

Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTIme objects
4.) Observation naming
6.) DO Corrections
6.a) DO table & DO correction Plot Check
7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
8.) Analysis, Respirometry - Creating the Slope Function
9.) Merging ds and dRESPmsr
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15.) Krill Sparkle Function (80% DO dataframe)
15.b) Krill Sparkle Function (1hr Trial dataframe)
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17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

Respirometry Trials for Summer Krill 2019

Hello World

Author: OA Lab, NWFSC Title: Respirometry Trials for Summer Krill 2019 Date: December 2020 - February 2021

Version Check

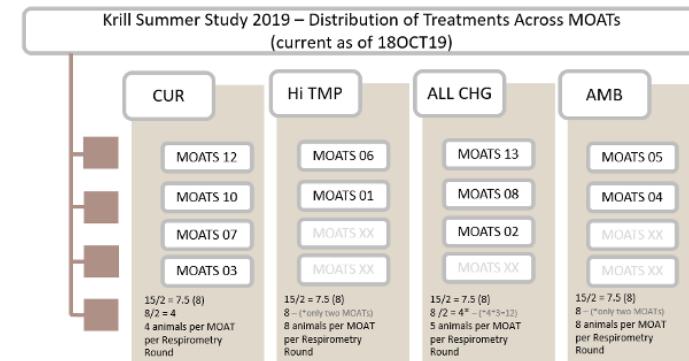
Libraries

Respirometry and Project End Determining Factors for Project End

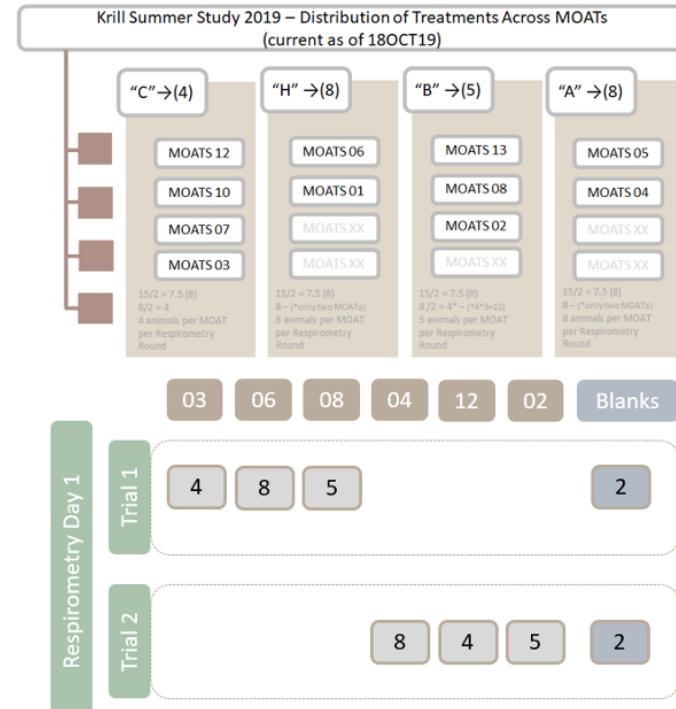
Goals Our goal is to have 4 lipid samples from each MOAT at the end of the study. A wild cohort was measured for both their size and wet weight. Whole body morts were measured to get a sense of the size for the animals. *End of Study Determinations*. End of the Study was biomass dependent to be able to accomplish Lipid analysis preparation.

In short 72 animals were selected for respirometry. Upwards of 200 animals (including those used in respirometry trials) were prepared in the last four days of the experiment to be included in lipid analysis.

Determining how to populate animals into respirometry trials Krill Doctrine 1. Krill needed to fast for 24hours prior to respirometry and lipids analysis preparation 2. Choose MOATs with the lowest number of animals remaining for the first round(s) of respirometry and follow on preparation for lipids analysis 3. Balance between MOATs across days of respirometry* 4. Balance between Treatments when choosing which respirometry round 5. Must achieve 4 vials per MOATs 6. Achieve 15-20 animals across treatments for respirometry 7. Wait until Night Time Conditions begin for the Krill to start Respirometry Trials. The night period for krill began at 1230pm.



Krill Doctrine Version 1



Krill Doctrine Version 1 Explained

1.) Setting Working Directory

Code

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 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
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 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

2.) DF Creation

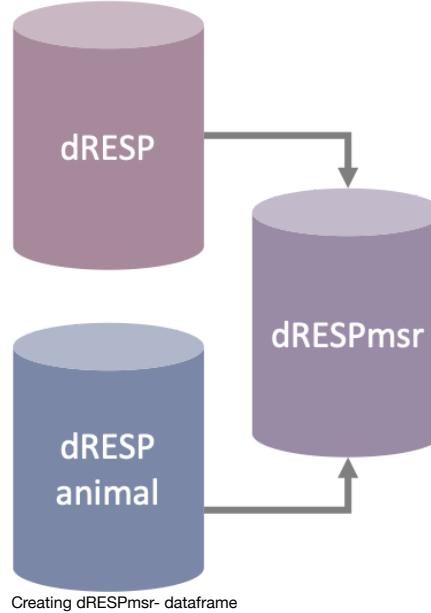
Code

```
## [1] 3756 52
```

Code

```
## [1] 76 11
```

Code



3.) dateTIme objects

Code

```
## [1] 3756 63
```

Code

4.) Observation naming

Code

```
## [1] 3756 63
```

Code

```

## [1] KrillR11 KrillR12 KrillR13 KrillR14 KrillR15 KrillR16 KrillR17 KrillR18
## [9] KrillR19 KrillR110 KrillR111 KrillR112 KrillR113 KrillR114 KrillR115 KrillR116
## [17] KrillR117 KrillR118 KrillR119 KrillR220 KrillR221 KrillR222 KrillR223 KrillR224
## [25] KrillR225 KrillR226 KrillR227 KrillR228 KrillR229 KrillR230 KrillR231 KrillR232
## [33] KrillR233 KrillR234 KrillR235 KrillR236 KrillR237 KrillR238 KRLr3_39 KRLr3_40
## [41] KRLr3_41 KRLr3_42 KRLr3_43 KRLr3_44 KRLr3_45 KRLr3_46 KRLr3_47 KRLr3_48
## [49] KRLr3_49 KRLr3_50 KRLr3_51 KRLr3_52 KRLr3_53 KRLr3_54 KRLr3_55 KRLr3_56
## [57] KRLr3_57 KRLr4_58 KRLr4_59 KRLr4_60 KRLr4_61 KRLr4_62 KRLr4_63 KRLr4_64
## [65] KRLr4_65 KRLr4_66 KRLr4_67 KRLr4_68 KRLr4_69 KRLr4_70 KRLr4_71 KRLr4_72
## [73] KRLr4_73 KRLr4_74 KRLr4_75 KRLr4_76
## 76 Levels: KrillR11 KrillR12 KrillR13 KrillR14 KrillR15 KrillR16 ... KRLr4_76

```

Code

#5.) Trial ID & Krill ID

5.a Round Variable

5.b KrillID (grp & time)

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6.) DO Corrections

Code

6.a) DO table & DO correction Plot Check

Code

6.b DO Selections

Code

7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

Trial01 Loading Map

Trial 01 of 2 (2019.10.28) Respirometry										
	A	B	C	D	E	F	G	H	I	J
1	12		6		12		8		6	
2		12						6		6
3			8					6		8
4		6							12	
5	BLNK		8		BLNK		6		8	

Trial01 Loading Map

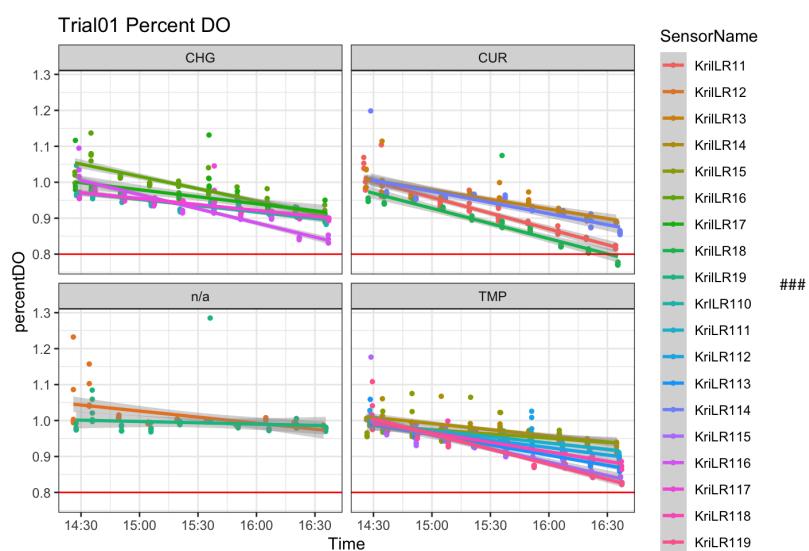
7.1a) PPlotting Percent DO filtering Trial 1

Code

```
## [1] "AMB" "CHG" "CUR" "n/a" "TMP"
```

Code

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



7.1a2) PPlotting Percent DO filtering Trial 1 Colored by Round

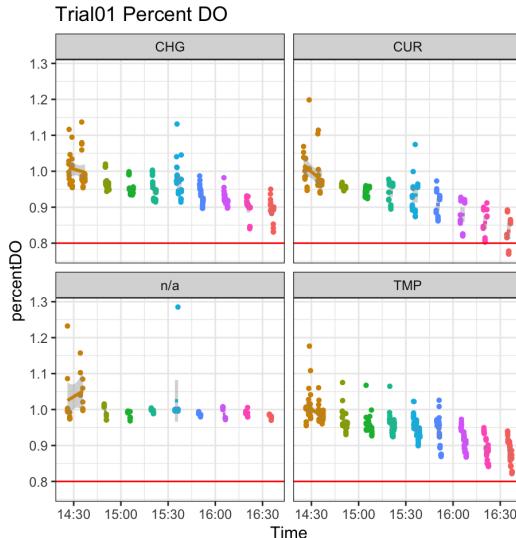
Code

```
## [1] "AMB" "CHG" "CUR" "n/a" "TMP"
```

Code

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

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 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff



T1dRESPmsr\$RESPRound

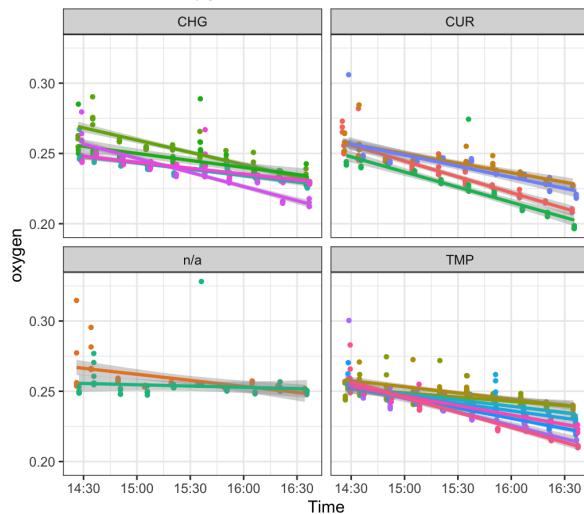
- other
- T1Round1
- T1Round2
- T1Round3
- T1Round4
- T1Round5
- T1Round6
- T1Round7
- T1Round8

7.1b) Trial 1 Vial Oxygen over Time

Code

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

Trial01 Vial Oxygen over Time



KrillID

- Trial01_KrilLR11
- Trial01_KrilLR12
- Trial01_KrilLR13
- Trial01_KrilLR14
- Trial01_KrilLR15
- Trial01_KrilLR16
- Trial01_KrilLR17
- Trial01_KrilLR18
- Trial01_KrilLR19
- Trial01_KrilLR10
- Trial01_KrilLR110
- Trial01_KrilLR111
- Trial01_KrilLR112
- Trial01_KrilLR113
- Trial01_KrilLR114
- Trial01_KrilLR115
- Trial01_KrilLR116
- Trial01_KrilLR117
- Trial01_KrilLR118
- Trial01_KrilLR119

7.1c) Trial01 Vial Oxygen over Time Organized by Round (1 of 8)

Depending on ordering there were animals that went all the way to ten rounds Likely that we will only consider rounds 01 through 08 due to 80% curve.

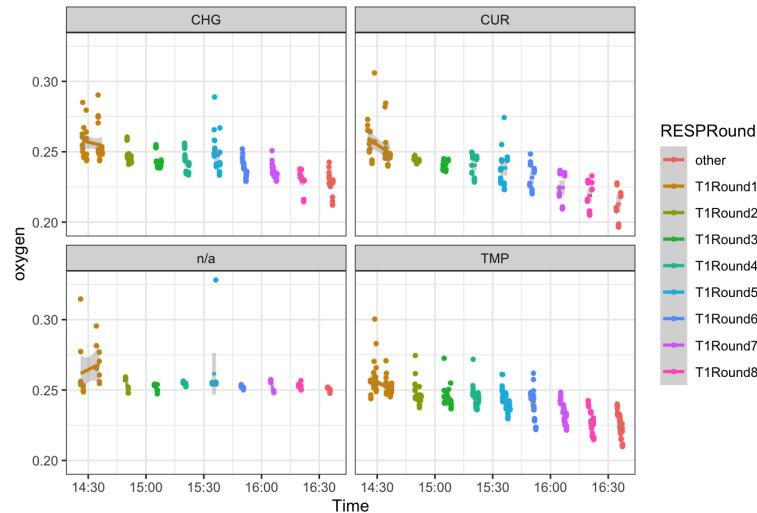
Goal in plotting animals by round is to see if there is a "temporal panic profile". Do we need to wait long for an acclimation period? This will have implications on future respirometry protocols if a chase period is introduced.

