

Raw Data

Yuxiang

```
#packages
```

```
library(reshape2)
library(readxl)
library(lubridate)
```

```
##
## Attaching package: 'lubridate'

## The following objects are masked from 'package:base':
##
##   date, intersect, setdiff, union
```

```
library(ggplot2)
library(ggpubr)
library(ggpmisc)
```

```
## Loading required package: ggpp
```

```
##
## Attaching package: 'ggpp'

## The following object is masked from 'package:ggplot2':
##
##   annotate
```

```
library(reshape2)
library(readr)
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.2
## --
```

```
## v tibble  3.1.8    v dplyr   1.1.0
## v tidyr   1.3.0    v stringr 1.5.0
## v purrr   1.0.1    v forcats 1.0.0
## -- Conflicts ----- tidyverse_conflicts() --
## x ggpp::annotate()      masks ggplot2::annotate()
## x lubridate::as.difftime() masks base::as.difftime()
## x lubridate::date()      masks base::date()
## x dplyr::filter()        masks stats::filter()
```

```
## x lubridate::intersect() masks base::intersect()
## x dplyr::lag() masks stats::lag()
## x lubridate::setdiff() masks base::setdiff()
## x lubridate::union() masks base::union()
```

```
library(here)
```

```
## here() starts at /Users/min/Desktop/TSA/FinalProject/FinalProject_ENV790
```

```
library(cowplot)
```

```
##
## Attaching package: 'cowplot'
##
## The following object is masked from 'package:ggpubr':
##
##     get_legend
##
## The following object is masked from 'package:lubridate':
##
##     stamp
```

```
library(tseries)
```

```
## Registered S3 method overwritten by 'quantmod':
##   method      from
##   as.zoo.data.frame zoo
```

```
#install.packages("vegan")
#install.packages("permute")
#install.packages("lattice")
library(permute)
library(lattice)
library(mgcv)
```

```
## Loading required package: nlme
##
## Attaching package: 'nlme'
##
## The following object is masked from 'package:dplyr':
##
##     collapse
##
## This is mgcv 1.8-42. For overview type 'help("mgcv-package")'.
```

```
library(vegan)
```

```
## This is vegan 2.6-4
```

```
#install.packages("relaimpo")  
library(relaimpo)
```

```
## Loading required package: MASS  
##  
## Attaching package: 'MASS'  
##  
## The following object is masked from 'package:dplyr':  
##  
##     select  
##  
## Loading required package: boot  
##  
## Attaching package: 'boot'  
##  
## The following object is masked from 'package:lattice':  
##  
##     melanoma  
##  
## Loading required package: survey  
## Loading required package: grid  
## Loading required package: Matrix  
##  
## Attaching package: 'Matrix'  
##  
## The following objects are masked from 'package:tidyr':  
##  
##     expand, pack, unpack  
##  
## Loading required package: survival  
##  
## Attaching package: 'survival'  
##  
## The following object is masked from 'package:boot':  
##  
##     aml  
##  
## Attaching package: 'survey'  
##  
## The following object is masked from 'package:vegan':  
##  
##     calibrate  
##  
## The following object is masked from 'package:graphics':  
##  
##     dotchart  
##  
## Loading required package: mitools  
## This is the global version of package relaimpo.  
##  
## If you are a non-US user, a version with the interesting additional metric pmvd is available  
##
```

```
## from Ulrike Groempings web site at prof.beuth-hochschule.de/groemping.
```

```
library(zoo)
```

```
##  
## Attaching package: 'zoo'  
##  
## The following objects are masked from 'package:base':  
##  
##    as.Date, as.Date.numeric
```

```
#install.packages("magrittr")  
library(magrittr)
```

```
##  
## Attaching package: 'magrittr'  
##  
## The following object is masked from 'package:purrr':  
##  
##    set_names  
##  
## The following object is masked from 'package:tidyr':  
##  
##    extract
```

```
library(knitr)  
library(dplyr)  
#install.packages("kableExtra")  
#install.packages("mgcv")
```

```
#phyto
```

```
phyto <- read.csv( file = "./Data/Phyto_raw.csv")  
phyto$sampldate <- ymd(phyto$sampldate)
```

infomation

```
###site_observation
```

```
## # A tibble: 4 x 2  
##   lakeid Observation_Count  
##   <chr>             <int>  
## 1 ME                402  
## 2 MO                355  
## 3 WI                 23  
## 4 FI                 1
```

Table 1: Site Information

Site	Observation Date	Count
ME		402
MO		355
WI		23
FI		1

###Division level Total Biomass

Table 2: Division level Total Biomass (*mg/L*)

Genus	Count	Total Biomass	Max Biomass	Min Biomass	Mean Biomass
Cyanophyta	8581	1824.2521267	76.0000000	0.0000000	0.2125920
Bacillariophyta	1914	378.0188786	13.4027978	0.0000319	0.1975020
Chlorophyta	4368	244.9520459	84.6924000	0.0000000	0.0560788
Cryptophyta	1876	76.1100881	2.9630000	0.0000363	0.0405704
Pyrrhophyta	415	29.1295004	5.3194000	0.0000000	0.0701916
Chrysophyta	871	11.3487339	0.5268000	0.0000000	0.0130295
Haptophyta	190	7.4487959	0.7395927	0.0000256	0.0392042
Miscellaneous	387	4.4740805	0.1359000	0.0000000	0.0115609
Euglenophyta	44	1.1695524	0.3695402	0.0002000	0.0265807
Xanthophyta	7	0.0690431	0.0517453	0.0005859	0.0098633
Rhodophyta	1	0.0309404	0.0309404	0.0309404	0.0309404

###Genus level Total Biomass

Table 3: Genus level Total Biomass (*mg/L*)

Division	Genus	Count	Total Biomass	Max Biomass	Min Biomass	Mean Biomass
Cyanophyta	Aphanizomenon	812	923.88321	76.000000	0.0004000	1.1377872
Cyanophyta	Microcystis	1065	436.73355	23.370568	0.0000284	0.4100785
Bacillariophyta	Stephanodiscus	501	259.59263	13.402798	0.0001000	0.5181490
Chlorophyta	Coelastrum	42	85.44968	84.692400	0.0004569	2.0345162
Chlorophyta	Actinastrum	53	84.45011	84.070000	0.0001421	1.5933983
Cyanophyta	Anabaena	525	79.18206	5.336000	0.0003000	0.1508230
Cyanophyta	Planktothrix	96	70.65535	8.519000	0.0004000	0.7359932
Cyanophyta	Lyngbya	247	50.47694	9.042087	0.0000570	0.2043601
Cryptophyta	Cryptomonas	880	47.31605	2.963000	0.0000363	0.0537682
Bacillariophyta	Aulacoseira	180	44.14470	4.202500	0.0005140	0.2452483