

Q1: Are lake and terrestrial primary productivity coherent?

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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))})),]
```

```
##      lagslakeid      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))}),]
```

```

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$lakedata[[lind]])))
  chlaXaccndvi<-coh(lakedat.ii[1,], lakedat.ii[2,], as.numeric(colnames(analysislakes$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)

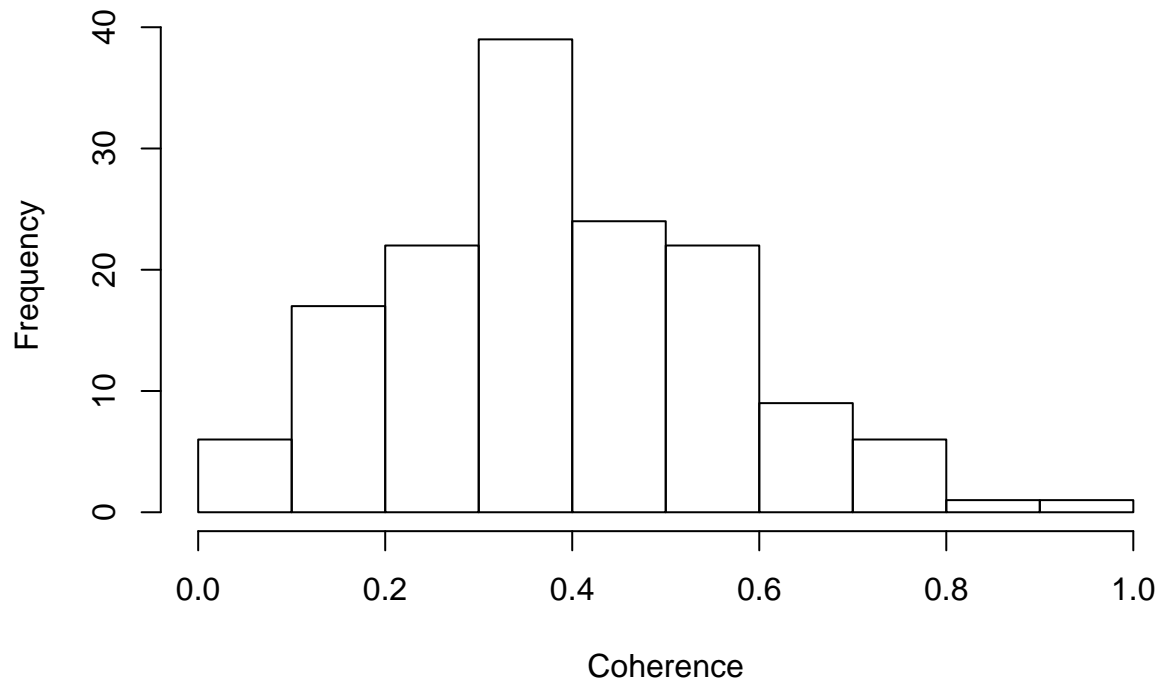
colnames(coh.chlaXaccndvi)<-paste0("accndvi",c("p.ts1","phi.ts1","coh.ts1","p.ts2","phi.ts2","coh.ts2"),
colnames(coh.chlaXmaxndvi)<-paste0("maxndvi",c("p.ts1","phi.ts1","coh.ts1","p.ts2","phi.ts2","coh.ts2"),

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

#short timescales
hist(coh.chlaXaccndvi$accndvicoh.ts1, main="Accumulated NDVI, short timescales", xlab="Coherence", ylab="")

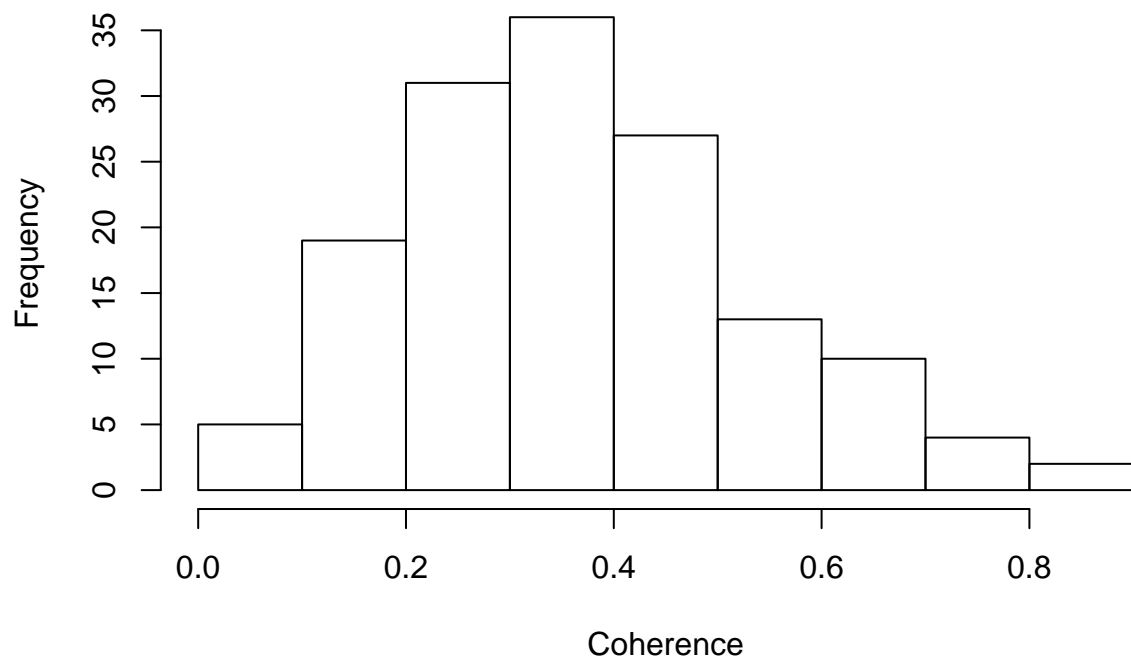
```

Accumulated NDVI, short timescales



```
hist(coh.chlaXmaxndvi$maxndvicoh.ts1, main="Maximum NDVI, short timescales", xlab="Coherence", ylab="Fr
```

Maximum NDVI, short timescales



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

```
##          0%          25%          50%          75%         100%
## 0.04230519 0.26855267 0.37281647 0.51749522 0.92134749
```

```

quantile(coh.chlaXmaxndvi$maxndvicoh.ts1)

