metadata

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knitr::opts\_chunk$set(echo = TRUE)  
require(tidyverse)

## Loading required package: tidyverse

## Loading tidyverse: ggplot2  
## Loading tidyverse: tibble  
## Loading tidyverse: tidyr  
## Loading tidyverse: readr  
## Loading tidyverse: purrr  
## Loading tidyverse: dplyr

## Conflicts with tidy packages ----------------------------------------------

## filter(): dplyr, stats  
## lag(): dplyr, stats

require(knitr)

## Loading required package: knitr

require(pander)

## Loading required package: pander

setwd("~/Dropbox/Projects/population\_genomics/maps")  
  
a = read\_csv("metadata.csv")

## Parsed with column specification:  
## cols(  
## Sample = col\_character(),  
## Environment = col\_character(),  
## WaterType = col\_character(),  
## Salinity = col\_double(),  
## Temperature = col\_double(),  
## Location = col\_character(),  
## Region = col\_character(),  
## Latitude = col\_double(),  
## Longitude = col\_double(),  
## Continent = col\_character(),  
## Code = col\_character()  
## )

a = filter(a, Sample %in% c("V1E", "MAE", "BRE", "MIE")) %>%  
 select(-Continent, -Region, -Code)  
  
kable(a)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Environment | WaterType | Salinity | Temperature | Location | Latitude | Longitude |
| BRE | Copepod | Fresh | 0.0 | 29.7 | Braddock Bay | 43.307 | -77.706 |
| MAE | Copepod | Salt | 5.0 | NA | Montmagnay | 46.990 | -70.550 |
| MIE | Copepod | Fresh | 0.1 | 15.7 | Milwaukee | 43.051 | -87.882 |
| V1E | Copepod | Salt | 13.7 | 5.9 | Lisle Verte | 48.002 | -69.423 |