Code

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

Trial01 Vial Oxygen over Time Organized by Round (1 of 8)

Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTime objects
4.) Observation naming
6.) DO Corrections
6.a) DO table & DO correction Plot Check
7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
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21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff



Trial02 Loading Map

Trial 02 of 2 (2019.10.28) Respirometry

	A	B	C	D	E	F	G	H	I	J
1	12			4		4		BLNK		12
2		2							2	4
3	4			12				4		2
4			BLNK							4
5	4		2		2		12		4	

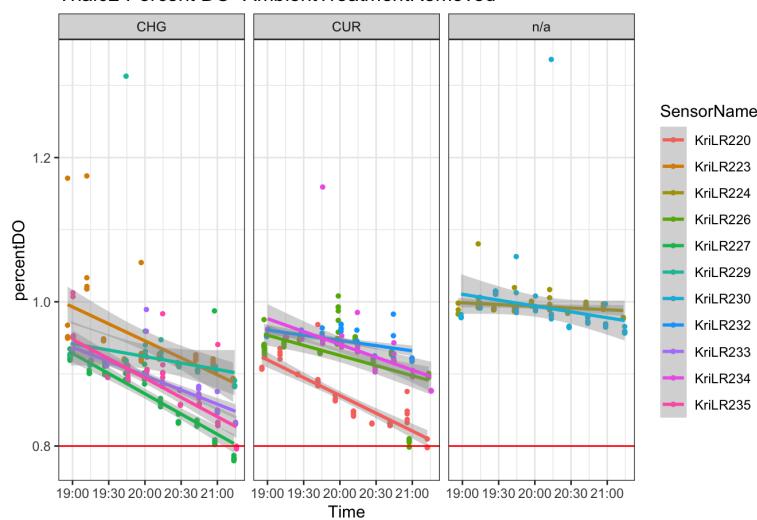
Trial02 Loading Map

7.2a) PPlotting Percent DO filtering Trial 2

Code

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

Trial02 Percent DO- AmbientTreatmentRemoved



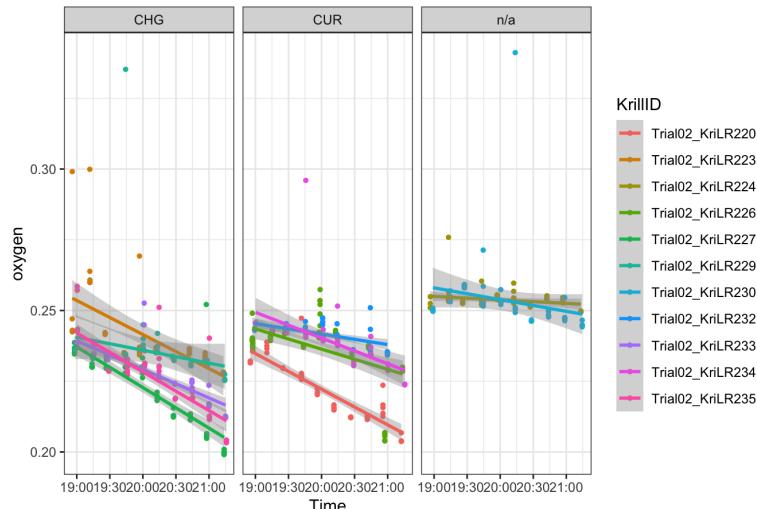
7.2a) Trial 2 Vial Oxygen over Time

Code

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

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17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
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Trial02 Vial Oxygen over Time



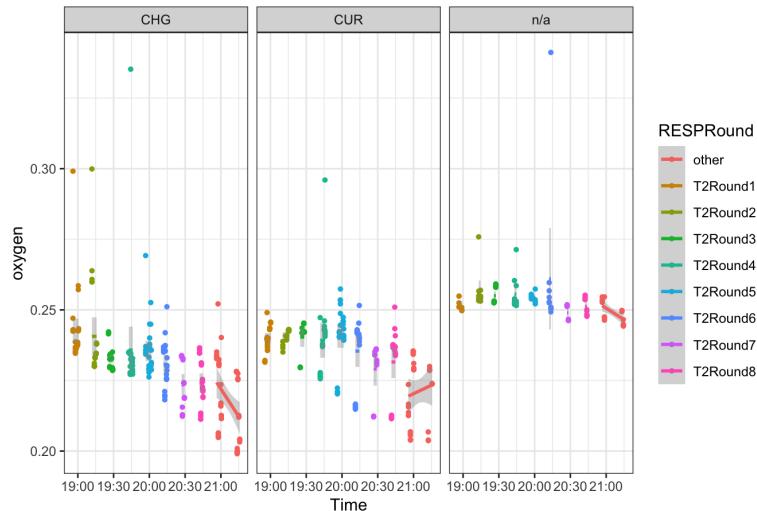
7.2c) Trial02 Vial Oxygen over Time Organized by Round (1 of 8)

Second Trial, Round 1 on 2019-10-28 began 18:50:01 Second Trial, Round 8 on 2019-10-28 ended 20:50:59

Code

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

Trial02 Vial Oxygen over Time Organized by Round (1 of 8)



Trial03 Loading Map

Trial 01 of 2 (2019.10.29) Respirometry

	A	B	C	D	E	F	G	H	I	J
1		7		13		13		7		1
2	1			1				1		
3		13						BLNK		13
4	1			1				1		1
5		BLNK		7				13		7

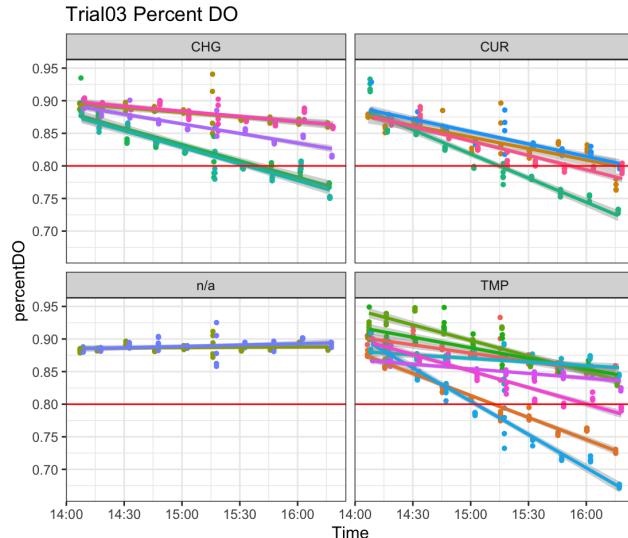
Trial03 Loading Map

7.3) PPlotting Percent DO filtering Trial 3

Code

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

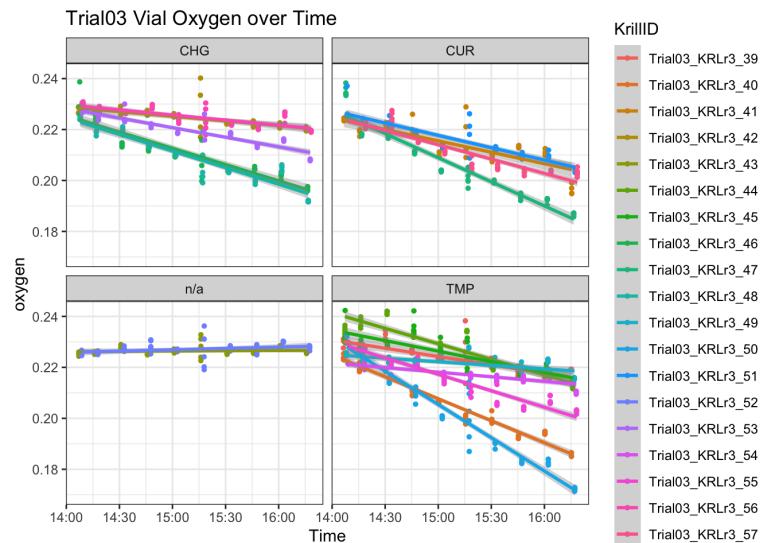
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 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff



7.3a) Trial 3 Vial Oxygen over Time

Code

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



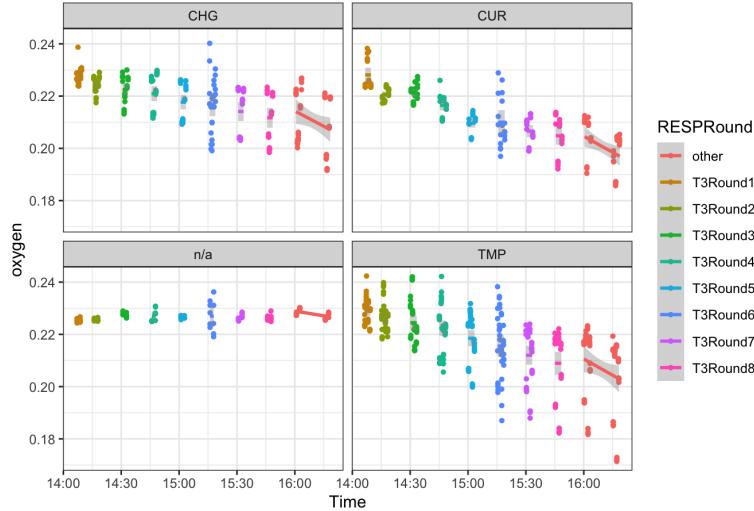
7.3c) Trial03 Vial Oxygen over Time Organized by Round (1 of 8)

Code

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

Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTIme objects
4.) Observation naming
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6.a) DO table & DO correction Plot Check
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17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
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21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
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Trial03 Vial Oxygen over Time Organized by Round (1 of 8)



Trial04 Loading Map

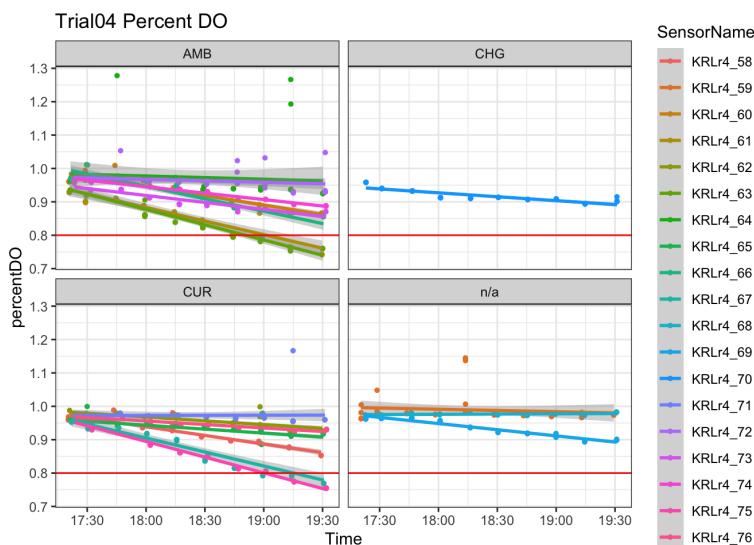
Trial 02 of 2 (2019.10.29) Respirometry

	A	B	C	D	E	F	G	H	I	J
1		5		7		5		10		10
2	10		10				BLNK		5	
3								5		10
4	BLNK		5				13		10	
5		5		5		10		5		

7.4) PPlotting Percent DO filtering Trial 4

Code

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



SensorName

KRLr4_58
KRLr4_59
KRLr4_60
KRLr4_61
KRLr4_62
KRLr4_63
KRLr4_64
KRLr4_65
KRLr4_66
KRLr4_67
KRLr4_68
KRLr4_69
KRLr4_70
KRLr4_71
KRLr4_72
KRLr4_73
KRLr4_74
KRLr4_75
KRLr4_76

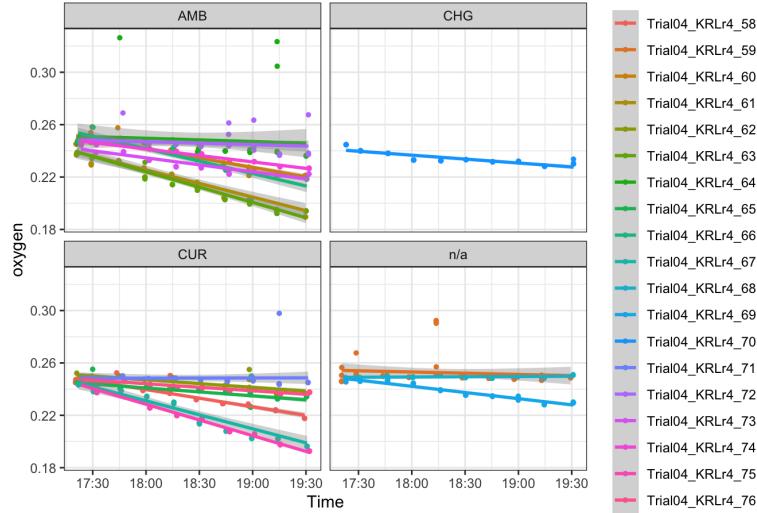
7.4a) Trial 4 Vial Oxygen over Time

Code

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

- Version Check
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- 9.) Respirometry Table
- 13.) Investigating Outliers
- 14.) Krill Sparkle Function (standard krillslopes dataframe)
- 15.) Krill Sparkle Function (80% DO dataframe)
- 15.b) Krill Sparkle Function (1hr Trial dataframe)
- 16.) Plots Following Filtering
- 17.x) Analysis, Respirometry - outliers removed (investigating krillslopes)
- 18.) Merging ks... and krillslopes...
- 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
- 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
- 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
- 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
- 21.) Analysis, Respirometry - Correcting the Slope for Blanks
- 21. Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
- 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

