0.3268675 0.2102010 -1.5550233  0.1224
## huc2_code08            0.1902009 0.7452006  0.2552345  0.7990
## huc2_code09            0.0523097 0.3767608  0.1388407  0.8898
## huc2_code10           -0.1565033 0.2967110 -0.5274604  0.5988
## huc2_code11           -0.0743011 0.5471063 -0.1358073  0.8922
##
##  Correlation:
##                       (Intr) mxdpth nh_436 lk_r_h pct.ag chla   ts.cth
## maxdepth              -0.319
## nhd_ftype436          -0.018 -0.034
## lake_area_ha           0.169 -0.572  0.019
## pct.ag                 0.133 -0.109  0.074  0.085
## chla                  -0.648  0.209  0.035 -0.114 -0.239
## tsi.cathypereutrophic  0.459 -0.103 -0.385  0.048 -0.088 -0.751
## tsi.catmesotrophic    -0.591  0.011  0.032 -0.032 -0.130  0.671 -0.455
## tsi.catoligotrophic   -0.530 -0.110  0.037  0.106 -0.095  0.645 -0.456
## huc2_code02           -0.274 -0.366  0.009  0.213  0.059 -0.161  0.104
## huc2_code04           -0.504  0.038 -0.021 -0.127 -0.213 -0.022  0.069
## huc2_code07           -0.511 -0.042 -0.011  0.027 -0.049 -0.125  0.065
## huc2_code08           -0.051 -0.058 -0.008  0.014  0.046 -0.225  0.180
## huc2_code09           -0.293 -0.038 -0.017  0.032 -0.199 -0.017  0.061
## huc2_code10           -0.256 -0.214 -0.012  0.068 -0.002 -0.311  0.270
## huc2_code11           -0.200 -0.216  0.009  0.062  0.038 -0.048  0.033
##                       ts.ctm ts.ctl hc2_02 hc2_04 hc2_07 hc2_08 hc2_09
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic    0.702
## huc2_code02           -0.087  0.042
## huc2_code04           -0.067 -0.144  0.489
## huc2_code07           -0.102 -0.101  0.590  0.737
## huc2_code08           -0.082 -0.086  0.201  0.199  0.248
## huc2_code09           -0.103  0.004  0.344  0.438  0.460  0.122
```

```
## huc2_code10           -0.049 -0.037  0.508  0.506  0.598  0.253  0.324
## huc2_code11            0.089  0.097  0.299  0.256  0.306  0.114  0.162
##                       hc2_10
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02
## huc2_code04
## huc2_code07
## huc2_code08
## huc2_code09
## huc2_code10
## huc2_code11            0.295
##
## Standardized residuals:
##           Min            Q1           Med            Q3           Max
## -1.891458e+00 -8.586243e-01 -1.591653e-16  7.499843e-01  1.679299e+00
##
## Residual standard error: 0.6975283
## Degrees of freedom: 143 total; 127 residual
```

```
dredge.phi.accndvi.st<-dredge(fm.phi.accndvi.st, beta="sd") #intercept only is best model. Disappointin
```

```
## Warning in dredge(fm.phi.accndvi.st, beta = "sd"): comparing models fitted
## by REML
```

```
## Warning in dredge(fm.phi.accndvi.st, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored
```

```
## Fixed term is "(Intercept)"
```

```
print(head(dredge.phi.accndvi.st))
```

```
## Global model call: gls(model = cos(accndviphi.ts1) ~ maxdepth + nhd_ftype + lake_area_ha +
##     pct.ag + chla + tsi.cat + huc2_code, data = modvars.accndvi,
##     correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##       (Int)      chl nhd_fty tsi.cat df   logLik  AICc delta weight
## 17  0.03424                +          4 -154.101 316.5  0.00  0.519
## 1   0.02840                           3 -155.367 316.9  0.41  0.422
## 18 -0.09982 0.011900       +          5 -155.828 322.1  5.60  0.032
## 81  0.10400                +       +  7 -154.432 323.7  7.20  0.014
## 65  0.10400                        +  6 -156.166 324.9  8.46  0.008
## 2  -0.05062 0.007465                  4 -158.520 325.3  8.84  0.006
## Models ranked by AICc(x)
```

```
#long timescales
fm.coh.accndvi.lt<-gls(accndvicoh.ts2 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.cat +
                       correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(fm.coh.accndvi.lt)
```