##          0%          25%          50%          75%         100%
## 0.03432407 0.24526250 0.35174752 0.47476306 0.80601025

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

## [1] 0.06802721

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

## [1] 0.03401361

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

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

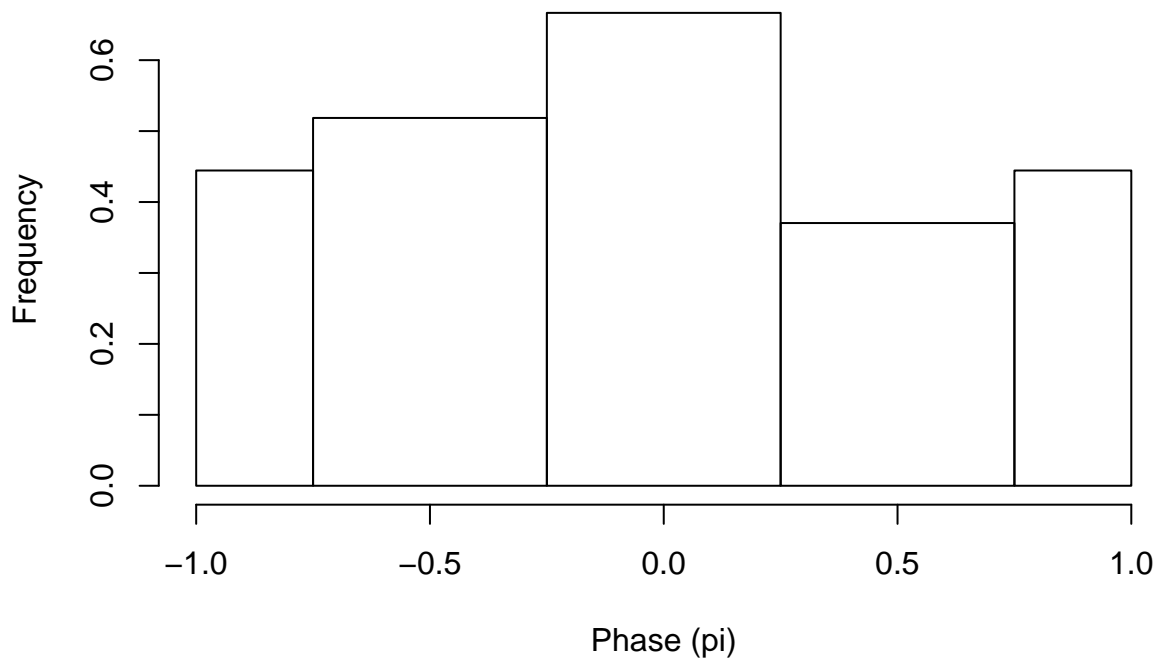
## [1] 0.3030499 0.1624359 -0.9406033 -0.5034587 -0.8338166

phicls<-c(-1,-.75,-0.25,0.25,0.75,1)

hist(coh.chlaXaccndvi$accndviphi.ts1[coh.chlaXaccndvi$accndvip.ts1<0.2]/pi, main="Accumulated NDVI, short

```

Accumulated NDVI, short timescales

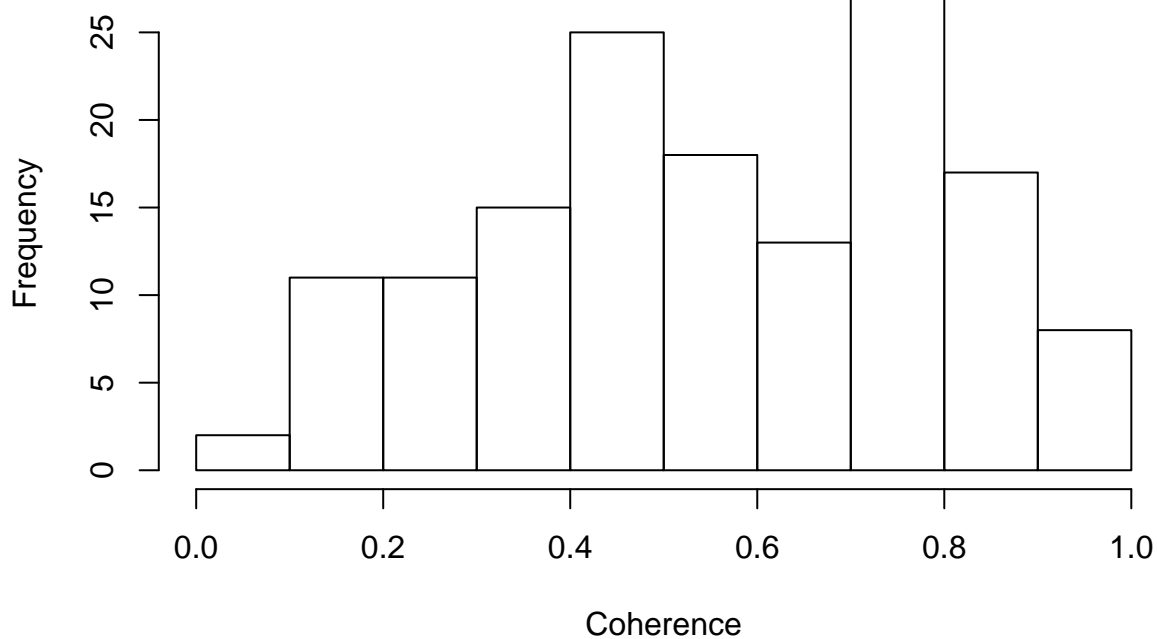


```

#hist(coh.chlaXmaxndvi$maxndviphi.ts1[coh.chlaXmaxndvi$maxndvip.ts1<0.2]/pi, main="Maximum NDVI, short
#long timescales
hist(coh.chlaXaccndvi$accndvicoh.ts2, main="Accumulated NDVI, long timescales", xlab="Coherence", ylab=