Trial04 Vial Oxygen over Time



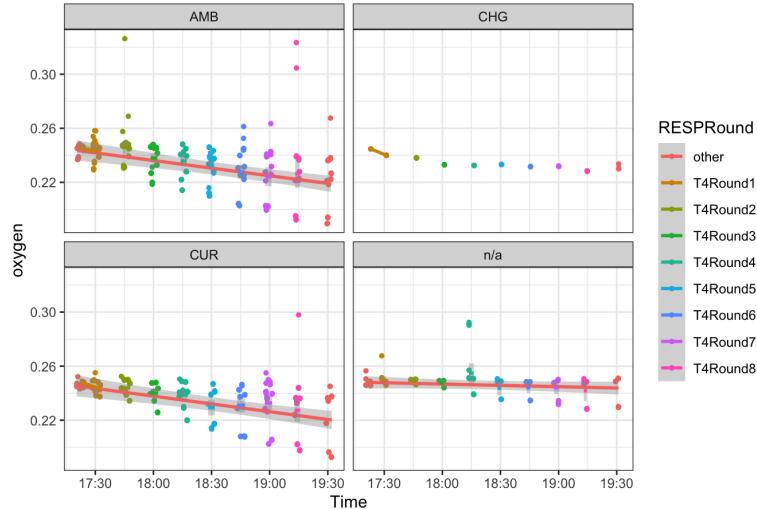
7.4c) Trial04 Vial Oxygen over Time Organized by Round (1 of 8)

Acclimation period snuck in from the start Second Trial, Round 1 on 2019-10-29 began 17:23:01 Second Trial, Round 8 on 2019-10-29 ended 19:23:59

Code

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

Trial04 Vial Oxygen over Time Organized by Round (1 of 8)



8.) Analysis, Respirometry - Creating the Slope Function

Code

9.) Merging ds and dRESPmsr

Code

10.) Krill ID as a factor & Grouping by Krill ID

Code

```
## [1] 76
```

60 is the number of vials when Ambient Treatment is excluded

11.) Analysis, Respirometry - Creating Slope Functions & Linear Models

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot
 Check
 7.) Initial Dataframe dRESPmsr Plots,
 80% DO, Oxygen Per Vial, Actual
 DOmg/L
 8.) Analysis, Respirometry - Creating
 the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by
 Krill ID
 11.) Analysis, Respirometry - Creating
 Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard
 krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO
 dataframe)
 15.b) Krill Sparkle Function (1hr Trial
 dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers
 removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by
 Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating
 Slope Functions & Linear Models
 20.1a) Analysis, Respirometry -
 Creating Slope Functions & Linear
 Models 80% cutoff
 20.1b) Analysis, Respirometry -
 Creating Slope Functions & Linear
 Models 70% cutoff
 20.1c) Analysis, Respirometry -
 Creating Slope Functions & Linear
 Models 1hr cutoff
 21.) Analysis, Respirometry -
 Correcting the Slope for Blanks
 21. Summary Statistics on the
 Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry -
 Correcting the Slope for Blanks - 80%
 cutoff
 21.c) Summary Statistics on the
 Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry -
 Correcting the Slope for Blanks - 70%
 cutoff

12.0) Filtering krillslopes by each Trial

Code

9.5) Filtering dtotl by each Trial and finding the 80% time

Code

```
## [1] "2019-10-28 14:25:01 UTC" "2019-10-28 14:25:02 UTC"
## [3] "2019-10-28 14:25:03 UTC" "2019-10-28 14:25:53 UTC"
## [5] "2019-10-28 14:25:54 UTC" "2019-10-28 14:25:55 UTC"
```

Code

```
## [1] "2019-10-28 16:35:20 UTC"
```

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRlr4_76
```

Code

```
## [1] 4.5
```

Code

```
## [1] "2019-10-28 18:55:21 UTC"
```

Code

```
## [1] "2019-10-28 21:12:23 UTC"
```

Code

```
## [1] Trial02_KrillR20 Trial02_KrillR21 Trial02_KrillR22 Trial02_KrillR23
## [5] Trial02_KrillR24 Trial02_KrillR25 Trial02_KrillR26 Trial02_KrillR27
## [9] Trial02_KrillR28 Trial02_KrillR29 Trial02_KrillR30 Trial02_KrillR231
## [13] Trial02_KrillR232 Trial02_KrillR233 Trial02_KrillR234 Trial02_KrillR235
## [17] Trial02_KrillR236 Trial02_KrillR237 Trial02_KrillR238
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRlr4_76
```

Code

```
## [1] 51.33333
```

Code

```
## [1] "2019-10-29 14:06:22 UTC" "2019-10-29 14:06:23 UTC"
## [3] "2019-10-29 14:06:24 UTC" "2019-10-29 14:06:25 UTC"
## [5] "2019-10-29 14:15:17 UTC" "2019-10-29 14:15:18 UTC"
```

Code

```
## [1] "2019-10-29 15:45:19 UTC"
```

Code

```
## [1] Trial03_KRlr3_39 Trial03_KRlr3_40 Trial03_KRlr3_41 Trial03_KRlr3_42
## [5] Trial03_KRlr3_43 Trial03_KRlr3_44 Trial03_KRlr3_45 Trial03_KRlr3_46
## [9] Trial03_KRlr3_47 Trial03_KRlr3_48 Trial03_KRlr3_49 Trial03_KRlr3_50
## [13] Trial03_KRlr3_51 Trial03_KRlr3_52 Trial03_KRlr3_53 Trial03_KRlr3_54
## [17] Trial03_KRlr3_55 Trial03_KRlr3_56 Trial03_KRlr3_57
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRlr4_76
```

Code

```
## [1] 57.3
```

Code

Version Check

Libraries

1.) Setting Working Directory

2.) DF Creation

3.) dateTIme objects

4.) Observation naming

6.) DO Corrections

6.a) DO table & DO correction Plot Check

7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

8.) Analysis, Respirometry - Creating the Slope Function

9.) Merging ds and dRESPmsr

10.) Krill ID as a factor & Grouping by Krill ID

11.) Analysis, Respirometry - Creating Slope Functions & Linear Models

12.) Filtering krillslopes by each Trial

9.) Respirometry Table

13.) Investigating Outliers

14.) Krill Sparkle Function (standard krillslopes dataframe)

15.) Krill Sparkle Function (80% DO dataframe)

15.b) Krill Sparkle Function (1hr Trial dataframe)

16.) Plots Following Filtering

17.) Analysis, Respirometry - outliers removed (investigating krillslopes)

18.) Merging ks... and krillslopes...

19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs

20.) Analysis, Respirometry - Creating Slope Functions & Linear Models

20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff

20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff

20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

21.) Analysis, Respirometry - Correcting the Slope for Blanks

21. Summary Statistics on the Unfiltered Dataframe dSlopes

21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

21.c) Summary Statistics on the Unfiltered Dataframe dSlopes

21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## [1] "2019-10-29 17:20:22 UTC" "2019-10-29 17:20:23 UTC"
## [3] "2019-10-29 17:20:24 UTC" "2019-10-29 17:20:25 UTC"
## [5] "2019-10-29 17:43:31 UTC" "2019-10-29 17:43:32 UTC"
```

Code

```
## [1] "2019-10-29 18:43:56 UTC"
```

Code

```
## [1] Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_60 Trial04_KRLr4_61
## [5] Trial04_KRLr4_62 Trial04_KRLr4_63 Trial04_KRLr4_64 Trial04_KRLr4_65
## [9] Trial04_KRLr4_66 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [13] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_72 Trial04_KRLr4_73
## [17] Trial04_KRLr4_74 Trial04_KRLr4_75 Trial04_KRLr4_76
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

```
## [1] "2019-10-29 17:20:22 UTC"
```

Code

```
## [1] "2019-10-29 19:31:51 UTC"
```

Code

```
## [1] 131.4833
```

8.6) Bringing all trials back together following 80% DO selection)

Code

8.7) Filtering krill slopes by each Trial and finding the 70% time

Code

```
## [1] "2019-10-28 14:25:01 UTC" "2019-10-28 14:25:02 UTC"
## [3] "2019-10-28 14:25:03 UTC" "2019-10-28 14:25:53 UTC"
## [5] "2019-10-28 14:25:54 UTC" "2019-10-28 14:25:55 UTC"
```

Code

```
## POSIXct of length 0
```

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

```
## [1] 132.4667
```

Code

```
## [1] "2019-10-28 18:55:21 UTC" "2019-10-28 18:55:22 UTC"
## [3] "2019-10-28 18:55:23 UTC" "2019-10-28 18:55:24 UTC"
## [5] "2019-10-28 18:55:33 UTC" "2019-10-28 18:55:34 UTC"
```

Code

```
## POSIXct of length 0
```

Code

```
## [1] Trial02_KrilR220 Trial02_KrilR221 Trial02_KrilR222 Trial02_KrilR223
## [5] Trial02_KrilR224 Trial02_KrilR225 Trial02_KrilR226 Trial02_KrilR227
## [9] Trial02_KrilR228 Trial02_KrilR229 Trial02_KrilR230 Trial02_KrilR231
## [13] Trial02_KrilR232 Trial02_KrilR233 Trial02_KrilR234 Trial02_KrilR235
## [17] Trial02_KrilR236 Trial02_KrilR237 Trial02_KrilR238
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

Code

Version Check

[1] 141.4

Code

Libraries

1.) Setting Working Directory

2.) DF Creation

3.) dateTIme objects

4.) Observation naming

6.) DO Corrections

6.a) DO table & DO correction Plot Check

7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

8.) Analysis, Respirometry - Creating the Slope Function

9.) Merging ds and dRESPmsr

10.) Krill ID as a factor & Grouping by Krill ID

11.) Analysis, Respirometry - Creating Slope Functions & Linear Models

12.0) Filtering krillslopes by each Trial

9.) Respirometry Table

13.) Investigating Outliers

14.) Krill Sparkle Function (standard krillslopes dataframe)

15.) Krill Sparkle Function (80% DO dataframe)

15.b) Krill Sparkle Function (1hr Trial dataframe)

16.) Plots Following Filtering

17.x) Analysis, Respirometry - outliers removed (investigating krillslopes)

18.) Merging ks... and krillslopes...

19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs

20.) Analysis, Respirometry - Creating Slope Functions & Linear Models

20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff

20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff

20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

21.) Analysis, Respirometry - Correcting the Slope for Blanks

21. Summary Statistics on the Unfiltered Dataframe dSlopes

21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

21.c) Summary Statistics on the Unfiltered Dataframe dSlopes

21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

[1] "2019-10-29 14:06:22 UTC" "2019-10-29 14:06:23 UTC"
[3] "2019-10-29 14:06:24 UTC" "2019-10-29 14:06:25 UTC"
[5] "2019-10-29 14:06:32 UTC" "2019-10-29 14:06:33 UTC"

Code

[1] "2019-10-29 16:17:06 UTC"

Code

[1] Trial03_KRLr3_39 Trial03_KRLr3_40 Trial03_KRLr3_41 Trial03_KRLr3_42
[5] Trial03_KRLr3_43 Trial03_KRLr3_44 Trial03_KRLr3_45 Trial03_KRLr3_46
[9] Trial03_KRLr3_47 Trial03_KRLr3_48 Trial03_KRLr3_49 Trial03_KRLr3_50
[13] Trial03_KRLr3_51 Trial03_KRLr3_52 Trial03_KRLr3_53 Trial03_KRLr3_54
[17] Trial03_KRLr3_55 Trial03_KRLr3_56 Trial03_KRLr3_57 Trial03_KRLr3_58
76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76

Code

[1] 130.75

Code

[1] "2019-10-29 17:20:22 UTC" "2019-10-29 17:20:23 UTC"
[3] "2019-10-29 17:20:24 UTC" "2019-10-29 17:20:25 UTC"
[5] "2019-10-29 17:20:30 UTC" "2019-10-29 17:20:31 UTC"

Code

POSIXct of length 0

Code

[1] Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_60 Trial04_KRLr4_61
[5] Trial04_KRLr4_62 Trial04_KRLr4_63 Trial04_KRLr4_64 Trial04_KRLr4_65
[9] Trial04_KRLr4_66 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
[13] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_72 Trial04_KRLr4_73
[17] Trial04_KRLr4_74 Trial04_KRLr4_75 Trial04_KRLr4_76 Trial04_KRLr4_77
76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76

Code

[1] "2019-10-29 17:20:22 UTC"

Code

[1] "2019-10-29 19:32:01 UTC"

Code

[1] 131.65

Code

8.8) bringing all trials back together following 70% DO selection)