```
## Generalized least squares fit by REML
##   Model: accndvicoh.ts2 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag +      chla + tsi.cat + huc2_
##   Data: modvars.accndvi
##        AIC      BIC    logLik
##   92.70797 143.9033 -28.35398
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~nhd_lat + nhd_long
##  Parameter estimate(s):
##     range
## 0.0317292
##
## Coefficients:
##                            Value  Std.Error   t-value p-value
## (Intercept)            0.6267287 0.09341037  6.709413  0.0000
## maxdepth              -0.0012909 0.00172968 -0.746341  0.4568
## nhd_ftype436           0.4738853 0.28283750  1.675469  0.0963
## lake_area_ha          -0.0000002 0.00000246 -0.099489  0.9209
## pct.ag                 0.0026158 0.00246775  1.059978  0.2912
## chla                   0.0009980 0.00388382  0.256965  0.7976
## tsi.cathypereutrophic -0.1490334 0.27994212 -0.532372  0.5954
## tsi.catmesotrophic    -0.0075659 0.06213026 -0.121774  0.9033
## tsi.catoligotrophic    0.0829907 0.07725160  1.074291  0.2847
## huc2_code02           -0.0449029 0.09934088 -0.452008  0.6520
## huc2_code04           -0.0477740 0.08075671 -0.591579  0.5552
## huc2_code07           -0.1425729 0.07506912 -1.899221  0.0598
## huc2_code08            0.2055679 0.24671465  0.833221  0.4063
## huc2_code09           -0.1816884 0.12854881 -1.413380  0.1600
## huc2_code10           -0.0876704 0.10094829 -0.868468  0.3868
## huc2_code11            0.0520844 0.18198034  0.286209  0.7752
##
##  Correlation:
##                       (Intr) mxdpth nh_436 lk_r_h pct.ag chla   ts.cth
## maxdepth              -0.297
## nhd_ftype436          -0.017 -0.036
## lake_area_ha           0.154 -0.570  0.020
## pct.ag                 0.131 -0.106  0.075  0.085
## chla                  -0.619  0.186  0.036 -0.101 -0.236
## tsi.cathypereutrophic  0.438 -0.085 -0.386  0.039 -0.089 -0.751
## tsi.catmesotrophic    -0.563 -0.023  0.033 -0.009 -0.137  0.681 -0.467
## tsi.catoligotrophic   -0.517 -0.130  0.037  0.115 -0.102  0.643 -0.454
## huc2_code02           -0.346 -0.339  0.009  0.198  0.051 -0.136  0.089
## huc2_code04           -0.561  0.047 -0.020 -0.127 -0.211 -0.005  0.057
## huc2_code07           -0.570 -0.024 -0.011  0.017 -0.065 -0.097  0.045
## huc2_code08           -0.081 -0.051 -0.008  0.011  0.042 -0.221  0.177
## huc2_code09           -0.345 -0.024 -0.016  0.023 -0.196 -0.004  0.053
## huc2_code10           -0.320 -0.195 -0.012  0.060 -0.009 -0.291  0.255
## huc2_code11           -0.235 -0.210  0.009  0.061  0.034 -0.040  0.028
##                       ts.ctm ts.ctl hc2_02 hc2_04 hc2_07 hc2_08 hc2_09
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
```

```
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic    0.719
## huc2_code02           -0.055  0.068
## huc2_code04           -0.047 -0.102  0.527
## huc2_code07           -0.067 -0.053  0.611  0.750
## huc2_code08           -0.084 -0.078  0.219  0.219  0.262
## huc2_code09           -0.075  0.023  0.369  0.464  0.480  0.138
## huc2_code10           -0.042 -0.015  0.539  0.543  0.623  0.269  0.356
## huc2_code11            0.094  0.108  0.323  0.285  0.329  0.125  0.185
##                       hc2_10
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02
## huc2_code04
## huc2_code07
## huc2_code08
## huc2_code09
## huc2_code10
## huc2_code11            0.317
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -2.24713790 -0.55609526 -0.07660139  0.62180817  1.84642434
##
## Residual standard error: 0.2297714
## Degrees of freedom: 143 total; 127 residual
```

```
dredge.coh.accndvi.lt<-dredge(fm.coh.accndvi.lt, beta="sd") #intercept only is best model. Disappointin
```

```
## Warning in dredge(fm.coh.accndvi.lt, beta = "sd"): comparing models fitted
## by REML
```