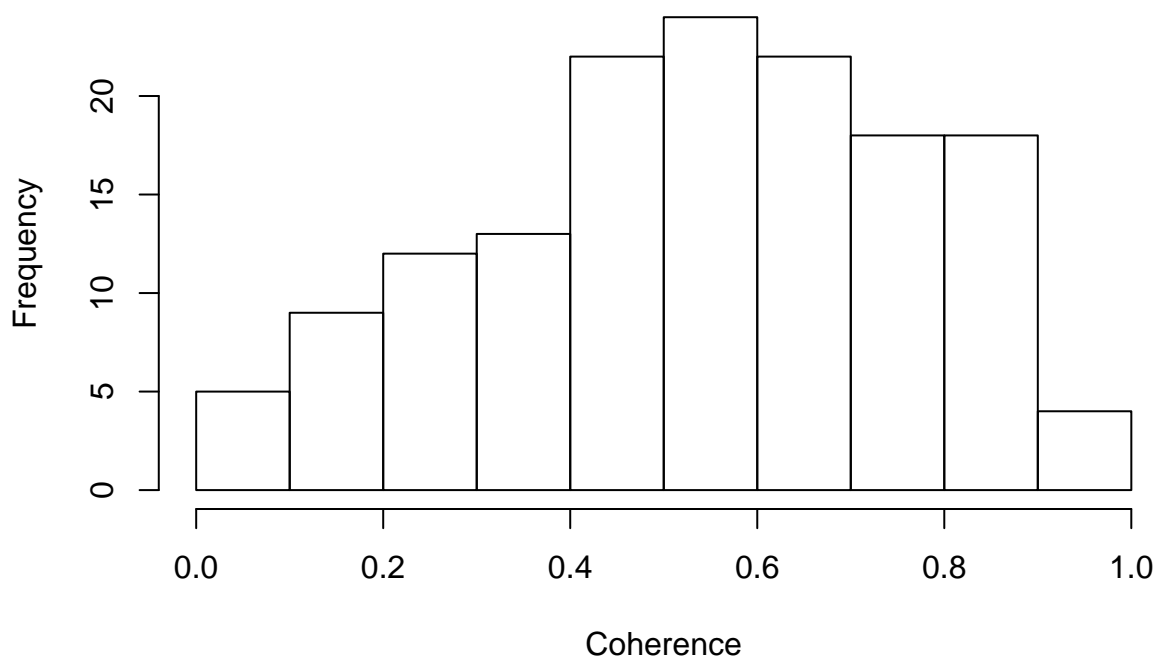
```

Accumulated NDVI, long timescales



```
hist(coh.chlaXmaxndvi$maxndvicoh.ts2, main="Maximum NDVI, long timescales", xlab="Coherence", ylab="Frequency")
```

Maximum NDVI, long timescales



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

```
##          0%          25%          50%          75%          100%
## 0.07654579 0.39401711 0.54402381 0.75143055 0.95309993
```

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

```
##          0%          25%          50%          75%          100%
## 0.02843414 0.39347021 0.54275391 0.72063540 0.95965507
```

```
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)
```

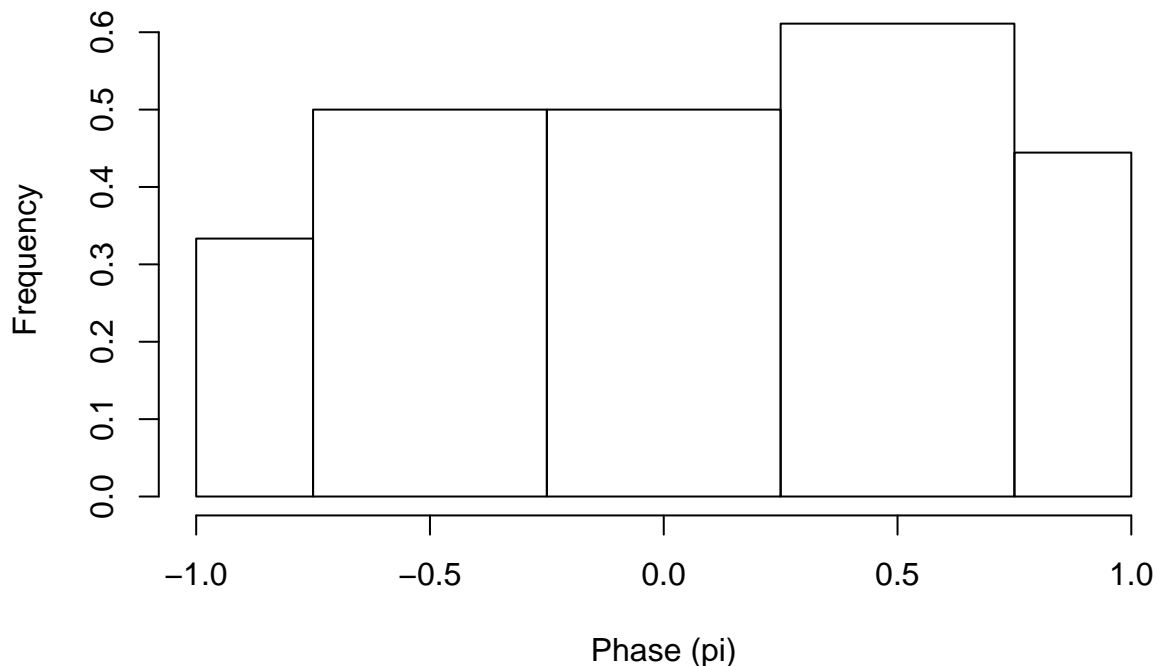
```
## [1] 0.73992662 -0.90124264 0.53888310 0.27521830 -0.95606597
## [6] 0.52712388 0.66512195 -0.68599147 -0.91773670 -0.29662433
## [11] -0.10820287 -0.40541240 -0.22793834 -0.04840174 -0.57269988
## [16] -0.52827164 0.88106993
```

```
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
```

```
hist(coh.chlaXaccndvi$accndviphi.ts1[coh.chlaXaccndvi$accndvip.ts2<0.2]/pi, main="Accumulated NDVI, long
```

Accumulated NDVI, long timescales



```
#hist(coh.chlaXmaxndvi$maxndviphi.ts1[coh.chlaXmaxndvi$maxndvicoh.ts2>0.6]/pi, main="Maximum NDVI, short
```

```
#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 huc2 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),]

modvars.accndvi.phist<-modvars.accndvi[modvars.accndvi$accndvip.ts1<0.2,]
modvars.accndvi.philt<-modvars.accndvi[modvars.accndvi$accndvip.ts2<0.2,]

#short timescales
gls.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(gls.coh.accndvi.st)

```

```

## Generalized least squares fit by REML
## Model: accndvicoh.tsi ~ 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.ct1 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(gls.coh.accndvi.st, beta="sd") #intercept only is best model. Disappointi