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR21 Trial02_KrillR22 Trial02_KrillR23 Trial02_KrillR24
## [25] Trial02_KrillR25 Trial02_KrillR26 Trial02_KrillR27 Trial02_KrillR28
## [29] Trial02_KrillR29 Trial02_KrillR230 Trial02_KrillR231 Trial02_KrillR232
## [33] Trial02_KrillR233 Trial02_KrillR234 Trial02_KrillR235 Trial02_KrillR236
## [37] Trial02_KrillR237 Trial02_KrillR238 Trial03_KRLr3_39 Trial03_KRLr3_40
## [41] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [45] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [49] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [53] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [57] Trial03_KRLr3_57 Trial04_KRLr4_56 Trial04_KRLr4_59 Trial04_KRLr4_60
## [61] Trial04_KRLr4_61 Trial04_KRLr4_62 Trial04_KRLr4_63 Trial04_KRLr4_64
## [65] Trial04_KRLr4_65 Trial04_KRLr4_66 Trial04_KRLr4_67 Trial04_KRLr4_68
## [69] Trial04_KRLr4_69 Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_72
## [73] Trial04_KRLr4_73 Trial04_KRLr4_74 Trial04_KRLr4_75 Trial04_KRLr4_76
## 76 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

8.9) Filtering krillslopes to give each Trial only 1hr

Code

```
## [1] "2019-10-28 14:25:01 UTC" "2019-10-28 14:25:02 UTC"
## [3] "2019-10-28 14:25:03 UTC" "2019-10-28 14:25:53 UTC"
## [5] "2019-10-28 14:25:54 UTC" "2019-10-28 14:25:55 UTC"
```

Code

```
## [1] "2019-10-28 14:25:01 UTC"
```

Code

```
## [1] 57.7
```

Code

```
## [1] "2019-10-28 18:55:21 UTC" "2019-10-28 18:55:22 UTC"
## [3] "2019-10-28 18:55:23 UTC" "2019-10-28 18:55:24 UTC"
## [5] "2019-10-28 18:55:33 UTC" "2019-10-28 18:55:34 UTC"
```

Code

```
## [1] 51.36667
```

Code

```
## [1] "2019-10-29 14:06:22 UTC" "2019-10-29 14:06:23 UTC"
## [3] "2019-10-29 14:06:24 UTC" "2019-10-29 14:06:25 UTC"
## [5] "2019-10-29 14:06:32 UTC" "2019-10-29 14:06:33 UTC"
```

Code

```
## [1] 57.38333
```

Code

```
## [1] "2019-10-29 17:20:22 UTC"
```

Code

```
## [1] "2019-10-29 18:17:41 UTC"
```

Code

```
## [1] 57.31667
```

Code

8.10) bringing all trials back together following the 1hr selection)

Code

Code

9.) Respirometry Table

Code

13.) Investigating Outliers

The krillslopes dataframe is broken up into four different dataframes based on Trial ID. These dataframes will be further filtered to remove the Ambient Treatment. Some rounds of respirometry featured a greater number ambient treatment animals and should account for the differences in number of observations between dataframes.

13.1 Investigating Outliers by Trial- cleaning up Trials Removing AMB from the 80% Threshold

- Version Check
- Libraries
- 1.) Setting Working Directory
- 2.) DF Creation
- 3.) dateTIme objects
- 4.) Observation naming
- 6.) DO Corrections
- 6.a) DO table & DO correction Plot Check
- 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
- 8.) Analysis, Respirometry - Creating the Slope Function
- 9.) Merging ds and dRESPmsr
- 10.) Krill ID as a factor & Grouping by Krill ID
- 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 12.) Filtering krillslopes by each Trial
- 9.) Respirometry Table
- 13.) Investigating Outliers
- 14.) Krill Sparkle Function (standard krillslopes dataframe)
- 15.) Krill Sparkle Function (80% DO dataframe)
- 15.b) Krill Sparkle Function (1hr Trial dataframe)
- 16.) Plots Following Filtering
- 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
- 18.) Merging ks... and krillslopes...
- 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
- 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
- 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
- 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
- 21.) Analysis, Respirometry - Correcting the Slope for Blanks
- 21. Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
- 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a"
```

Code

```
## [1] "CHG" "CUR" "n/a"
```

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a"
```

Code

```
## [1] "CHG" "CUR" "n/a"
```

Code

13.1a Investigating Outliers by Trial- cleaning up Trials Removing AMB from the 70% Threshold

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a"
```

Code

```
## [1] "CHG" "CUR" "n/a"
```

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

```
## [1] "CHG" "CUR" "n/a" "TMP"
```

Code

Version Check

Libraries

1.) Setting Working Directory

2.) DF Creation

3.) dateTIme objects

4.) Observation naming

6.) DO Corrections

6.a) DO table & DO correction Plot Check

7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

8.) Analysis, Respirometry - Creating the Slope Function

9.) Merging ds and dRESPmsr

10.) Krill ID as a factor & Grouping by Krill ID

11.) Analysis, Respirometry - Creating Slope Functions & Linear Models

12.) Filtering krillslopes by each Trial

9.) Respirometry Table

13.) Investigating Outliers

14.) Krill Sparkle Function (standard krillslopes dataframe)

15.) Krill Sparkle Function (80% DO dataframe)

15.b) Krill Sparkle Function (1hr Trial dataframe)

16.) Plots Following Filtering

17.) Analysis, Respirometry - outliers removed (investigating krillslopes)

18.) Merging ks... and krillslopes...

19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs

20.) Analysis, Respirometry - Creating Slope Functions & Linear Models

20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff

20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff

20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

21.) Analysis, Respirometry - Correcting the Slope for Blanks

21. Summary Statistics on the Unfiltered Dataframe dSlopes

21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

21.c) Summary Statistics on the Unfiltered Dataframe dSlopes

21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

[1] "CHG" "CUR" "n/a"

Code

[1] "CHG" "CUR" "n/a"

Code

13.1a Investigating Outliers by Trial- cleaning up Trials Removing AMB from the 1hr Threshold

Code

[1] "CHG" "CUR" "n/a" "TMP"

Code

[1] "CHG" "CUR" "n/a" "TMP"

Code

[1] "CHG" "CUR" "n/a"

Code

[1] "CHG" "CUR" "n/a"

Code

[1] "CHG" "CUR" "n/a" "TMP"

Code

[1] "CHG" "CUR" "n/a" "TMP"

Code

[1] "CHG" "CUR" "n/a"

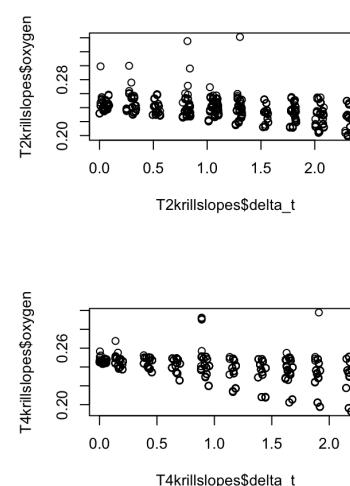
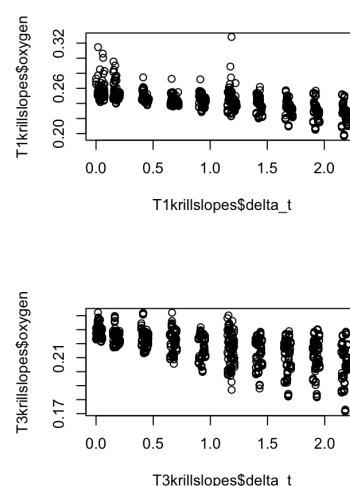
Code

[1] "CHG" "CUR" "n/a"

Code

Time Series Plot for the unfiltered Krill Slopes Dataframe ####13.1a.1 Investigating Outliers by Trial- timeseries plots showing the four distinct dataframes

Code



Time Series Plot for Krill selected before 1st vial reached 80% DO ####13.1b Investigating Outliers by Trial- timeseries plots showing the four distinct dataframes

Version Check

Libraries

1.) Setting Working Directory

2.) DF Creation

3.) dateTIme objects

4.) Observation naming

6.) DO Corrections

6.a) DO table & DO correction Plot

Check

7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

8.) Analysis, Respirometry - Creating the Slope Function

9.) Merging ds and dRESPmsr

10.) Krill ID as a factor & Grouping by Krill ID

11.) Analysis, Respirometry - Creating Slope Functions & Linear Models

12.) Filtering krillslopes by each Trial

9.) Respirometry Table

13.) Investigating Outliers

14.) Krill Sparkle Function (standard krillslopes dataframe)

15.) Krill Sparkle Function (80% DO dataframe)

15.b) Krill Sparkle Function (1hr Trial dataframe)

16.) Plots Following Filtering

17.) Analysis, Respirometry - outliers removed (investigating krillslopes)

18.) Merging ks... and krillslopes...

19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs

20.) Analysis, Respirometry - Creating Slope Functions & Linear Models

20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff

20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff

20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

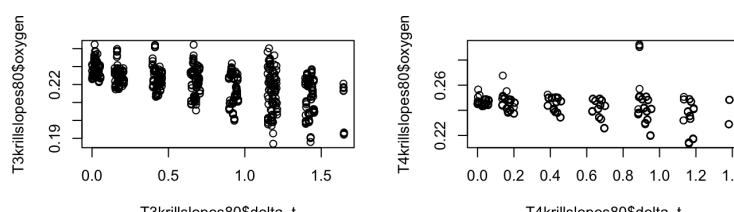
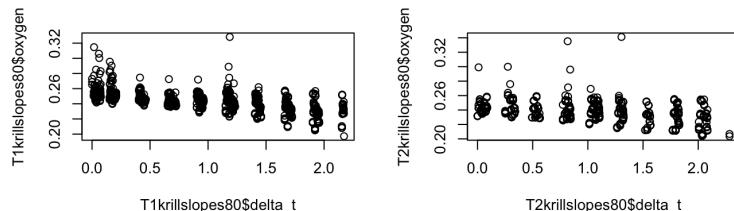
21.) Analysis, Respirometry - Correcting the Slope for Blanks

21. Summary Statistics on the Unfiltered Dataframe dSlopes

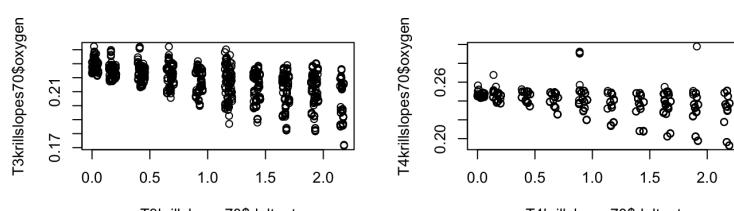
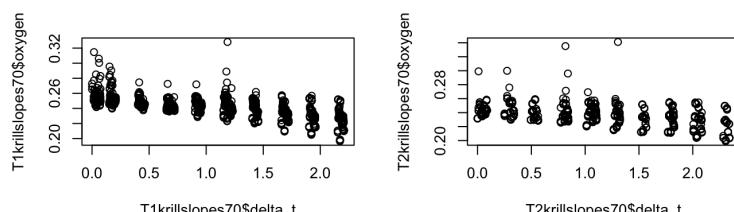
21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

21.c) Summary Statistics on the Unfiltered Dataframe dSlopes

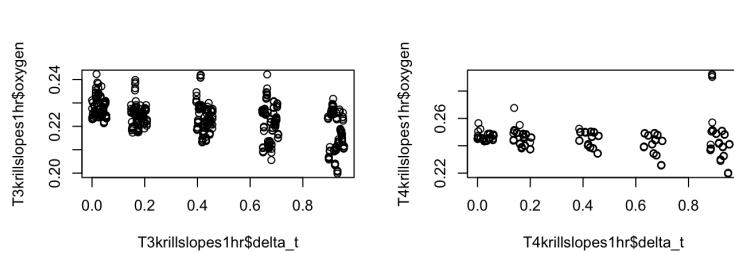
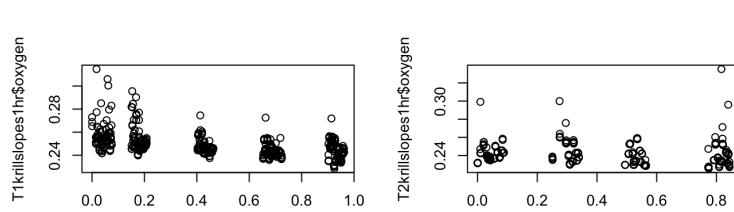
21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff



Time Series Plot for Krill selected before 1st vial reached 70% DO ####13.1c Investigating Outliers by Trial- timeseries plots showing the four distinct dataframes



Time Series Plot for Krill selected (1hour) per trial ####13.1d Investigating Outliers by Trial- timeseries plots showing the four distinct dataframes



Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

13.e Example of loop and function writting Kate is trying to for each krill

13.2e) take 1 df at a time

Code

```
## [1] 932 77
```

Code

13.2f) Use the unique tool to get names for each krill

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19
## 19 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial01_KrillR19
```

Code

13.2g) Create a linear model object for 1 krill

Code

13.2h) Use the fortify function to get the residuals and cook.sd for each observation