```
## Warning in dredge(fm.coh.accndvi.lt, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored
```

```
## Fixed term is "(Intercept)"
```

```
print(head(dredge.coh.accndvi.lt))
```

```
## Global model call: gls(model = accndvicoh.ts2 ~ maxdepth + nhd_ftype + lake_area_ha +
##     pct.ag + chla + tsi.cat + huc2_code, data = modvars.accndvi,
##     correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##     (Int)       chl        mxd nhd_fty   pct.ag df logLik AICc delta
## 1  0.5542                                        3  6.491 -6.8  0.00
## 17 0.5512                              +         4  7.315 -6.3  0.47
## 33 0.5426                                0.002276  4  1.835  4.6 11.43
## 49 0.5428                              + 0.001707  5  2.393  5.7 12.46
```

```
## 2  0.5448 0.0008675                                4  1.080  6.1 12.94
## 9  0.5693          -0.0007822                      4  0.928  6.4 13.24
##    weight
## 1   0.556
## 17  0.439
## 33  0.002
## 49  0.001
## 2   0.001
## 9   0.001
## Models ranked by AICc(x)
```

```
fm.p.accndvi.lt<-gls(accndvip.ts2 ~ tslength + maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + ts
                     correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(fm.p.accndvi.lt)
```

```
## Generalized least squares fit by REML
##   Model: accndvip.ts2 ~ tslength + maxdepth + nhd_ftype + lake_area_ha +      pct.ag + chla + tsi.ca
##   Data: modvars.accndvi
##        AIC      BIC    logLik
##   181.3168 235.2061 -71.65839
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~nhd_lat + nhd_long
##  Parameter estimate(s):
##       range
## 0.0005203966
##
## Coefficients:
##                            Value Std.Error    t-value p-value
## (Intercept)            0.1703609 0.3227742  0.5278020  0.5986
## tslength               0.0013143 0.0139902  0.0939450  0.9253
## maxdepth               0.0023092 0.0023565  0.9799216  0.3290
## nhd_ftype436          -0.2740421 0.3839574 -0.7137305  0.4767
## lake_area_ha           0.0000016 0.0000033  0.4962372  0.6206
## pct.ag                -0.0014182 0.0033373 -0.4249647  0.6716
## chla                   0.0072056 0.0052726  1.3666126  0.1742
## tsi.cathypereutrophic -0.6021940 0.3780162 -1.5930375  0.1137
## tsi.catmesotrophic     0.0407581 0.0876744  0.4648802  0.6428
## tsi.catoligotrophic    0.1091835 0.1048805  1.0410274  0.2999
## huc2_code02            0.0523082 0.1297168  0.4032496  0.6874
## huc2_code04            0.1540052 0.1031885  1.4924644  0.1381
## huc2_code07            0.1746925 0.0933342  1.8716870  0.0636
## huc2_code08           -0.0481973 0.3330675 -0.1447073  0.8852
## huc2_code09            0.2813430 0.1677966  1.6766905  0.0961
## huc2_code10            0.0961973 0.1329634  0.7234875  0.4707
## huc2_code11           -0.0703673 0.2455461 -0.2865749  0.7749
##
##  Correlation:
##                       (Intr) tslngt mxdpth nh_436 lk_r_h pct.ag chla
## tslength              -0.927
## maxdepth              -0.004 -0.124
## nhd_ftype436          -0.118  0.120 -0.049
## lake_area_ha           0.015  0.052 -0.574  0.025
## pct.ag                -0.061  0.120 -0.122  0.087  0.091
## chla                  -0.185 -0.062  0.215  0.028 -0.117 -0.244
```