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

## Warning in dredge(gls.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
## 17 0.3879      +
## 33 0.3976      -0.001869
## 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)

gls.p.accndvi.st<-gls(accndvip.ts1 ~ tslength + maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.ca
                        correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(gls.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) tslngr 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(gls.p.accndvi.st, beta="sd") #intercept only is best model. Disappointing.
## Warning in dredge(gls.p.accndvi.st, beta = "sd"): comparing models fitted

```

```

## by REML

## Warning in dredge(gls.p.accndvi.st, beta = "sd"): do not know how to
## standardize coefficients of 'glms', 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
## 17   0.4862          +
## 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)
gls.phi.accndvi.st<-gls(cos(accndviphi.ts1) ~ maxdepth + lake_area_ha + pct.ag + chla + tsi.cat + huc2_
summary(gls.phi.accndvi.st)

## Generalized least squares fit by REML
##      Model: cos(accndviphi.ts1) ~ maxdepth + lake_area_ha + pct.ag + chla +      tsi.cat + huc2_code
##      Data: modvars.accndvi.phist
##           AIC      BIC    logLik
##    103.2394 111.7136 -36.61969
##
## Coefficients:
##              Value Std.Error    t-value p-value
## (Intercept)    0.5571571  0.708438  0.7864588  0.4457
## maxdepth      -0.0413294  0.030556 -1.3525847  0.1992
## lake_area_ha    0.0002658  0.000378  0.7027756  0.4946
## pct.ag         -0.0160235  0.028486 -0.5625123  0.5833
## chla           0.0337431  0.034275  0.9844887  0.3428
## tsi.cathypereutrophic -2.6661267  2.025591 -1.3162218  0.2108
## tsi.catmesotrophic   0.3635161  0.622191  0.5842514  0.5691
## tsi.catoligotrophic  0.4300884  0.764512  0.5625657  0.5833
## huc2_code02        -1.0094495  0.722341 -1.3974697  0.1857
## huc2_code04        -0.8564502  0.619617 -1.3822260  0.1902
## huc2_code07        -0.2526052  0.564918 -0.4471534  0.6621
## huc2_code09        -1.0480555  0.970545 -1.0798630  0.2998
## huc2_code10         0.0099709  0.675156  0.0147683  0.9884
## huc2_code11        -1.2055855  4.259894 -0.2830084  0.7816
##
##      Correlation:
##              (Intr) mxdpth lk_r_h pct.ag chla    ts.cth ts.ctm
## maxdepth      -0.411
## lake_area_ha    0.062 -0.580
## pct.ag         0.179 -0.034  0.276
## chla          -0.670  0.185 -0.181 -0.433
## tsi.cathypereutrophic 0.605 -0.165  0.144  0.382 -0.919

```

```

## tsi.catmesotrophic      -0.330 -0.290  0.093 -0.173  0.604 -0.501
## tsi.catoligotrophic     -0.276 -0.454  0.052 -0.379  0.597 -0.503  0.733
## huc2_code02             -0.416 -0.043 -0.195 -0.214  0.188 -0.151  0.193
## huc2_code04             -0.494  0.337 -0.111 -0.179  0.013 -0.036 -0.304
## huc2_code07             -0.330 -0.050  0.347  0.218 -0.307  0.210 -0.344
## huc2_code09             -0.284  0.037  0.074 -0.188 -0.010 -0.016 -0.313
## huc2_code10             -0.123 -0.385  0.251 -0.158 -0.259  0.242 -0.108
## huc2_code11             0.044  0.268 -0.923 -0.291  0.111 -0.076  0.001
##                          ts.ct1 hc2_02 hc2_04 hc2_07 hc2_09 hc2_10
## maxdepth
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## huc2_code02             0.307
## huc2_code04            -0.313  0.325
## huc2_code07            -0.291  0.277  0.589
## huc2_code09            -0.056  0.233  0.445  0.458
## huc2_code10             0.125  0.387  0.371  0.577  0.394
## huc2_code11             0.123  0.302  0.053 -0.303 -0.059 -0.065
##
## Standardized residuals:
##           Min           Q1           Med           Q3           Max
## -1.31683e+00 -3.69501e-01  1.516748e-16  2.866973e-01  1.378857e+00
##
## Residual standard error: 0.7319761
## Degrees of freedom: 27 total; 13 residual

dredge.ph1.accndvi.st<-dredge(gls.ph1.accndvi.st, beta="sd") #intercept only is best model. Disappointi

## Warning in dredge(gls.ph1.accndvi.st, beta = "sd"): comparing models fitted
## by REML

## Warning in dredge(gls.ph1.accndvi.st, beta = "sd"): do not know how to
## standardize coefficients of 'gls', argument 'beta' ignored

## Fixed term is "(Intercept)"

print(head(dredge.ph1.accndvi.st))

## Global model call: gls(model = cos(accndviphi.ts1) ~ maxdepth + lake_area_ha + pct.ag +
##           chla + tsi.cat + huc2_code, data = modvars.accndvi.phist)
## ---
## Model selection table
##           (Int)      chl hc2_cod    pct.ag tsi.cat df  logLik AICc delta weight
## 1    0.11240
## 33   0.40590
## 17   0.16480      -0.01501
## 2    -0.02266 0.01113
## 3     0.46800      +
## 34   -0.31370 0.04378      + 6 -29.867 75.9 9.34 0.008
## Models ranked by AICc(x)

#long timescales
gls.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(gls.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.ct1 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(gls.coh.accndvi.lt, beta="sd") #intercept only is best model. Disappointi

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

## Warning in dredge(gls.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)

gls.p.accndvi.lt<-gls(accndvip.ts2 ~ tslength + maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.ca
correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(gls.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) tslngr 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(gls.p.accndvi.lt, beta="sd") #intercept only is best model. Disappointing.
```

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

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

```
glms.phi.accndvi.lt<-glms(cos(accndviphi.ts2) ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi
                        correlation=corExp(form = ~ nhd_lat + nhd_long))
summary(glms.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.philt
##      AIC      BIC    logLik
## 128.9434 145.6558 -48.4717
##
## Correlation Structure: Exponential spatial correlation
## Formula: ~nhd_lat + nhd_long
## Parameter estimate(s):
##      range
## 0.2064398
##
## Coefficients:
##              Value Std.Error    t-value p-value
## (Intercept)  -0.3078653  0.8876303  -0.3468395  0.7322
## maxdepth      0.0022125  0.0155863   0.1419549  0.8885
## nhd_ftype436  -1.3100328  1.2113344  -1.0814791  0.2917
## lake_area_ha   0.0000590  0.0000456   1.2936721  0.2098
## pct.ag         0.0039218  0.0217802   0.1800649  0.8588
```