Code

13.2i) Identify which observations have a cooksd score above 4/n

n is the whole number of observations on that krill in the vial

Code

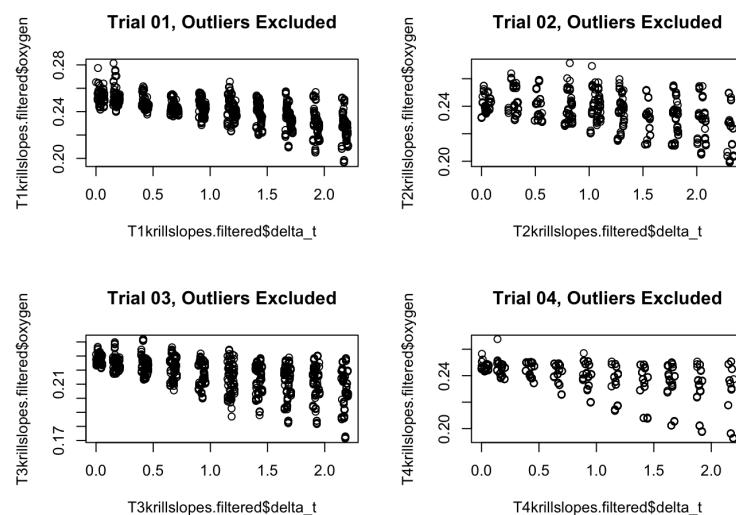
13.2j) Use one dataframe to sort another

Code

```
## [1] FALSE FALSE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE
## [5] TRUE TRUE
## [25] TRUE TRUE
## [37] TRUE TRUE
```

14.) Krill Sparkle Function (standard krillslopes dataframe)

Code



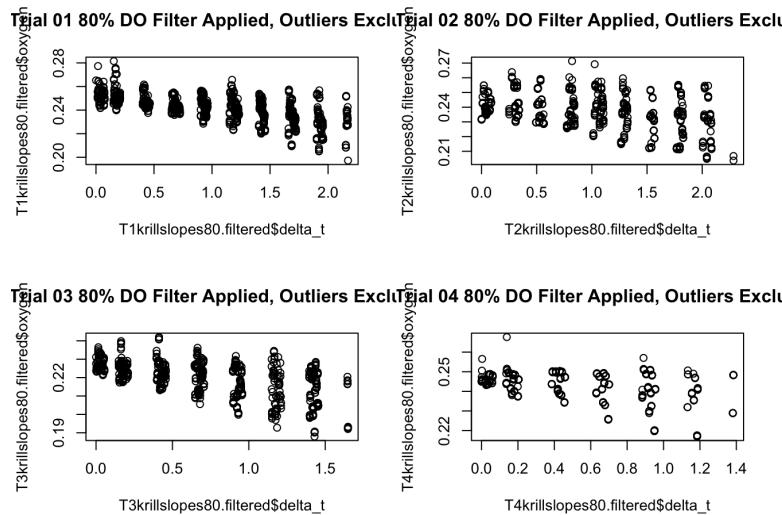
Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

14.) Rbind back the filtered dataframes following the sparkle function

Code

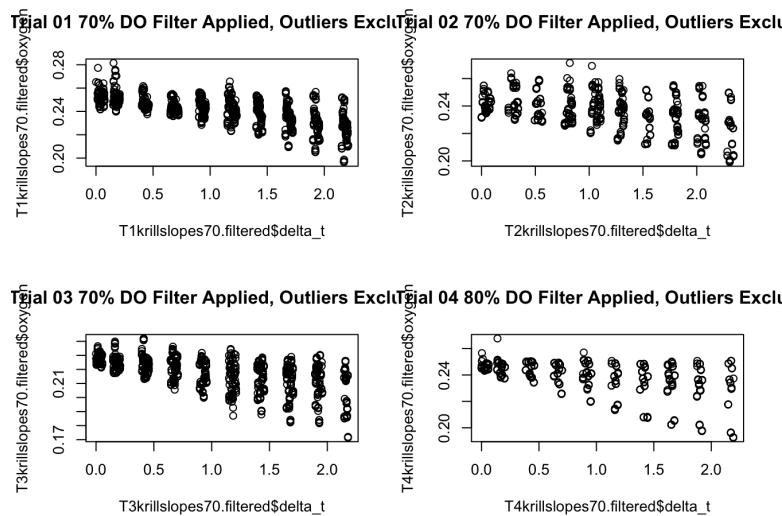
15.) Krill Sparkle Function (80% DO dataframe)

Code



15.a) Krill Sparkle Function (70% DO dataframe)

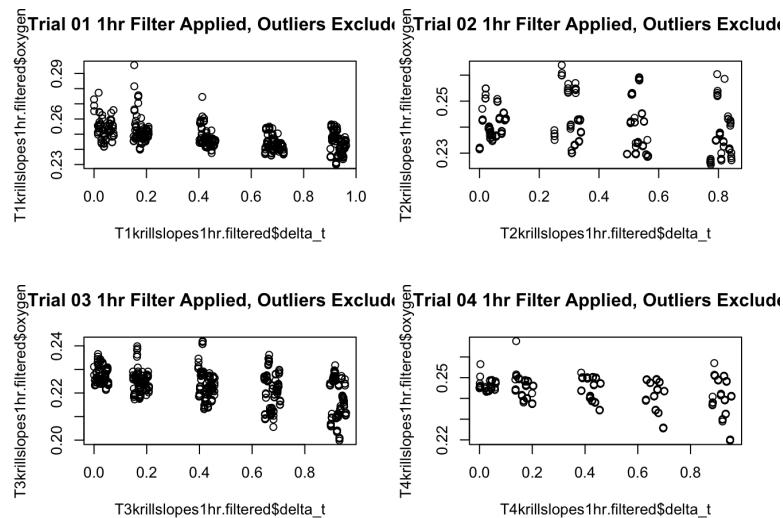
Code



15.b) Krill Sparkle Function (1hr Trial dataframe)

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot
 Check
 7.) Initial Dataframe dRESPmsr Plots,
 80% DO, Oxygen Per Vial, Actual
 DOmg/L
 8.) Analysis, Respirometry - Creating
 the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by
 Krill ID
 11.) Analysis, Respirometry - Creating
 Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard
 krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO
 dataframe)
 15.b) Krill Sparkle Function (1hr Trial
 dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers
 removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by
 Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating
 Slope Functions & Linear Models
 20.1a) Analysis, Respirometry -
 Creating Slope Functions & Linear
 Models 80% cutoff
 20.1b) Analysis, Respirometry -
 Creating Slope Functions & Linear
 Models 70% cutoff
 20.1c) Analysis, Respirometry -
 Creating Slope Functions & Linear
 Models 1hr cutoff
 21.) Analysis, Respirometry -
 Correcting the Slope for Blanks
 21. Summary Statistics on the
 Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry -
 Correcting the Slope for Blanks - 80%
 cutoff
 21.c) Summary Statistics on the
 Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry -
 Correcting the Slope for Blanks - 70%
 cutoff



15.d Bringing all trials back together 80%, 70% and 1hr

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR223 Trial02_KrillR224 Trial02_KrillR226 Trial02_KrillR227
## [25] Trial02_KrillR229 Trial02_KrillR230 Trial02_KrillR232 Trial02_KrillR233
## [29] Trial02_KrillR234 Trial02_KrillR235 Trial03_KRLr3_39 Trial03_KRLr3_40
## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62
## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76
## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR223 Trial02_KrillR224 Trial02_KrillR226 Trial02_KrillR227
## [25] Trial02_KrillR229 Trial02_KrillR230 Trial02_KrillR232 Trial02_KrillR233
## [29] Trial02_KrillR234 Trial02_KrillR235 Trial03_KRLr3_39 Trial03_KRLr3_40
## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62
## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76
## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

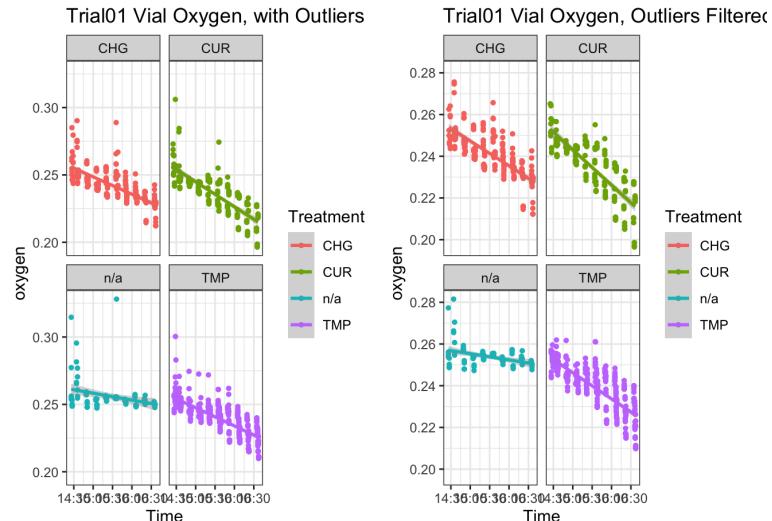
```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR223 Trial02_KrillR224 Trial02_KrillR226 Trial02_KrillR227
## [25] Trial02_KrillR229 Trial02_KrillR230 Trial02_KrillR232 Trial02_KrillR233
## [29] Trial02_KrillR234 Trial02_KrillR235 Trial03_KRLr3_39 Trial03_KRLr3_40
## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62
## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76
## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

16.) Plots Following Filtering

16.1a Trial 1 Vial Oxygen over Time

Code

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

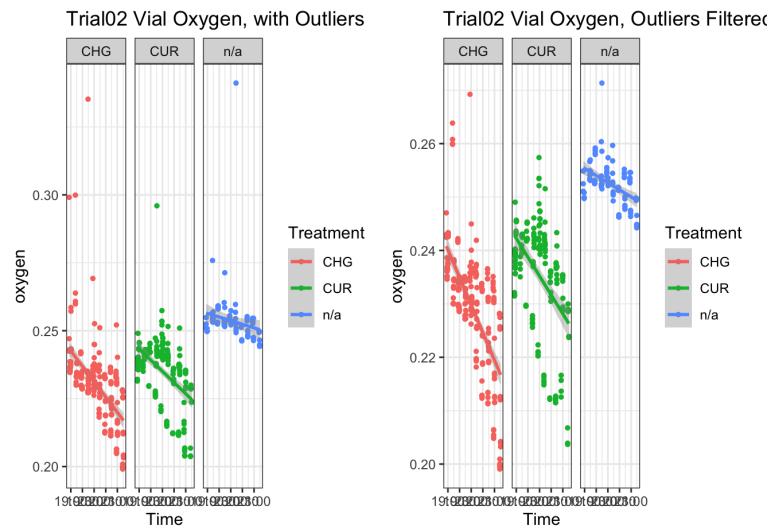


Code

16.1b After Filtering Trial 02

Code

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

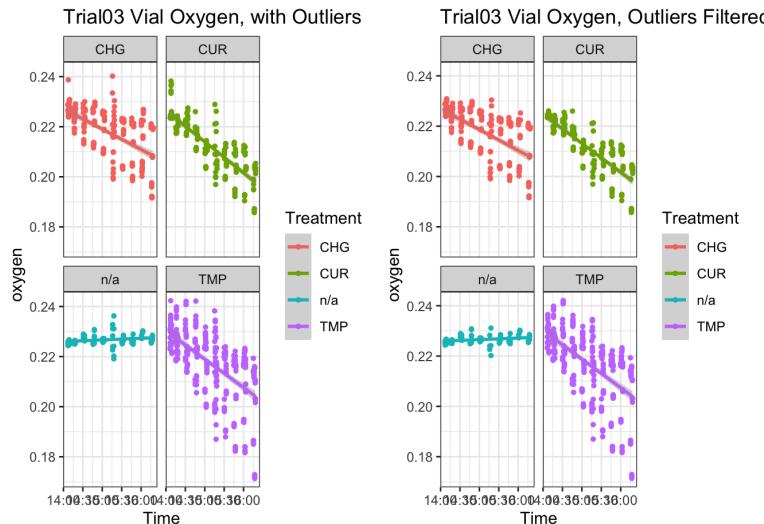


Code

16.1c After Filtering Trial 03

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

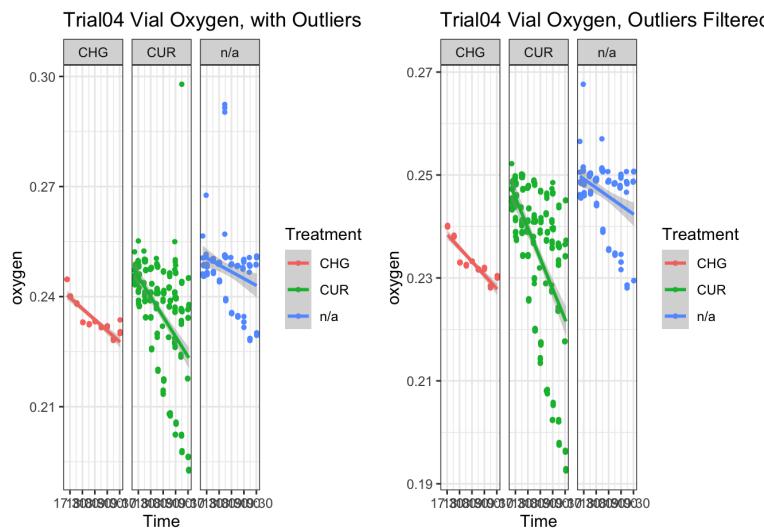
Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTime objects
4.) Observation naming
6.) DO Corrections
6.a) DO table & DO correction Plot Check
7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
8.) Analysis, Respirometry - Creating the Slope Function
9.) Merging ds and dRESPmsr
10.) Krill ID as a factor & Grouping by Krill ID
11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
12.) Filtering krillslopes by each Trial
9.) Respirometry Table
13.) Investigating Outliers
14.) Krill Sparkle Function (standard krillslopes dataframe)
15.) Krill Sparkle Function (80% DO dataframe)
15.b) Krill Sparkle Function (1hr Trial dataframe)
16.) Plots Following Filtering
17.x) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff



16.1d After Filtering Trial 04

Code

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



(patchwork learning in this chunk ignore for now)

Code

17.x) Analysis, Respirometry - outliers removed (investigating krillslopes)

Code

KrillID	SensorNa...	Date	Time	User	SensorID
3 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:25:03	default	159906405
4 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:25:53	default	159906405
5 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:25:54	default	159906405
6 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:25:55	default	159906405
7 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:25:56	default	159906405
79 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:34:05	default	159906405
80 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:34:06	default	159906405
81 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:34:07	default	159906405
162 Trial01_KrilLR11	KrilLR11	28-Oct-19	2019-10-28 14:49:11	default	159906405

Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTIme objects
4.) Observation naming
6.) DO Corrections
6.a) DO table & DO correction Plot Check
7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
8.) Analysis, Respirometry - Creating the Slope Function
9.) Merging ds and dRESPmsr
10.) Krill ID as a factor & Grouping by Krill ID
11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
12.) Filtering krillslopes by each Trial
9.) Respirometry Table
13.) Investigating Outliers
14.) Krill Sparkle Function (standard krillslopes dataframe)
15.) Krill Sparkle Function (80% DO dataframe)
15.b) Krill Sparkle Function (1hr Trial dataframe)
16.) Plots Following Filtering
17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

KrillID	SensorNa...	Date	Time	User	SensorID							
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>							
163	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:49:12	default							
1-10 of 2,773 rows 1-7 of 84 columns												
			Previous	1	2	3	4	5	6	...	278	Next

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR23 Trial02_KrillR24 Trial02_KrillR25 Trial02_KrillR26 Trial02_KrillR27
## [25] Trial02_KrillR29 Trial02_KrillR23 Trial02_KrillR23 Trial02_KrillR23 Trial02_KrillR23
## [29] Trial02_KrillR24 Trial02_KrillR25 Trial03_KRLr3_39 Trial03_KRLr3_40
## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62
## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76
## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

KrillID	SensorNa...	Date	Time	User	SensorID							
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>							
3	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:03	default							
4	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:53	default							
5	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:54	default							
6	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:55	default							
7	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:56	default							
8	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 15:34:11	default							
9	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 15:04:11	default							
10	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 15:04:12	default							
11	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 15:04:13	default							
12	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 15:04:14	default							
1-10 of 2,240 rows 1-7 of 84 columns												
			Previous	1	2	3	4	5	6	...	224	Next

Code