```
## tsi.cathypereutrophic  0.236 -0.070 -0.093 -0.390  0.045 -0.096 -0.744
## tsi.catmesotrophic    -0.209 -0.014  0.012  0.030 -0.033 -0.131  0.671
## tsi.catoligotrophic   -0.201  0.003 -0.109  0.037  0.106 -0.094  0.644
## huc2_code02           -0.111  0.009 -0.364  0.010  0.213  0.060 -0.161
## huc2_code04           -0.254  0.071  0.029 -0.012 -0.122 -0.203 -0.026
## huc2_code07           -0.208  0.018 -0.044 -0.008  0.028 -0.046 -0.126
## huc2_code08            0.088 -0.116 -0.043 -0.022  0.008  0.031 -0.215
## huc2_code09           -0.036 -0.080 -0.027 -0.026  0.028 -0.206 -0.012
## huc2_code10            0.031 -0.136 -0.194 -0.028  0.060 -0.018 -0.299
## huc2_code11            0.062 -0.147 -0.193 -0.009  0.054  0.020 -0.038
##                       ts.cth ts.ctm ts.ctl hc2_02 hc2_04 hc2_07 hc2_08
## tslength
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic    -0.453
## tsi.catoligotrophic   -0.455  0.702
## huc2_code02            0.103 -0.087  0.042
## huc2_code04            0.063 -0.067 -0.143  0.488
## huc2_code07            0.064 -0.102 -0.100  0.590  0.736
## huc2_code08            0.187 -0.080 -0.086  0.199  0.189  0.244
## huc2_code09            0.067 -0.102  0.003  0.342  0.430  0.457  0.130
## huc2_code10            0.277 -0.047 -0.037  0.502  0.491  0.590  0.265
## huc2_code11            0.043  0.090  0.096  0.294  0.243  0.300  0.129
##                       hc2_09 hc2_10
## tslength
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02
## huc2_code04
## huc2_code07
## huc2_code08
## huc2_code09
## huc2_code10            0.331
## huc2_code11            0.171  0.309
##
## Standardized residuals:
##         Min          Q1         Med          Q3         Max
## -1.77046431 -0.84318300  0.04109281  0.78457936  1.70675570
##
## Residual standard error: 0.3096696
## Degrees of freedom: 143 total; 126 residual
```

```
dredge.p.accndvi.lt<-dredge(fm.p.accndvi.lt, beta="sd") #intercept only is best model. Disappointing.
```

```
## Warning in dredge(fm.p.accndvi.lt, beta = "sd"): comparing models fitted by
```

```
## REML

## Warning in dredge(fm.p.accndvi.lt, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored

## Fixed term is "(Intercept)"
```

```
print(head(dredge.p.accndvi.lt))
```

```
## Global model call: gls(model = accndvip.ts2 ~ tslength + maxdepth + nhd_ftype +
##     lake_area_ha + pct.ag + chla + tsi.cat + huc2_code, data = modvars.accndvi,
##     correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##      (Int)      mxd nhd_fty     pct.ag       tsl df  logLik AICc delta
## 1   0.4720                                        3 -36.419 79.0  0.00
## 17  0.4753               +                        4 -35.486 79.3  0.25
## 129 0.4527                           0.0008790   4 -39.873 88.0  9.03
## 145 0.4723               +           0.0001351   5 -38.947 88.3  9.32
## 9   0.4342 0.002011                              4 -41.173 90.6 11.62
## 33  0.4759                 -0.0008419            4 -41.361 91.0 12.00
##     weight
## 1    0.524
## 17   0.462
## 129  0.006
## 145  0.005
## 9    0.002
## 33   0.001
## Models ranked by AICc(x)
```

```
fm.phi.accndvi.lt<-gls(cos(accndviphi.ts2) ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.
                       correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(fm.phi.accndvi.lt)
```

```
## Generalized least squares fit by REML
##   Model: cos(accndviphi.ts2) ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag +      chla + tsi.cat + l
##   Data: modvars.accndvi
##        AIC      BIC    logLik
##   376.0792 427.2746 -170.0396
##
## Correlation Structure: Exponential spatial correlation
##  Formula: ~nhd_lat + nhd_long
##  Parameter estimate(s):
##       range
## 0.009545035
##
## Coefficients:
##                            Value Std.Error    t-value p-value
## (Intercept)           -0.1507349 0.2724725 -0.5532113  0.5811
## maxdepth               0.0047576 0.0052142  0.9124475  0.3633
## nhd_ftype436          -0.3473762 0.8476126 -0.4098290  0.6826
## lake_area_ha          -0.0000054 0.0000074 -0.7386528  0.4615
## pct.ag                -0.0043727 0.0073719 -0.5931575  0.5541
## chla                   0.0035586 0.0117019  0.3041060  0.7615
## tsi.cathypereutrophic  0.2139450 0.8388836  0.2550354  0.7991
## tsi.catmesotrophic     0.1600129 0.1934211  0.8272776  0.4096
```

