multi-variate

Getting Started

Libraries

Data

```
dust<- read_csv(here("data", "processed_data", "dust_master.csv")) #Different Dust attribut</pre>
Rows: 32 Columns: 9
-- Column specification ------
Delimiter: ","
dbl (8): t1, t7, t13, t19, tsum, tavg, t7sum, t7avg
date (1): date
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.
  data<- read_csv(here("data", "processed_data", "tx_master.csv")) #Master Data</pre>
New names:
Rows: 1005 Columns: 26
-- Column specification
----- Delimiter: "," chr
(3): hr_cst, site, Type dbl (22): ...1, SUM, dust, chl, sal, temp, do_mgl,
do_per, pH, secchi, amm,... date (1): date
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.
* `` -> `...1`
```

Cleaning

Clean and Trim

Make into one data set

```
master<-
    dust %>% full_join(data) %>%
    filter(hr_cst %in% "01") #While this is technically not for hour 1, this gets ride of al

Joining, by = "date"

master<- master %>%
    select(site, sal, temp, copies_mL,t7sum, date, orthop,nn, don,doc) %>%
    mutate(t7sum = log10(t7sum))
```

Site-specific Data sets and Clean df

```
b<- master %>%
  filter(site %in% "Gulf" | date %in% as.Date('2022-07-05') : as.Date('2022-07-06'))
b<- b %>%
mutate(
  lag =Lag(b$t7sum, shift = 1)) %>% #Create 1 day lag
filter(between(date, as.Date('2022-07-07'), as.Date('2022-07-19'))) %>%
select(!c(date,t7sum,site)) %>%
  rename("log10dust" = "lag")
```

Models

0. Null Model:

Create 5 Fold

```
fold <- vfold_cv(b, v = 5, repeats = 5) #Data was too small to stratify (<20)</pre>
```

Make Models

Get Metrics for Null

RMSE

AIC

```
null_mod<-
   lm(copies_mL ~ 1, data = b)
aic0<-AIC(null_mod) %>% round(digits = 2)
```

1. Dust Model

Model

```
#Create Recipe for Growth
  growth_recipe1<- recipe(copies_mL ~ log10dust, data = b)</pre>
  #Workflow that adds recipe to model
  Growth_wflow1<-
    workflow() %>%
    add_model(lm_mod) %>%
    add_recipe(growth_recipe1)
  #Use workflow to fit model to data set
  growth_fit1<- Growth_wflow1 %>%
    fit(data = b)
  #View as Tibble
  growth_fit1 %>%
    extract_fit_parsnip() %>%
    tidy()
# A tibble: 2 x 5
              estimate std.error statistic p.value
  <chr>
               <dbl> <dbl> <dbl> <dbl> <dbl>
1 (Intercept) 135834.
                         29387.
                                     4.62 0.000947
2 log10dust
            101960. 36063.
                                 2.83 0.0179
Metrics
  aug_test1 <- augment(growth_fit1, b)</pre>
  rmse1 <- aug_test1 %>% rmse(truth = copies_mL, .pred)
  rsq1 <- aug_test1 %>% rsq(truth = copies_mL, .pred)
  mod1<- lm(copies_mL ~ log10dust, b)</pre>
  aic1<-AIC(mod1) %>% round(digits = 2)
  metrics1<- full_join(rmse1, rsq1)</pre>
Joining, by = c(".metric", ".estimator", ".estimate")
  metrics1
```

2. Water Chemistry Model

Model

```
#Create Recipe for Growth
  growth_recipe2<- recipe(copies_mL ~ sal+temp, data = b)</pre>
  #Workflow that adds recipe to model
  Growth_wflow2<-
    workflow() %>%
    add_model(lm_mod) %>%
    add_recipe(growth_recipe2)
  #Use workflow to fit model to data set
  growth_fit2<- Growth_wflow2 %>%
    fit(data = b)
  #View as Tibble
  growth_fit2 %>%
    extract_fit_parsnip() %>%
    tidy()
# A tibble: 3 x 5
             estimate std.error statistic p.value
 term
  <chr>
                <dbl>
                          <dbl>
                                    <dbl> <dbl>
1 (Intercept) 659851. 826558.
                                    0.798 0.445
                                  0.500 0.629
                      19373.
2 sal
                9688.
3 temp
              -33450.
                        11891. -2.81 0.0203
```