```
## [1] 4
```

Code

KrillID	SensorNa...	Date	Time	User	SensorID
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14 ## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18 ## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12 ## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16 ## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20 ## [21] Trial02_KrillR23 Trial02_KrillR24 Trial02_KrillR25 Trial02_KrillR26 Trial02_KrillR27 ## [25] Trial02_KrillR29 Trial02_KrillR23 Trial02_KrillR23 Trial02_KrillR23 Trial02_KrillR23 ## [29] Trial02_KrillR24 Trial02_KrillR25 Trial03_KRLr3_39 Trial03_KRLr3_40 ## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44 ## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48 ## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52 ## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56 ## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62 ## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69 ## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76 ## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76					

Code

KrillID	SensorNa...	Date	Time	User	SensorID
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>
3	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:03	default
4	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:53	default
5	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:54	default
6	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:55	default
7	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:56	default
79	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:05	default
80	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:06	default

Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTIme objects
4.) Observation naming
6.) DO Corrections
6.a) DO table & DO correction Plot Check
7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
8.) Analysis, Respirometry - Creating the Slope Function
9.) Merging ds and dRESPmsr
10.) Krill ID as a factor & Grouping by Krill ID
11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
12.) Filtering krillslopes by each Trial
9.) Respirometry Table
13.) Investigating Outliers
14.) Krill Sparkle Function (standard krillslopes dataframe)
15.) Krill Sparkle Function (80% DO dataframe)
15.b) Krill Sparkle Function (1hr Trial dataframe)
16.) Plots Following Filtering
17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

KrillID	SensorNa...	Date	Time	User	SensorID	▶
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>	▶
81	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:07	default	159906405
162	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:49:11	default	159906405
163	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:49:12	default	159906405

1-10 of 2,733 rows | 1-7 of 84 columns

Previous 1 2 3 4 5 6 ... 274 Next

Code

[1] "CHG" "CUR" "n/a" "TMP"

Code

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR223 Trial02_KrillR224 Trial02_KrillR226 Trial02_KrillR227
## [25] Trial02_KrillR229 Trial02_KrillR230 Trial02_KrillR232 Trial02_KrillR233
## [29] Trial02_KrillR234 Trial02_KrillR235 Trial03_KRLr3_39 Trial03_KRLr3_40
## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62
## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76
## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

KrillID	SensorNa...	Date	Time	User	SensorID	▶
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>	▶
1	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:01	default	159906405
2	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:02	default	159906405
3	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:03	default	159906405
4	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:53	default	159906405
5	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:54	default	159906405
6	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:55	default	159906405
7	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:56	default	159906405
79	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:05	default	159906405
80	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:06	default	159906405
81	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:07	default	159906405

1-10 of 1,337 rows | 1-7 of 84 columns

Previous 1 2 3 4 5 6 ... 134 Next

Code

KrillID	SensorNa...	Date	Time	User	SensorID	▶
<fctr>	<fctr>	<chr>	<S3: POSIXct>	<chr>	<int>	▶
1	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:01	default	159906405
2	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:02	default	159906405
3	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:03	default	159906405
4	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:53	default	159906405
5	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:54	default	159906405
6	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:55	default	159906405
7	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:25:56	default	159906405
79	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:05	default	159906405
80	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:06	default	159906405
81	Trial01_KrillR11	KrillR11	28-Oct-19	2019-10-28 14:34:07	default	159906405

1-10 of 1,337 rows | 1-7 of 84 columns

Previous 1 2 3 4 5 6 ... 134 Next

Code

[1] "CHG" "CUR" "n/a" "TMP"

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## [1] Trial01_KrillR11 Trial01_KrillR12 Trial01_KrillR13 Trial01_KrillR14
## [5] Trial01_KrillR15 Trial01_KrillR16 Trial01_KrillR17 Trial01_KrillR18
## [9] Trial01_KrillR19 Trial01_KrillR10 Trial01_KrillR11 Trial01_KrillR12
## [13] Trial01_KrillR13 Trial01_KrillR14 Trial01_KrillR15 Trial01_KrillR16
## [17] Trial01_KrillR17 Trial01_KrillR18 Trial01_KrillR19 Trial02_KrillR20
## [21] Trial02_KrillR23 Trial02_KrillR24 Trial02_KrillR226 Trial02_KrillR227
## [25] Trial02_KrillR229 Trial02_KrillR230 Trial02_KrillR232 Trial02_KrillR233
## [29] Trial02_KrillR234 Trial02_KrillR235 Trial03_KRLr3_39 Trial03_KRLr3_40
## [33] Trial03_KRLr3_41 Trial03_KRLr3_42 Trial03_KRLr3_43 Trial03_KRLr3_44
## [37] Trial03_KRLr3_45 Trial03_KRLr3_46 Trial03_KRLr3_47 Trial03_KRLr3_48
## [41] Trial03_KRLr3_49 Trial03_KRLr3_50 Trial03_KRLr3_51 Trial03_KRLr3_52
## [45] Trial03_KRLr3_53 Trial03_KRLr3_54 Trial03_KRLr3_55 Trial03_KRLr3_56
## [49] Trial03_KRLr3_57 Trial04_KRLr4_58 Trial04_KRLr4_59 Trial04_KRLr4_62
## [53] Trial04_KRLr4_65 Trial04_KRLr4_67 Trial04_KRLr4_68 Trial04_KRLr4_69
## [57] Trial04_KRLr4_70 Trial04_KRLr4_71 Trial04_KRLr4_75 Trial04_KRLr4_76
## 60 Levels: Trial01_KrillR11 Trial01_KrillR12 ... Trial04_KRLr4_76
```

Code

18.) Merging ks... and krillslopes...

Code

19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs

Code

60 is the number of vials when Ambient Treatment is excluded

20.) Analysis, Respirometry - Creating Slope Functions & Linear Models

Code

20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff

Code

20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff

Code

20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

Code

21.) Analysis, Respirometry - Correcting the Slope for Blanks

Code

21. Summary Statistics on the Unfiltered Dataframe dSlopes

Code

```
## [1] Trial01 Trial01 Trial01 Trial01 Trial01 Trial01 Trial01 Trial01
## [10] Trial01 Trial01 Trial01 Trial01 Trial01 Trial01 Trial01 Trial01
## [19] Trial01 Trial02 Trial02 Trial02 Trial02 Trial02 Trial02 Trial02
## [28] Trial02 Trial02 Trial02 Trial02 Trial02 Trial02 Trial02 Trial02
## [37] Trial02 Trial02 Trial03 Trial03 Trial03 Trial03 Trial03 Trial03
## [46] Trial03 Trial03 Trial03 Trial03 Trial03 Trial03 Trial03 Trial03
## [55] Trial03 Trial03 Trial04 Trial04 Trial04 Trial04 Trial04 Trial04
## [64] Trial04 Trial04 Trial04 Trial04 Trial04 Trial04 Trial04 Trial04
## [73] Trial04 Trial04 Trial04 Trial04 Trial04 Trial04 Trial04 Trial04
## Levels: Trial01 Trial02 Trial03 Trial04
```

Code

Version Check

Libraries

1.) Setting Working Directory

2.) DF Creation

3.) dateTime objects

4.) Observation naming

6.) DO Corrections

6.a) DO table & DO correction Plot Check

7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

8.) Analysis, Respirometry - Creating the Slope Function

9.) Merging ds and dRESPmsr

10.) Krill ID as a factor & Grouping by Krill ID

11.) Analysis, Respirometry - Creating Slope Functions & Linear Models

12.) Filtering krillslopes by each Trial

9.) Respirometry Table

13.) Investigating Outliers

14.) Krill Sparkle Function (standard krillslopes dataframe)

15.) Krill Sparkle Function (80% DO dataframe)

15.b) Krill Sparkle Function (1hr Trial dataframe)

16.) Plots Following Filtering

17.) Analysis, Respirometry - outliers removed (investigating krillslopes)

18.) Merging ks... and krillslopes...

19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs

20.) Analysis, Respirometry - Creating Slope Functions & Linear Models

20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff

20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff

20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

21.) Analysis, Respirometry - Correcting the Slope for Blanks

21. Summary Statistics on the Unfiltered Dataframe dSlopes

21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

21.c) Summary Statistics on the Unfiltered Dataframe dSlopes

21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

`summarise()` ungrouping output (override with `groups` argument)

Code

Treatment	sd	mean	median	IQR	n	se	dt
<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dbl>	<dbl>
CHG	0.004265618	-0.008106896	-0.007795664	0.007238001	16	0.001066405	0.00209018
CUR	0.006674893	-0.010331173	-0.009898894	0.009208639	19	0.001531325	0.00300138
TMP	0.006783077	-0.009752567	-0.008601520	0.009479005	16	0.001695769	0.0033237

3 rows

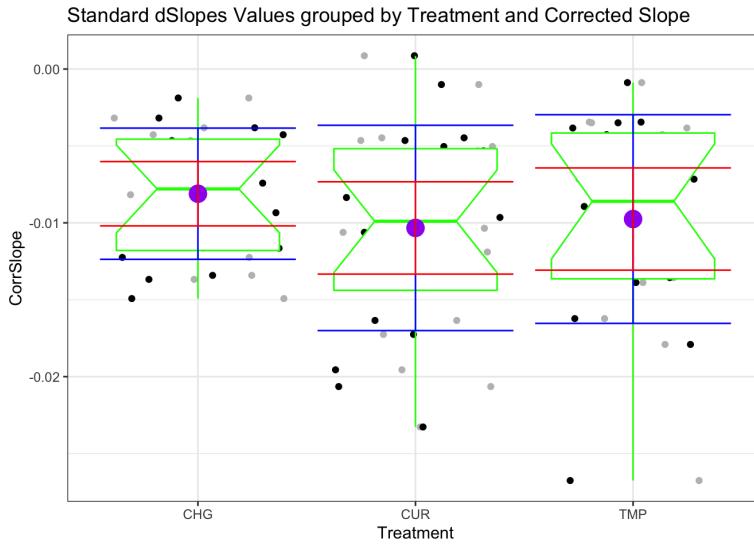
Code

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.0043-0.0081	-0.00780.0072160.00110.0021					
CUR	0.0067-0.0103	-0.00990.0092190.00150.0030					
TMP	0.0068-0.0098	-0.00860.0095160.00170.0033					

Code

21.a) Summary Statistics Graphed with Standard dSlope Values

Code



Code

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.0043-0.0081	-0.00780.0072160.00110.0021					
CUR	0.0067-0.0103	-0.00990.0092190.00150.0030					
TMP	0.0068-0.0098	-0.00860.0095160.00170.0033					

Code

21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

Code

21.c) Summary Statistics on the Unfiltered Dataframe dSlopes

Code

`summarise()` ungrouping output (override with `groups` argument)