```
## tsi.catoligotrophic   -0.1165299 0.2337879 -0.4984428  0.6190
## huc2_code02           -0.0664997 0.2903827 -0.2290071  0.8192
## huc2_code04            0.0667821 0.2320811  0.2877533  0.7740
## huc2_code07           -0.0286506 0.2116802 -0.1353487  0.8926
## huc2_code08            0.9902682 0.7365668  1.3444378  0.1812
## huc2_code09            0.2651725 0.3739325  0.7091454  0.4795
## huc2_code10           -0.0789391 0.2950886 -0.2675097  0.7895
## huc2_code11            0.9141921 0.5411328  1.6894044  0.0936
##
##  Correlation:
##                       (Intr) mxdpth nh_436 lk_r_h pct.ag chla   ts.cth
## maxdepth              -0.322
## nhd_ftype436          -0.017 -0.035
## lake_area_ha           0.170 -0.573  0.019
## pct.ag                 0.133 -0.109  0.074  0.085
## chla                  -0.641  0.208  0.036 -0.113 -0.238
## tsi.cathypereutrophic  0.454 -0.102 -0.385  0.048 -0.089 -0.751
## tsi.catmesotrophic    -0.582  0.006  0.032 -0.028 -0.132  0.673 -0.457
## tsi.catoligotrophic   -0.524 -0.113  0.037  0.109 -0.097  0.643 -0.454
## huc2_code02           -0.289 -0.356  0.009  0.209  0.056 -0.156  0.101
## huc2_code04           -0.519  0.047 -0.021 -0.130 -0.213 -0.018  0.066
## huc2_code07           -0.526 -0.032 -0.011  0.022 -0.053 -0.119  0.062
## huc2_code08           -0.058 -0.055 -0.008  0.013  0.044 -0.224  0.180
## huc2_code09           -0.307 -0.031 -0.017  0.029 -0.199 -0.014  0.060
## huc2_code10           -0.271 -0.206 -0.012  0.065 -0.004 -0.307  0.267
## huc2_code11           -0.207 -0.212  0.009  0.061  0.037 -0.047  0.033
##                       ts.ctm ts.ctl hc2_02 hc2_04 hc2_07 hc2_08 hc2_09
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic    0.703
## huc2_code02           -0.083  0.047
## huc2_code04           -0.065 -0.137  0.497
## huc2_code07           -0.097 -0.089  0.596  0.741
## huc2_code08           -0.083 -0.084  0.205  0.204  0.252
## huc2_code09           -0.100  0.008  0.352  0.447  0.468  0.126
## huc2_code10           -0.049 -0.032  0.515  0.515  0.605  0.257  0.333
## huc2_code11            0.089  0.099  0.304  0.262  0.311  0.116  0.167
##                       hc2_10
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02
## huc2_code04
## huc2_code07
```

```
## huc2_code08
## huc2_code09
## huc2_code10
## huc2_code11            0.299
##
## Standardized residuals:
##           Min            Q1           Med            Q3           Max
## -1.883535e+00 -8.895194e-01 -9.874969e-16  8.702264e-01  1.636105e+00
##
## Residual standard error: 0.6886215
## Degrees of freedom: 143 total; 127 residual
```

```
dredge.phi.accndvi.lt<-dredge(fm.phi.accndvi.lt, beta="sd") #intercept only is best model. Disappointin
```

```
## Warning in dredge(fm.phi.accndvi.lt, beta = "sd"): comparing models fitted
## by REML
```

```
## Warning in dredge(fm.phi.accndvi.lt, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored
```

```
## Fixed term is "(Intercept)"
```

```
print(head(dredge.phi.accndvi.lt))
```

```
## Global model call: gls(model = cos(accndviphi.ts2) ~ maxdepth + nhd_ftype + lake_area_ha +
##     pct.ag + chla + tsi.cat + huc2_code, data = modvars.accndvi,
##     correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##        (Int)      mxd nhd_fty    pct.ag tsi.cat df   logLik  AICc delta
## 1   0.001102                                     3 -148.850 303.9  0.00
## 17  0.002009                +                    4 -148.295 304.9  1.01
## 65 -0.010000                                   +  6 -149.564 311.7  7.87
## 81 -0.009983                +                  +  7 -148.766 312.4  8.49
## 33  0.009313                  -0.001692          4 -153.003 314.3 10.42
## 9  -0.056060 0.003022                            4 -153.194 314.7 10.81
##    weight
## 1   0.607
## 17  0.367
## 65  0.012
## 81  0.009
## 33  0.003
## 9   0.003
## Models ranked by AICc(x)
```