Metrics

```
aug_test2 <- augment(growth_fit2, b)
rmse2 <- aug_test2 %>% rmse(truth = copies_mL, .pred)
rsq2 <- aug_test2 %>% rsq(truth = copies_mL, .pred)
```

3. Chemistry + Dust

Model

```
#Create Recipe for Growth
growth_recipe3<- recipe(copies_mL ~ sal+temp + log10dust, data = b)

#Workflow that adds recipe to model
Growth_wflow3<-
    workflow() %>%
    add_model(lm_mod) %>%
    add_recipe(growth_recipe3)

#Use workflow to fit model to data set
growth_fit3<- Growth_wflow3 %>%
    fit(data = b)

#View as Tibble
growth_fit3 %>%
    extract_fit_parsnip() %>%
    tidy()
```

A tibble: 4 x 5

```
estimate std.error statistic p.value
 term
 <chr>
               <dbl>
                         <dbl>
                                  <dbl>
                                          <dbl>
1 (Intercept) 972372.
                      787547.
                                          0.252
                                  1.23
2 sal
              -5385.
                        20210.
                                 -0.266
                                          0.797
3 temp
             -23395.
                       12646.
                                -1.85
                                          0.101
4 log10dust
              70187.
                       43844.
                                  1.60
                                          0.148
```

Metrics

```
aug_test3 <- augment(growth_fit3, b)</pre>
  rmse3 <- aug_test3 %>% rmse(truth = copies_mL, .pred)
  rsq3 <- aug_test3 %>% rsq(truth = copies_mL, .pred)
  mod3<- lm(copies_mL ~ sal+temp + log10dust, b)</pre>
  aic3<- AIC(mod3)%>% round(digits = 2)
  metrics3<- full_join(rmse3, rsq3)</pre>
Joining, by = c(".metric", ".estimator", ".estimate")
  metrics3
# A tibble: 2 x 3
  .metric .estimator .estimate
 <chr> <chr>
                          <dbl>
1 rmse
          standard
                    29952.
2 rsq
          standard
                         0.618
```

4. Model 3 + Nutrients

Model

```
#Create Recipe for Growth
growth_recipe4<- recipe(copies_mL ~ sal+temp+orthop+log10dust+nn, data = b)

#Workflow that adds recipe to model
Growth_wflow4<-
workflow() %>%
add_model(lm_mod) %>%
```

```
add_recipe(growth_recipe4)
  #Use workflow to fit model to data set
  growth_fit4<- Growth_wflow4 %>%
    fit(data = b)
  #View as Tibble
  growth_fit4 %>%
    extract_fit_parsnip() %>%
    tidy()
# A tibble: 6 x 5
 term
             estimate std.error statistic p.value
 <chr>
                <dbl>
                        <dbl>
                                    <dbl>
                                            <dbl>
1 (Intercept) 1110980.
                      821260.
                                    1.35
                                            0.225
2 sal
              -15150.
                        22242.
                                 -0.681
                                            0.521
                                  -1.28
3 temp
              -17676.
                        13802.
                                            0.248
              42986. 260706.
                                  0.165 0.874
4 orthop
5 log10dust
              92110.
                        51339.
                                  1.79
                                            0.123
                                0.613 0.562
              286931. 467807.
6 nn
Metrics
  aug_test4 <- augment(growth_fit4, b)</pre>
  rmse4 <- aug_test4 %>% rmse(truth = copies_mL, .pred)
  rsq4 <- aug_test4 %>% rsq(truth = copies_mL, .pred)
  mod4<- lm(copies_mL ~ sal+temp+orthop+log10dust+nn, b)</pre>
  aic4<- AIC(mod4)%>% round(digits = 2)
  metrics4<- full_join(rmse4, rsq4)</pre>
Joining, by = c(".metric", ".estimator", ".estimate")
  metrics4
# A tibble: 2 x 3
  .metric .estimator .estimate
 <chr> <chr>
                        <dbl>
```

```
1 rmse standard 26604.
2 rsq standard 0.699
```