Code

Treatment	sd	mean	median	IQR	n	se	dt
<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dbl>	<dbl>

Version Check
Libraries
1.) Setting Working Directory
2.) DF Creation
3.) dateTIme objects
4.) Observation naming
6.) DO Corrections
6.a) DO table & DO correction Plot Check
7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
8.) Analysis, Respirometry - Creating the Slope Function
9.) Merging ds and dRESPmsr
10.) Krill ID as a factor & Grouping by Krill ID
11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
12.) Filtering krillslopes by each Trial
9.) Respirometry Table
13.) Investigating Outliers
14.) Krill Sparkle Function (standard krillslopes dataframe)
15.) Krill Sparkle Function (80% DO dataframe)
15.b) Krill Sparkle Function (1hr Trial dataframe)
16.) Plots Following Filtering
17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
18.) Merging ks... and krillslopes...
19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

Treatment	sd	mean	median	IQR	n	se	ci
<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dbl>	>
CHG	0.004065527	0.0005785529	0.0014299211	0.002052282	16	0.0010163817	
CUR	0.003283892	-0.0010072002	-0.0006882532	0.003677814	19	0.0007533765	
TMP	0.003494196	0.0010753163	0.0006012823	0.005156133	16	0.0008735490	

3 rows | 1-7 of 8 columns

Code

Treatment	sd	mean	median	IQR	n	se	ci
<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dbl>	>
CHG	0.0041	0.0006	0.00140.0021161e-030.0020				
CUR	0.0033	-0.0010-0.00070.0037198e-040.0015					
TMP	0.0035	0.0011	0.00060.0052169e-040.0017				

Code

21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

Code

21.e Summary Statistics on the Unfiltered Dataframe dSlopes

Code

```
## `summarise()` ungrouping output (override with `groups` argument)
```

Code

Treatment	sd	mean	median	IQR	n	se	ci
<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dbl>	>
CHG	0.003173232	-0.0004976462	-4.158713e-05	0.002900971	16	0.0007933080	
CUR	0.002298790	-0.0003071082	-2.570656e-05	0.002418887	19	0.0005273785	
TMP	0.002813950	0.0002339053	4.077097e-04	0.003848429	16	0.0007034875	

3 rows | 1-7 of 8 columns

Code

```
Treatment sd mean median IQR n se ci
```

CHG	0.0032-5e-04	0e+000.0029168e-040.0016	
CUR	0.0023-3e-04	0e+000.0024195e-040.0010	
TMP	0.0028 2e-04	4e-040.0038167e-040.0014	

Code

21.f) Analysis, Respirometry - Correcting the Slope for Blanks - 1hr cutoff

Code

Executive Summary

21.g Summary Statistics on the Unfiltered Dataframe dSlopes

Code

```
## `summarise()` ungrouping output (override with `groups` argument)
```

Code

Treatment	sd	mean	median	IQR	n	se	ci
<fctr>	<dbl>	<dbl>	<dbl>	<dbl>	<int>	<dbl>	>
CHG	0.005583358	-0.001776208	-0.002036407	0.004907458	16	0.001395839	0.0027358
CUR	0.011298257	0.002379594	0.001020978	0.005144002	19	0.002591998	0.0050803
TMP	0.004838440	-0.002500531	-0.003650568	0.005695567	16	0.001209610	0.0023708

3 rows

Code

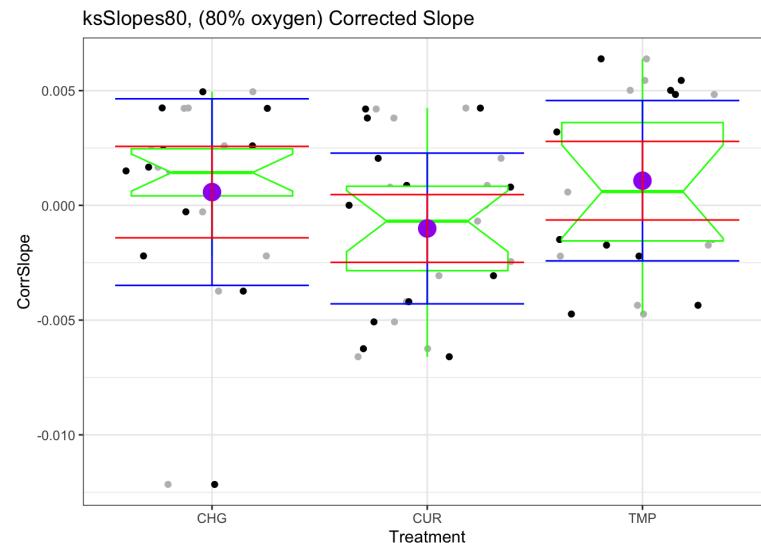
Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.0056	-0.0018	-0.0020	0.0049	160	0.00140	0.0027
CUR	0.0113	0.0024	0.00100	0.0051	190	0.00260	0.0051
TMP	0.0048	-0.0025	-0.00370	0.00571	60	0.00120	0.0024

Code

22.) 80% Slope for Corrected Slopes

Code

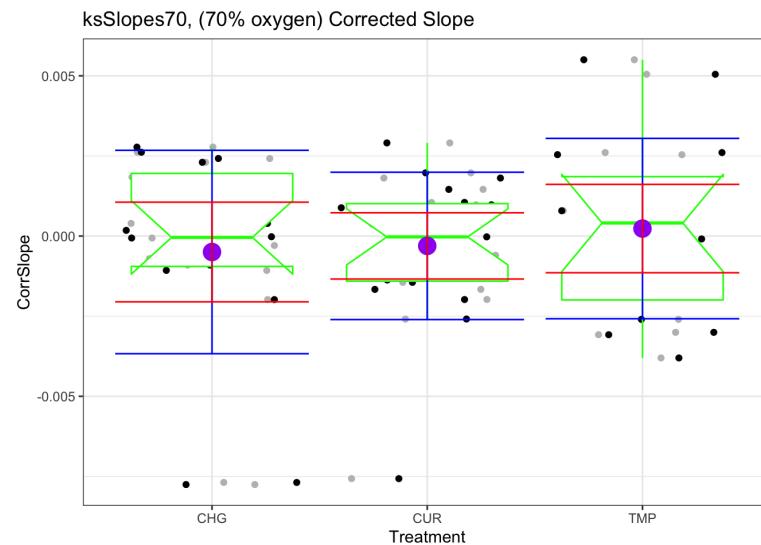


The purple dots represent the mean- all trials included Confidence Intervals set to 95 Green boxplots show from the 25th percentile to the 75th percentile error bars +/- SD shown in blue error bars(CI) +/- our confidence intervals- shown in red

23.) 70% Slope for Corrected Slopes

Code

```
## notch went outside hinges. Try setting notch=FALSE.
## notch went outside hinges. Try setting notch=FALSE.
```



The purple dots represent the mean- all trials included Confidence Intervals set to 95 Green boxplots show from the 25th percentile to the 75th percentile error bars +/- SD shown in blue error bars(CI) +/- our confidence intervals- shown in red

24.) 1hr cutoff Slope for Corrected Slopes

Code

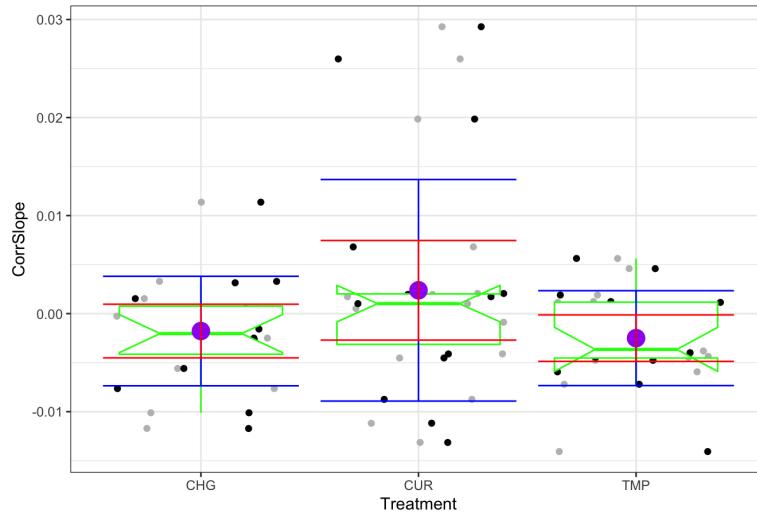
Version Check

Libraries

- 1.) Setting Working Directory
- 2.) DF Creation
- 3.) dateTime objects
- 4.) Observation naming
- 6.) DO Corrections
- 6.a) DO table & DO correction Plot Check
- 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
- 8.) Analysis, Respirometry - Creating the Slope Function
- 9.) Merging ds and dRESPmsr
- 10.) Krill ID as a factor & Grouping by Krill ID
- 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 12.) Filtering krillslopes by each Trial
- 9.) Respirometry Table
- 13.) Investigating Outliers
- 14.) Krill Sparkle Function (standard krillslopes dataframe)
- 15.) Krill Sparkle Function (80% DO dataframe)
- 15.b) Krill Sparkle Function (1hr Trial dataframe)
- 16.) Plots Following Filtering
- 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
- 18.) Merging ks... and krillslopes...
- 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
- 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
- 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
- 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
- 21.) Analysis, Respirometry - Correcting the Slope for Blanks
21. Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
- 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## notch went outside hinges. Try setting notch=FALSE.
## notch went outside hinges. Try setting notch=FALSE.
```

ksSlopes1hr, (1hr cutoff) Corrected Slope



The purple dots represent the mean- all trials included Confidence Intervals set to 95 Green boxplots show from the 25th percentile to the 75th percentile error bars +/- SD shown in blue error bars(CI) +/- our confidence intervals- shown in red

25.) Descriptive Statistics

Code

	Avg All Points	Med All Points	Avg 80% DO Slopes	Med 80% DO Slopes	80% DO Slopes	Avg 70% DO Slopes	Med 70% DO Slopes	70% DO Slopes	Avg 1hr Slopes	Med 1hr Slopes
CHG	-0.0081069	-0.0077957	0.0042656	0.0005786	0.0014299	0.0040655	-0.00044976	-0.00004160	0.0031732	-0.0017762
CUR	-0.0103312	-0.0098989	0.0066749	-0.0010072	-0.0006883	0.0032839	-0.0003071	-0.00002570	0.0022988	0.0023796
TMP	-0.0097526	-0.0086015	0.0067831	0.0010753	0.00060130	0.0034942	0.0002339	0.00040770	0.0028139	-0.0025005

26.) Fitting my Linear Mixed-Effects Models to my Dataframes

Code

```
## [1] 51
```

Code

26.a) 1hr Dataframe - LMER

Code

- Version Check
- Libraries
- 1.) Setting Working Directory
- 2.) DF Creation
- 3.) dateTIme objects
- 4.) Observation naming
- 6.) DO Corrections
- 6.a) DO table & DO correction Plot Check
- 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
- 8.) Analysis, Respirometry - Creating the Slope Function
- 9.) Merging ds and dRESPmsr
- 10.) Krill ID as a factor & Grouping by Krill ID
- 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 12.) Filtering krillslopes by each Trial
- 9.) Respirometry Table
- 13.) Investigating Outliers
- 14.) Krill Sparkle Function (standard krillslopes dataframe)
- 15.) Krill Sparkle Function (80% DO dataframe)
- 15.b) Krill Sparkle Function (1hr Trial dataframe)
- 16.) Plots Following Filtering
- 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
- 18.) Merging ks... and krillslopes...
- 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
- 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
- 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
- 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
- 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
- 21.) Analysis, Respirometry - Correcting the Slope for Blanks
- 21. Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
- 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
- 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.lhr
##
## REML criterion at convergence: -329.1
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -1.68638 -0.47569  0.00437  0.51632  2.75955
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS    (Intercept) 3.441e-05 0.005866
##   Residual           4.178e-05 0.006464
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept) -0.001302  0.003369 8.777260 -0.386   0.708
## TreatmentCUR  0.004016  0.004212 14.743842  0.953   0.356
## TreatmentTMP -0.001199  0.005583  6.333602 -0.215   0.837
##
## Correlation of Fixed Effects:
##   (Intr) TrtCUR
## TreatmentCUR -0.670
## TreatmentTMP -0.604  0.405
```

Code

"1hr Dataset" - No Treatment Effect Found

Random Effects Model variance accounting for a possible MOATs effect remains significantly small. No treatment effect observed. Neither correlation or T values between "All Change(CHG)" to "Current(CUR)" and "High Temperature(TMP)" This model doesn't consider High Temperature directly against Current Model re-organized/re-leveled below

