A report on Lake Ontario's microbes

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#Prepare the R environment

```
#Load libraries/packages
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.4     v tidyr     1.3.1
## v purrr     1.0.4
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

#Load in the Lake Ontario Data

```
# load in Lake Ontario microbial community data
sample_and_taxon <-
  read_csv("data/sample_and_taxon.csv")
```

```
## Rows: 71 Columns: 15
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr  (2): sample_id, env_group
## dbl (13): depth, cells_per_ml, temperature, total_nitrogen, total_phosphorus...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
#inspect the data
glimpse(sample_and_taxon)
```

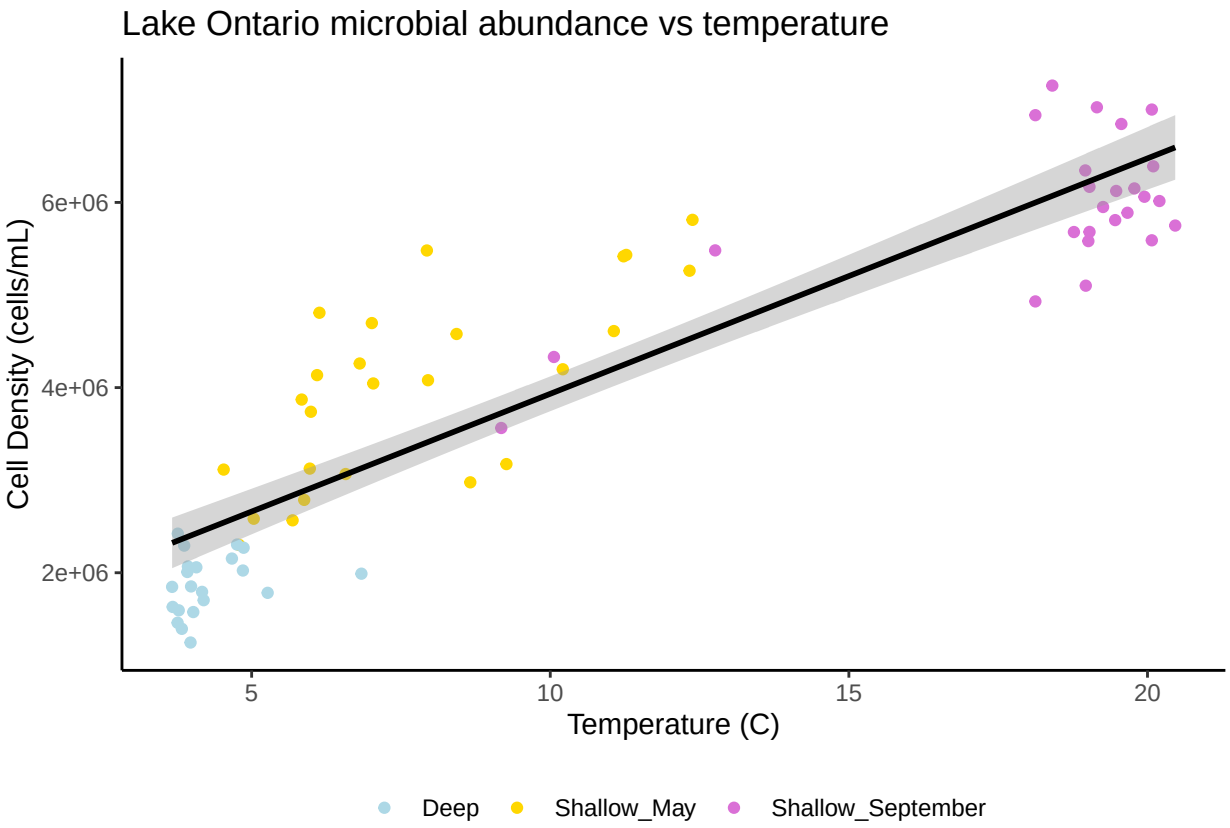
```
## Rows: 71
## Columns: 15
## $ sample_id         <chr> "May_12_B", "May_12_E", "May_12_M", "May_17_E", "May~
## $ env_group         <chr> "Deep", "Shallow_May", "Shallow_May", "Shallow_May",~
## $ depth             <dbl> 102.8, 5.0, 15.0, 5.0, 27.0, 5.0, 19.0, 135.0, 5.0, ~
## $ cells_per_ml      <dbl> 2058864, 4696827, 4808339, 3738681, 2153086, 3124920~
```

```
## $ temperature       <dbl> 4.07380, 7.01270, 6.13500, 5.99160, 4.66955, 5.97390~
## $ total_nitrogen    <dbl> 465, 465, 474, 492, 525, 521, 539, 505, 473, 515, 47~
## $ total_phosphorus  <dbl> 3.78, 4.39, 5.37, 4.67, 4.44, 3.71, 4.23, 4.18, 6.64~
## $ diss_org_carbon   <dbl> 2.478, 2.380, 2.601, 2.435, 2.396, 2.283, 2.334, 2.3~
## $ chlorophyll       <dbl> 0.05, 2.53, 3.20, 0.55, 0.48, 0.79, 0.44, 0.22, 3.44~
## $ Proteobacteria    <dbl> 0.4120986, 0.3389293, 0.2762080, 0.4351188, 0.410063~
## $ Actinobacteriota  <dbl> 0.1288958, 0.1861232, 0.2866884, 0.1910769, 0.280123~
## $ Bacteroidota      <dbl> 0.08065717, 0.23470807, 0.21659843, 0.21576244, 0.11~
## $ Chloroflexi       <dbl> 0.19463564, 0.08086689, 0.07032061, 0.08498357, 0.13~
## $ Verrucomicrobiota <dbl> 0.13249532, 0.10878214, 0.09991639, 0.05752092, 0.06~
## $ Cyanobacteria     <dbl> 2.482454e-04, 9.574640e-03, 1.262830e-02, 1.288730e-~
```

#Plot Lake Ontario microbial abundance vs temperature

```
ggplot(data = sample_and_taxon,
       aes(x=temperature, y=cells_per_ml)) +
  geom_point(aes(color=env_group)) +
  labs(title="Lake Ontario microbial abundance vs temperature",
       x = "Temperature (C)", y= "Cell Density (cells/mL)") +
  theme_classic() +
  theme(legend.position = "bottom",
        legend.title = element_blank()) +
  scale_color_manual(values=c("lightblue",
                              "gold",
                              "orchid")) +
  geom_smooth(method = "lm", color="black")
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



The above plot shows that:

- there's positive relationship between temperature and cell abundances
- for example: deep samples are the coldest and have the fewest files

The total number of samples is 71. For this set of samples, temperatures range from min of 3.67 to max of 20.46