```

## chla -0.0096330 0.0326000 -0.2954902 0.7705
## tsi.cathypereutrophic 1.8327966 1.9970116 0.9177696 0.3692
## tsi.catmesotrophic 0.4079637 0.4693381 0.8692321 0.3945
## tsi.catoligotrophic 0.0653412 0.5906597 0.1106241 0.9130
## huc2_code02 0.4026739 0.6840031 0.5887018 0.5623
## huc2_code04 0.0732165 0.6694618 0.1093663 0.9140
## huc2_code07 0.1421377 0.5992983 0.2371735 0.8148
## huc2_code09 0.7425994 0.9693689 0.7660648 0.4522
## huc2_code10 -0.3158615 0.7884389 -0.4006163 0.6927
##
## Correlation:
## (Intr) mxdepth nh_436 lk_r_h pct.ag chla ts.cth
## maxdepth -0.592
## nhd_ftype436 -0.022 -0.007
## lake_area_ha -0.142 -0.191 -0.110
## pct.ag 0.056 -0.066 -0.438 0.254
## chla -0.703 0.443 0.093 0.114 -0.155
## tsi.cathypereutrophic 0.612 -0.377 -0.339 -0.086 0.159 -0.911
## tsi.catmesotrophic -0.619 0.221 0.055 0.276 -0.075 0.761 -0.653
## tsi.catoligotrophic -0.592 0.101 0.060 0.327 -0.085 0.694 -0.600
## huc2_code02 -0.286 -0.207 -0.024 0.073 0.053 -0.212 0.198
## huc2_code04 -0.619 0.373 0.135 -0.259 -0.342 0.140 -0.123
## huc2_code07 -0.625 0.212 0.012 0.049 -0.061 0.032 -0.066
## huc2_code09 -0.396 0.157 0.061 -0.024 -0.156 0.071 -0.067
## huc2_code10 -0.222 -0.190 0.042 -0.008 -0.098 -0.202 0.185
## ts.ctm ts.ct1 hc2_02 hc2_04 hc2_07 hc2_09
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic 0.761
## huc2_code02 -0.135 0.026
## huc2_code04 0.041 0.014 0.486
## huc2_code07 0.025 0.100 0.641 0.737
## huc2_code09 -0.055 0.075 0.393 0.503 0.517
## huc2_code10 -0.142 0.001 0.579 0.470 0.559 0.360
##
## Standardized residuals:
## Min Q1 Med Q3 Max
## -1.526120e+00 -4.771919e-01 1.040424e-07 3.036786e-01 1.626510e+00
##
## Residual standard error: 0.7686352
## Degrees of freedom: 35 total; 21 residual
dredge.phil.accndvi.lt<-dredge(gls.phil.accndvi.lt, beta="sd") #intercept only is best model. Disappointi
## Warning in dredge(gls.phil.accndvi.lt, beta = "sd"): comparing models fitted
## by REML
## Warning in dredge(gls.phil.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.philt,
##   correlation = corExp(form = ~nhd_lat + nhd_long))
## ---
## Model selection table
##      (Int)      mxd nhd_fty    pct.ag tsi.cat df  logLik AICc delta
## 1  0.05658
## 17 0.06355      +
## 65 -0.10320      + 6 -35.354 85.7 6.26
## 81 -0.10700      + 7 -33.796 85.7 6.29
## 33 0.09438      -0.006614 4 -39.546 88.4 8.98
## 9  -0.05636 0.006575      4 -39.830 89.0 9.54
##   weight
## 1  0.622
## 17 0.312
## 65 0.027
## 81 0.027
## 33 0.007
## 9  0.005
## Models ranked by AICc(x)
```

GLS models sucked, but inspection of results suggested that mixed effects models with random effects of region on the intercept may likely be an improvement.

```
lme.coh.accndvi.st<-lmer(accndvicoh.ts1 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.cat
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lme.coh.accndvi.st)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: accndvicoh.ts1 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag +
##   chla + tsi.cat + (1 | huc2_code)
##   Data: modvars.accndvi
##
## REML criterion at convergence: -22.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.90600 -0.68182 -0.06535  0.64780  2.88041
##
## Random effects:
##   Groups      Name      Variance Std.Dev.
##   huc2_code (Intercept) 0.0005782 0.02405
##   Residual              0.0306185 0.17498
## Number of obs: 143, groups:  huc2_code, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
```

```

## (Intercept)          4.109e-01  5.846e-02  8.237e+01   7.029  5.54e-10
## maxdepth             -1.247e-03  1.179e-03  1.044e+02  -1.058   0.293
## nhd_ftype436          9.060e-02  2.153e-01  1.311e+02   0.421   0.675
## lake_area_ha          6.788e-07  1.782e-06  1.279e+02   0.381   0.704
## pct.ag               -2.604e-03  1.777e-03  1.294e+02  -1.465   0.145
## chla                 -5.612e-04  2.768e-03  1.298e+02  -0.203   0.840
## tsi.cathypereutrophic  1.160e-01  2.032e-01  1.330e+02   0.571   0.569
## tsi.catmesotrophic     2.119e-03  4.870e-02  1.328e+02   0.044   0.965
## tsi.catoligotrophic    8.296e-02  5.768e-02  1.340e+02   1.438   0.153
##
## (Intercept)          ***
## maxdepth
## nhd_ftype436
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) mxdpth nh_436 lk_r_h pct.ag chla   ts.cth ts.ctm
## maxdepth      -0.423
## nhd_ftyp436   -0.031 -0.028
## lake_area_h    0.176 -0.530  0.013
## pct.ag         0.055 -0.032  0.070  0.021
## chla           -0.836  0.143  0.038 -0.072 -0.211
## ts.cthyprtr   0.588 -0.051 -0.401  0.030 -0.114 -0.731
## ts.ctmstrph  -0.752  0.015  0.029 -0.025 -0.153  0.711 -0.468
## ts.ctlgrtrph -0.703 -0.047  0.032  0.061 -0.137  0.707 -0.480  0.714
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
dredge.coh.accndvi.st<-dredge(lme.coh.accndvi.st, beta="sd") #intercept only is best model. Disappointi
## Warning in dredge(lme.coh.accndvi.st, beta = "sd"): comparing models fitted
## by REML
## Fixed term is "(Intercept)"
## Warning: Some predictor variables are on very different scales: consider
## rescaling
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## Warning: Some predictor variables are on very different scales: consider
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## Warning: Some predictor variables are on very different scales: consider
## rescaling
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## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