5. Module 4 + DOM

Model

```
#Create Recipe for Growth
  growth_recipe5<- recipe(copies_mL ~ sal+temp+log10dust+orthop+nn+don+doc, data = b)</pre>
  #Workflow that adds recipe to model
  Growth_wflow5<-
    workflow() %>%
    add_model(lm_mod) %>%
    add_recipe(growth_recipe5)
  #Use workflow to fit model to data set
  growth_fit5<- Growth_wflow5 %>%
    fit(data = b)
  #View as Tibble
  growth_fit5 %>%
    extract_fit_parsnip() %>%
    tidy()
# A tibble: 8 x 5
 term
             estimate std.error statistic p.value
 <chr>>
                <dbl>
                          <dbl>
                                    <dbl>
                                            <dbl>
1 (Intercept) 783691. 1007915.
                                    0.778
                                            0.480
2 sal
                         25053.
                                  -0.454
              -11374.
                                            0.673
3 temp
              -10370.
                         17575.
                                   -0.590
                                            0.587
4 log10dust
                                   1.41
              84206.
                        59840.
                                            0.232
5 orthop
              185666.
                        354271.
                                    0.524 0.628
6 nn
              214439. 596064.
                                   0.360 0.737
                                  -0.836 0.450
7 don
               -4314.
                         5160.
```

-0.546 0.614

Metrics

8 doc

-149.

272.

```
aug_test5 <- augment(growth_fit5, b)</pre>
  rmse5 <- aug_test5 %>% rmse(truth = copies_mL, .pred)
  rsq5 <- aug_test5 %>% rsq(truth = copies_mL, .pred)
  mod5<- lm(copies_mL ~ sal+temp+log10dust+orthop+nn+don+doc, b)</pre>
  aic5<-AIC(mod5)%>% round(digits = 2)
  metrics5<- full_join(rmse5, rsq5)</pre>
Joining, by = c(".metric", ".estimator", ".estimate")
  metrics5
# A tibble: 2 x 3
  .metric .estimator .estimate
  <chr> <chr>
                          <dbl>
1 rmse
          standard 23880.
                          0.757
2 rsq
         standard
```

Tables

Label Metrics

```
#R2
rs1<- rsq1$.estimate %>% round(digits = 2)
rs2<- rsq2$.estimate %>% round(digits = 2)
rs3<- rsq3$.estimate %>% round(digits = 2)
rs4<- rsq4$.estimate %>% round(digits = 2)
rs5<- rsq5$.estimate %>% round(digits = 2)

#RMSE
rm1<- rmse1$.estimate
rm2<- rmse2$.estimate
rm3<- rmse3$.estimate
rm4<- rmse4$.estimate
rm5<- rmse5$.estimate</pre>
```

Make Table

Table 1: Gulf: Comparative linear regression analysis of Vibrio copies per mL between 6 operational models.

Model	R2	RMSE	AIC
Null Model	NA	50771.79	296.98
Model 1: Dust	0.44	36132.11	291.93
Model 2: Water Chemistry	0.5	34417.21	292.77
Model 3: Chemistry + Dust	0.62	29952.44	291.43
Model 4: Model 3 + Nutrients	0.7	26604.11	292.59
Model 5: Model 4 + DOM	0.76	23880.38	293.99

```
kable(data.frame(Model = c("Null Model", "Model 1: Dust", "Model 2: Water Chemistry", "Model
R2 = c(rs0,rs1,rs2,rs3,rs4,rs5),
RMSE = c(rm0,rm1,rm2,rm3,rm4,rm5),
AIC = c(aic0, aic1,aic2,aic3,aic4,aic5)),
caption = "Gulf: Comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear regression analysis of Vibrio copies per mL between the comparative linear re
```