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

```
## Global model call: lmer(formula = accndvip.ts1 ~ maxdepth + nhd_ftype + lake_area_ha +
##   pct.ag + chla + tsi.cat + (1 | huc2_code), data = modvars.accndvi,
##   na.action = "na.fail")
```

```
## ---
```

```
## Model selection table
```

##	(Int)	chl	mx	nhd_fty	pct.ag	tsi.cat	df	logLik	AICc	delta
## 1	0						3	42.253	-78.3	0.00
## 9	0			+			4	41.609	-74.9	3.40
## 17	0				-0.1153		4	37.637	-67.0	11.35
## 2	0	-0.05738					4	36.642	-65.0	13.34
## 5	0		-0.06052				4	36.495	-64.7	13.63
## 33	0					+	6	38.652	-64.7	13.65

```
## weight
```

```
## 1 0.841
```

```
## 9 0.153
```

```
## 17 0.003
```

```
## 2 0.001
```

```
## 5 0.001
```

```
## 33 0.001
```

```
## Models ranked by AICc(x)
```

```
## Random terms (all models):
```

```
## '1 | huc2_code'
```

```
lme.p.accndvi.st<-lmer(accndvip.ts1 ~ tslength + maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla +
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lme.p.accndvi.st)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
```

```
## lmerModLmerTest]
```

```
## Formula: accndvip.ts1 ~ tslength + maxdepth + nhd_ftype + lake_area_ha +
```

```
##   pct.ag + chla + tsi.cat + (1 | huc2_code)
```

```
## Data: modvars.accndvi
```

```

##
## REML criterion at convergence: 114.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.09352 -0.70997 -0.06146  0.80047  1.86426
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
## huc2_code (Intercept) 0.00000  0.0000
## Residual              0.08213  0.2866
## Number of obs: 143, groups: huc2_code, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    1.030e-01  2.773e-01  1.330e+02   0.371   0.7109
## tslength       1.227e-02  1.240e-02  1.330e+02   0.990   0.3242
## maxdepth       1.513e-03  1.922e-03  1.330e+02   0.787   0.4325
## nhd_ftype436   3.725e-01  3.549e-01  1.330e+02   1.050   0.2958
## lake_area_ha  -2.591e-06  2.886e-06  1.330e+02  -0.898   0.3710
## pct.ag         5.068e-03  2.900e-03  1.330e+02   1.747   0.0829
## chla          2.378e-03  4.522e-03  1.330e+02   0.526   0.5999
## tsi.cathypereutrophic -4.101e-01  3.299e-01  1.330e+02  -1.243   0.2160
## tsi.catmesotrophic  1.003e-01  7.960e-02  1.330e+02   1.260   0.2098
## tsi.catoligotrophic  4.460e-02  9.400e-02  1.330e+02   0.474   0.6359
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) tslngt mxdpth nh_436 lk_r_h pct.ag chla  ts.cth ts.ctm
## tslength    -0.943
## maxdepth     0.058 -0.203
## nhd_ftyp436 -0.119  0.115 -0.050
## lake_area_h -0.027  0.087 -0.527  0.021
## pct.ag      -0.122  0.147 -0.046  0.084  0.010
## chla        -0.152 -0.138  0.151  0.022 -0.071 -0.221
## ts.cthyprtr  0.204 -0.007 -0.035 -0.402  0.028 -0.114 -0.723
## ts.ctmstrph -0.257 -0.003  0.014  0.029 -0.021 -0.153  0.712 -0.473
## ts.ctlgrtrph -0.279  0.033 -0.037  0.035  0.051 -0.144  0.711 -0.489  0.717
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
dredge.p.accndvi.st<-dredge(lme.p.accndvi.st, beta="sd") #intercept only is best model. Disappointing.

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

## Fixed term is "(Intercept)"

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider

```


[illegible]

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

```
## Global model call: lmer(formula = accndvip.ts1 ~ tslength + maxdepth + nhd_ftype +
## lake_area_ha + pct.ag + chla + tsi.cat + (1 | huc2_code),
## data = modvars.accndvi, na.action = "na.fail")
## ---
```

```
## Model selection table
```

```
## (Int) nhd_fty pct.ag      tsl df  logLik AICc delta weight
## 1      0                                3 -26.080 58.3  0.00  0.760
## 9      0      +                                4 -26.261 60.8  2.48  0.220
## 65     0                                0.06570 4 -29.304 66.9  8.57  0.010
## 17     0      0.1236                        4 -30.057 68.4 10.07  0.005
## 73     0      +      0.06756                5 -29.467 69.4 11.04  0.003
## 25     0      + 0.1192                      5 -30.335 71.1 12.77  0.001
```

```
## Models ranked by AICc(x)
```

```
## Random terms (all models):
```

```
## '1 | huc2_code'
```

```
lme.phi.accndvi.st<-lmer(accndviphi.ts1 ~ maxdepth + lake_area_ha + pct.ag + chla + tsi.cat + (1|huc2_code))
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lme.phi.accndvi.st)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
```

```
## Formula:
```

```
## accndviphi.ts1 ~ maxdepth + lake_area_ha + pct.ag + chla + tsi.cat +
## (1 | huc2_code)
```

```
## Data: modvars.accndvi.phist
```

```
##
```

```
## REML criterion at convergence: 118.8
```

```
##
```

```
## Scaled residuals:
```

```
##      Min      1Q   Median      3Q      Max
## -1.41084 -0.70979  0.04223  0.74514  1.63422
```

```
##
```

```
## Random effects:
```

```
## Groups      Name      Variance Std.Dev.
## huc2_code (Intercept) 0.000    0.000
## Residual          2.729    1.652
```

```
## Number of obs: 27, groups: huc2_code, 7
```

```
##
```

```
## Fixed effects:
```

```
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   -1.012e+00  1.256e+00  1.900e+01  -0.806   0.4303
## maxdepth       3.899e-02  5.049e-02  1.900e+01   0.772   0.4494
## lake_area_ha   -6.788e-05  2.543e-04  1.900e+01  -0.267   0.7924
## pct.ag         9.842e-02  5.184e-02  1.900e+01   1.898   0.0729
## chla          -1.024e-02  6.569e-02  1.900e+01  -0.156   0.8778
## tsi.cathypereutrophic -4.689e-01  4.118e+00  1.900e+01  -0.114   0.9105
```

```

## tsi.catmesotrophic      1.340e+00  1.152e+00  1.900e+01  1.163  0.2593
## tsi.catoligotrophic    -7.614e-01  1.345e+00  1.900e+01  -0.566  0.5780
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) mxdpth lk_r_h pct.ag chla   ts.cth ts.ctm
## maxdepth    -0.425
## lake_area_h  0.287 -0.866
## pct.ag       0.159  0.026  0.042
## chla        -0.826  0.060 -0.051 -0.387
## ts.cthyprtr  0.686 -0.021  0.039  0.375 -0.907
## ts.ctmstrph -0.592 -0.241  0.281 -0.170  0.629 -0.528
## ts.ctlgtrph -0.560 -0.358  0.344 -0.336  0.707 -0.615  0.697
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
dredge.ph_i.acndvi.st<-dredge(lme.ph_i.acndvi.st, beta="sd") #model with TSI is unconvincingly better t

## Warning in dredge(lme.ph_i.acndvi.st, beta = "sd"): comparing models fitted
## by REML
## Fixed term is "(Intercept)"
## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
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```

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## Warning: Some predictor variables are on very different scales: consider
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## Warning: Some predictor variables are on very different scales: consider
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## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning in optwrap(optimizer, devfun, getStart(start, rho$lower, rho$pp), :
## convergence code 3 from bobyqa: bobyqa -- a trust region step failed to
## reduce q

## Warning: Some predictor variables are on very different scales: consider
## rescaling

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## rescaling

```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

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## rescaling
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## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

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

```
## Global model call: lmer(formula = accndviphi.ts1 ~ maxdepth + lake_area_ha + pct.ag +
##      chla + tsi.cat + (1 | huc2_code), data = modvars.accndvi.phist,
##      na.action = "na.fail")
```

```
## ---
```

```
## Model selection table
```

```
##      (Int)    chl    mxd pct.ag tsi.cat df  logLik  AICc delta weight
## 17      0
## 1      0
## 25      0          0.3546      + 7 -48.072 116.0  4.47  0.058
## 9       0          0.2974      + 4 -53.679 117.2  5.61  0.033
## 18      0 0.2803
## 21      0          0.1552      + 7 -50.142 120.2  8.61  0.007
```

```
## Models ranked by AICc(x)
```

```
## Random terms (all models):
```

```
## '1 | huc2_code'
```

```
lme.coh.accndvi.lt<-lmer(accndvicoh.ts2 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla + tsi.cat
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lme.coh.accndvi.lt)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
```

```
## lmerModLmerTest]
```

```
## Formula: accndvicoh.ts2 ~ maxdepth + nhd_ftype + lake_area_ha + pct.ag +
##      chla + tsi.cat + (1 | huc2_code)
```

```
##      Data: modvars.accndvi
```

```
##
```

```
## REML criterion at convergence: 47.3
```

```
##
```

```
## Scaled residuals:
```

```
##      Min      1Q   Median      3Q      Max
## -2.21276 -0.57031 -0.02055  0.75164  1.74788
```

```
##
```

```
## Random effects:
```

```
##      Groups      Name      Variance Std.Dev.
```

```
## huc2_code (Intercept) 0.001896 0.04354
```

```

## Residual          0.051117 0.22609
## Number of obs: 143, groups:  huc2_code, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    5.585e-01  7.738e-02  8.109e+01   7.217 2.55e-10
## maxdepth      -9.739e-04  1.548e-03  1.111e+02  -0.629  0.5306
## nhd_ftype436    4.656e-01  2.782e-01  1.311e+02   1.674  0.0965
## lake_area_ha   -2.708e-07  2.322e-06  1.308e+02  -0.117  0.9073
## pct.ag         2.006e-03  2.314e-03  1.321e+02   0.867  0.3876
## chla          9.604e-04  3.605e-03  1.310e+02   0.266  0.7903
## tsi.cathypereutrophic -1.544e-01  2.641e-01  1.335e+02  -0.585  0.5598
## tsi.catmesotrophic  -1.813e-02  6.301e-02  1.326e+02  -0.288  0.7740
## tsi.catoligotrophic  6.080e-02  7.478e-02  1.339e+02   0.813  0.4176
##
## (Intercept)      ***
## maxdepth
## nhd_ftype436      .
## lake_area_ha
## pct.ag
## chla
## tsi.cathypereutrophic
## tsi.catmesotrophic
## tsi.catoligotrophic
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) mxdpth nh_436 lk_r_h pct.ag chla  ts.cth ts.ctm
## maxdepth      -0.431
## nhd_ftyp436   -0.030 -0.029
## lake_area_h    0.183 -0.537  0.014
## pct.ag         0.058 -0.042  0.070  0.034
## chla          -0.824  0.154  0.037 -0.080 -0.214
## ts.cthyprtr   0.584 -0.060 -0.399  0.032 -0.113 -0.733
## ts.ctmstrph  -0.735  0.017  0.030 -0.027 -0.152  0.706 -0.465
## ts.ctlgrtrph -0.677 -0.056  0.033  0.068 -0.129  0.697 -0.475  0.712
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
dredge.coh.accndvi.lt<-dredge(lme.coh.accndvi.lt, beta="sd") #lake type is marginal improvement over in
## Warning in dredge(lme.coh.accndvi.lt, beta = "sd"): comparing models fitted
## by REML
## Fixed term is "(Intercept)"
## Warning: Some predictor variables are on very different scales: consider
## rescaling
## Warning: Some predictor variables are on very different scales: consider
## rescaling
## Warning: Some predictor variables are on very different scales: consider
## rescaling

```

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## Warning: Some predictor variables are on very different scales: consider
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## rescaling
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```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

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

```
## Global model call: lmer(formula = accndvcoh.ts2 ~ maxdepth + nhd_ftype + lake_area_ha +
##   pct.ag + chla + tsi.cat + (1 | huc2_code), data = modvars.accndvi,
##   na.action = "na.fail")
```

```
## ---
```

```
## Model selection table
```

##	(Int)	chl	mxl	nhd_fty	pct.ag	df	logLik	AICc	delta	weight
## 9	0			+		4	7.370	-6.5	0.00	0.510
## 1	0					3	6.264	-6.4	0.10	0.486
## 17	0				0.09355	4	1.599	5.1	11.54	0.002
## 25	0			+	0.06678	5	2.404	5.6	12.08	0.001
## 2	0	0.07609				4	1.074	6.1	12.59	0.001
## 5	0	-0.07076				4	0.853	6.6	13.03	0.001

```
## Models ranked by AICc(x)
```

```
## Random terms (all models):
```

```
## '1 | huc2_code'
```

```
lme.p.accndvi.lt<-lmer(accndvip.ts2 ~ tslength + maxdepth + nhd_ftype + lake_area_ha + pct.ag + chla +
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
summary(lme.p.accndvi.lt)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
```

```
## Formula: accndvip.ts2 ~ tslength + maxdepth + nhd_ftype + lake_area_ha +
##   pct.ag + chla + tsi.cat + (1 | huc2_code)
```

```
## Data: modvars.accndvi
```

```
##
```

```
## REML criterion at convergence: 134.2
```

```

##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.71395 -0.76388  0.02568  0.84056  1.74987
##
## Random effects:
##   Groups   Name      Variance Std.Dev.
## huc2_code (Intercept) 0.0005271 0.02296
## Residual              0.0949908 0.30821
## Number of obs: 143, groups: huc2_code, 8
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    3.443e-01  2.996e-01  1.243e+02   1.149   0.253
## tslength       -7.858e-04  1.336e-02  1.330e+02  -0.059   0.953
## maxdepth        1.321e-03  2.083e-03  1.017e+02   0.634   0.527
## nhd_ftype436    -2.605e-01  3.817e-01  1.298e+02  -0.683   0.496
## lake_area_ha     2.297e-06  3.120e-06  1.226e+02   0.736   0.463
## pct.ag           1.487e-04  3.135e-03  1.234e+02   0.047   0.962
## chla             6.813e-03  4.881e-03  1.295e+02   1.396   0.165
## tsi.cathypereutrophic -5.834e-01  3.559e-01  1.311e+02  -1.639   0.104
## tsi.catmesotrophic   6.490e-02  8.567e-02  1.318e+02   0.758   0.450
## tsi.catoligotrophic  1.395e-01  1.013e-01  1.330e+02   1.377   0.171
##
## Correlation of Fixed Effects:
##              (Intr)  tslngt  mxdpth  nh_436  lk_r_h  pct.ag  chla   ts.cth  ts.ctm
## tslength      -0.942
## maxdepth       0.050 -0.198
## nhd_ftyp436   -0.119  0.116 -0.050
## lake_area_h   -0.023  0.085 -0.529  0.021
## pct.ag        -0.119  0.145 -0.049  0.084  0.019
## chla          -0.156 -0.134  0.155  0.022 -0.075 -0.222
## ts.cthyprtr   0.208 -0.010 -0.039 -0.401  0.028 -0.115 -0.722
## ts.ctmstrph  -0.255 -0.004  0.015  0.029 -0.023 -0.153  0.710 -0.471
## ts.ctlgtrph  -0.274  0.031 -0.042  0.035  0.055 -0.140  0.707 -0.486  0.716
## fit warnings:
## Some predictor variables are on very different scales: consider rescaling
dredge.p.accndvi.lt<-dredge(lme.p.accndvi.lt, beta="sd") #intercept only is best model. Disappointing.

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

## Fixed term is "(Intercept)"

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
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## rescaling
```



```

## Model selection table
##      (Int)      mxd nhd_fty    pct.ag      tsl df  logLik AICc delta weight
## 1         0                                     3 -36.419 79.0  0.00  0.524
## 9         0               +                                     4 -35.486 79.3  0.25  0.462
## 65        0                                     4 -39.873 88.0  9.03  0.006
## 73        0               +      0.0058720 5 -38.947 88.3  9.32  0.005
## 5         0 0.1004                                     4 -41.173 90.6 11.62  0.002
## 17        0               -0.02605          4 -41.361 91.0 12.00  0.001
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | huc2_code'

lme.phi.accndvi.lt<-lmer(accndviphi.ts2 ~ maxdepth + lake_area_ha + pct.ag + chla + tsi.cat + (1|huc2_code)

## Warning: Some predictor variables are on very different scales: consider
## rescaling

## Warning: Some predictor variables are on very different scales: consider
## rescaling

summary(lme.phi.accndvi.lt)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula:
## accndviphi.ts2 ~ maxdepth + lake_area_ha + pct.ag + chla + tsi.cat +
##      (1 | huc2_code)
##      Data: modvars.accndvi.philt
##
## REML criterion at convergence: 159
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.46024 -0.72225  0.00125  0.57741  1.66743
##
## Random effects:
##      Groups      Name      Variance Std.Dev.
## huc2_code (Intercept) 0.000      0.000
## Residual              3.308      1.819
## Number of obs: 35, groups: huc2_code, 6
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   -3.944e-01  1.478e+00  2.700e+01  -0.267    0.792
## maxdepth       1.673e-02  2.752e-02  2.700e+01   0.608    0.548
## lake_area_ha   -5.263e-05  9.689e-05  2.700e+01  -0.543    0.591
## pct.ag         5.962e-02  4.166e-02  2.700e+01   1.431    0.164
## chla          -1.414e-02  7.100e-02  2.700e+01  -0.199    0.844
## tsi.cathypereutrophic 1.217e+00  4.108e+00  2.700e+01   0.296    0.769
## tsi.catmesotrophic  -7.606e-01  1.158e+00  2.700e+01  -0.657    0.517
## tsi.catoligotrophic  -1.656e-01  1.398e+00  2.700e+01  -0.118    0.907
##
## Correlation of Fixed Effects:
##              (Intr) mxdpth lk_r_h pct.ag chla    ts.cth ts.ctm
## maxdepth      -0.455

```



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

## Global model call: lmer(formula = accndviphi.ts2 ~ maxdepth + lake_area_ha + pct.ag +
##   chla + tsi.cat + (1 | huc2_code), data = modvars.accndvi.philt,
##   na.action = "na.fail")
## ---
## Model selection table
##   (Int)    chl      mxd pct.ag tsi.cat df  logLik  AICc delta weight
## 1      0
## 17     0
## 9      0          0.3005
## 25     0          0.2583
## 2      0 0.1398
## 5      0      0.01092
## Models ranked by AICc(x)
## Random terms (all models):
## '1 | huc2_code'
```

Adding random effects of huc2 region on intercept helped somewhat. Some possibilities are to add more detailed lake type classes, and to model 2-3 regions separately.