26.b) 1hr Dataframe - LMER relieved Current 1st

Code

```
## [1] "CHG" "CUR" "TMP"
```

Code

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.lhr
##
## REML criterion at convergence: -329.1
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -1.68638 -0.47569  0.00437  0.51632  2.75955
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS    (Intercept) 3.441e-05 0.005866
##   Residual           4.178e-05 0.006464
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept)  0.002713  0.003173 8.789085  0.855   0.415
## TreatmentCHG -0.004016  0.004212 14.743842 -0.953   0.356
## TreatmentTMP -0.005214  0.005467  6.253781 -0.954   0.376
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TreatmentCHG -0.616
## TreatmentTMP -0.580  0.357
```

The Current Conditions to Hight Temperature comparison did not display a treatment effect.

Possible reasons for such small amount of variance include only 51 animals in trial. 16 animals from the "All Change" treatment were in included across four trials. 19 animals from the "Current" treatment were in included across four trials. 16 animals from the "High Temperarure" treatment were in included across four trials. (totals 51 animals)

so signal over the noise- why?

1hr may not have allowed enough observations to show a discernable difference across treatments. However, Krill could just be proving to be a robust organism, able to withstand a cross stress environment. It's more likely that sample size was small.

26.c) 80% Threshold Dataframe - LMER

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.x) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.80
##
## REML criterion at convergence: -395.3
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -3.4943 -0.5586  0.1519  0.5739  1.4604
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS    (Intercept) 2.347e-07 0.0004845
##   Residual           1.287e-05 0.0035869
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.0005746 0.0009346 7.6538185  0.615   0.557
## TreatmentCUR -0.0016000 0.0012697 7.5087302 -1.260   0.245
## TreatmentTMP  0.0005007 0.0013398 4.4345996  0.374   0.726
##
## Correlation of Fixed Effects:
##   (Intr) TrtCUR
## TrtmntCUR -0.733
## TrtmntTMP -0.698  0.511
```

Code

The 80% (DO) Threshold t values are slightly smaller. The variance around a MOATS effect remains significantly small. No treatment effect observed. Model re-organized/re-leveled below to compare "Current" against "High Temperature" directly

26.d) 80% Threshold - LMER releved Current 1st

Code

```
## [1] "CHG" "CUR" "TMP"
```

Code

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.80
##
## REML criterion at convergence: -395.3
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -3.4943 -0.5586  0.1519  0.5739  1.4604
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS    (Intercept) 2.347e-07 0.0004845
##   Residual           1.287e-05 0.0035869
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) -0.0010254 0.0008642 5.6876601 -1.187   0.283
## TreatmentCHG  0.0016000 0.0012697 7.5087302  1.260   0.245
## TreatmentTMP  0.0021007 0.0012916 3.8400048  1.626   0.182
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TrtmntCHG -0.677
## TrtmntTMP -0.669  0.453
```

When comparing Current against "High Temperature" and "All Change" the T values remain small but the TMP to CUR is somewhat larger.

Still, no discernible treatment effect, no discernible MOATS effect.

26.e) 70% Threshold Dataframe - LMER

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method 
## lmerModLmerTest
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.70
##
## REML criterion at convergence: -431.4
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max 
## -3.1536 -0.5207  0.1268  0.5546  1.5776 
##
## Random effects:
##   Groups   Name        Variance Std.Dev. 
##   MOATS    (Intercept) 3.331e-06 0.001825 
##   Residual             5.069e-06 0.002251 
##   Number of obs: 51, groups: MOATS, 9 
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept) -3.876e-04 1.089e-03 9.300e+00 -0.356  0.730 
## TreatmentCUR 1.416e-05 1.384e-03 1.437e+01  0.010  0.992 
## TreatmentTMP 6.215e-04 1.780e-03 6.780e+00  0.349  0.738 
##
## Correlation of Fixed Effects:
##   (Intr) TrtCUR 
## TreatmentCUR -0.680 
## TreatmentTMP -0.612  0.416
```

Code

The variance around a MOATs effect remains significantly small in this 70% Threshold dataset. No treatment effect observed. Model re-organized/re-leveled below to compare "Current" against "High Temperature" directly

26.f) 70% Threshold - LMER relevel Current 1st

Code

```
## [1] "CHG" "CUR" "TMP"
```

Code

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method 
## lmerModLmerTest
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.70
##
## REML criterion at convergence: -431.4
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max 
## -3.1536 -0.5207  0.1268  0.5546  1.5776 
##
## Random effects:
##   Groups   Name        Variance Std.Dev. 
##   MOATS    (Intercept) 3.331e-06 0.001825 
##   Residual             5.069e-06 0.002251 
##   Number of obs: 51, groups: MOATS, 9 
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept) -3.734e-04 1.025e-03 9.401e+00 -0.364  0.724 
## TreatmentCHG -1.416e-05 1.384e-03 1.437e+01 -0.010  0.992 
## TreatmentTMP 6.073e-04 1.742e-03 6.715e+00  0.349  0.738 
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG 
## TreatmentCHG -0.628 
## TreatmentTMP -0.589  0.370
```

No discernible treatment effect, no discernible MOATS effect. None of the "threshold confined" datasets displayed a MOATs or Treatment Effect.

Below shows the comparison is slopes values when all data points were considered.

26.g) All Points "dSlopes" Dataframe - LMER

Code

```
## boundary (singular) fit: see ?isSingular
```

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: dSlopes
##
## REML criterion at convergence: -345.4
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -2.8039 -0.6542  0.1125  0.7677  1.8463
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS   (Intercept) 0.000e+00 0.000000
##   Residual           3.677e-05 0.006064
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept) -0.008107  0.001516 48.000000 -5.348 2.44e-06 ***
## TreatmentCUR -0.002224  0.002058 48.000000 -1.081  0.285
## TreatmentTMP -0.001646  0.002144 48.000000 -0.768  0.446
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##   (Intr) TrtCUR
## TreatmentCUR -0.737
## TreatmentTMP -0.707  0.521
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

Code

The variance around a MOATs effect remains so significantly small. No MOATs effect No treatment effect observed. Model re-organized/re-leveled below to compare "Current" against "High Temperature" directly

26.f) All Points - LMER relevel Current 1st

Code

```
## [1] "CHG" "CUR" "TMP"
```

Code

```
## boundary (singular) fit: see ?isSingular
```

Code

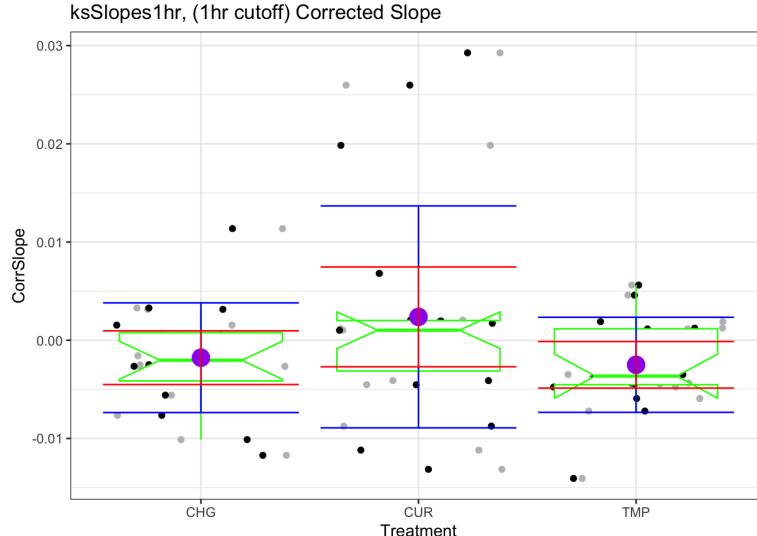
```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: dSlopes
##
## REML criterion at convergence: -345.4
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -2.8039 -0.6542  0.1125  0.7677  1.8463
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS   (Intercept) 0.000e+00 0.000000
##   Residual           3.677e-05 0.006064
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|) 
## (Intercept) -0.0103312 0.0013912 48.000000 -7.426 1.64e-09 ***
## TreatmentCHG  0.0022243 0.0020576 48.000000  1.081  0.285
## TreatmentTMP  0.0005786 0.0020576 48.000000  0.281  0.780
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TreatmentCHG -0.676
## TreatmentTMP -0.676  0.457
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular
```

Code

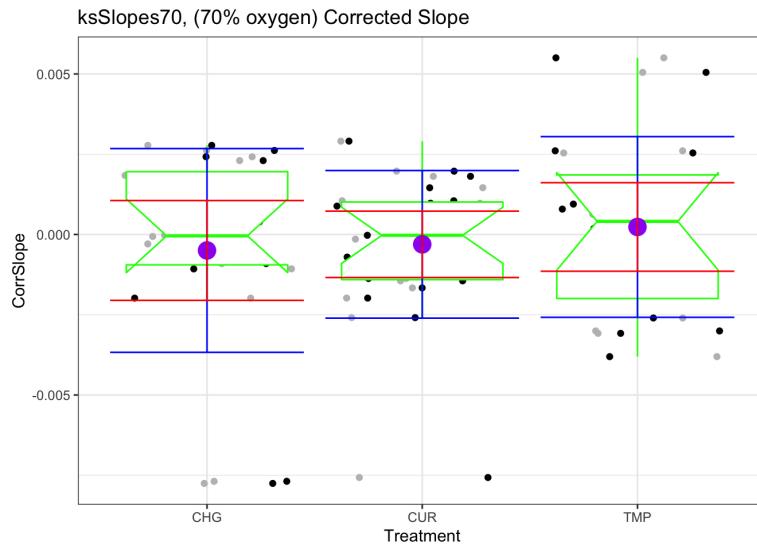
Code

```
## notch went outside hinges. Try setting notch=FALSE.
## notch went outside hinges. Try setting notch=FALSE.
```

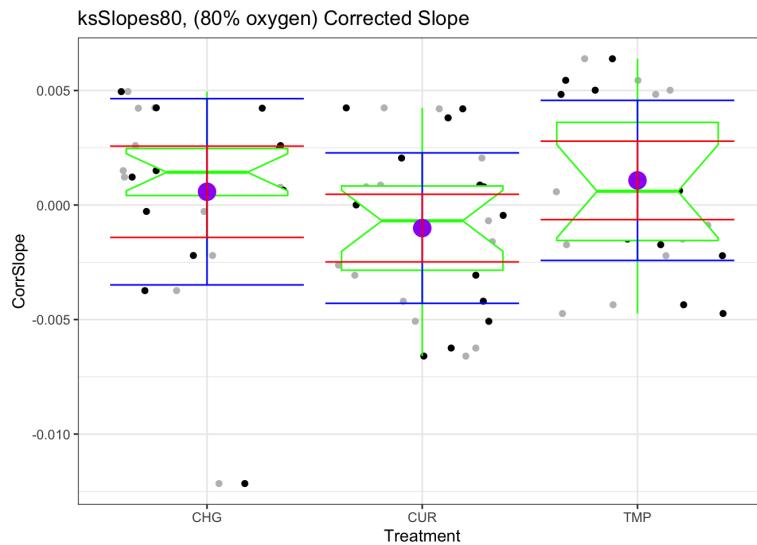
Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTime objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
 7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L
 8.) Analysis, Respirometry - Creating the Slope Function
 9.) Merging ds and dRESPmsr
 10.) Krill ID as a factor & Grouping by Krill ID
 11.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 12.) Filtering krillslopes by each Trial
 9.) Respirometry Table
 13.) Investigating Outliers
 14.) Krill Sparkle Function (standard krillslopes dataframe)
 15.) Krill Sparkle Function (80% DO dataframe)
 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.x) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
 20.1b) Analysis, Respirometry - Creating Slope Functions & Linear Models 70% cutoff
 20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff
 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff



```
## notch went outside hinges. Try setting notch=FALSE.
## notch went outside hinges. Try setting notch=FALSE.
```



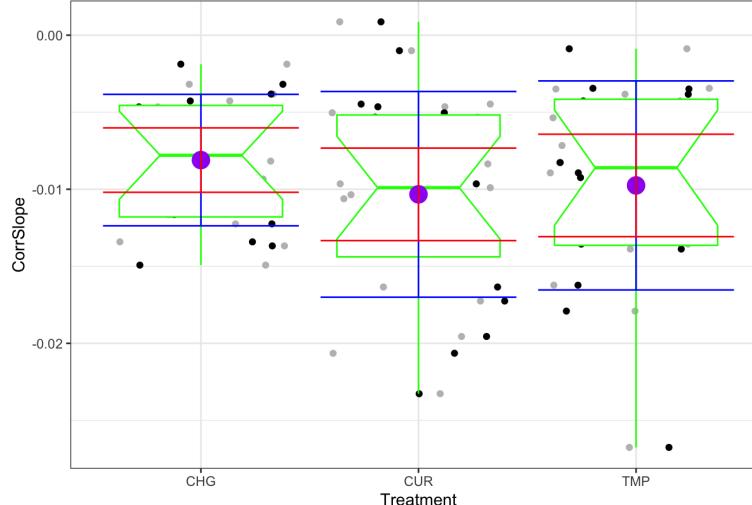
Code



Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTime objects
 4.) Observation naming
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 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
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 19.) Krill ID as a factor & Grouping by Krill ID - filtered DFs
 20.) Analysis, Respirometry - Creating Slope Functions & Linear Models
 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
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 21.) Analysis, Respirometry - Correcting the Slope for Blanks
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 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

Standard dSlopes Values grouped by Treatment and Corrected Slope



Slope Statistics

Code

	Avg All Points	Med All Points	All Points	Avg 80% DO	Med 80% DO	80% DO	Avg 70% DO	Med 70% DO	70% DO	Avg 1hr Slopes	Med 1hr Slopes
Corrected Slopes											
SD											
CHG	0.0081069	-0.0077957	0.0042656	0.0005786	0.0014299	0.0040655	-0.0004976	-0.00004160	0.0031732	-0.0017762	-0.0020364
CUR	-0.0103312	-0.0098989	0.0066749	-0.0010072	-0.0006883	0.0032839	-0.0003071	-0.0000257	0.0022988	0.0023796	0.0010210
TMP	-0.0097526	-0.0086015	0.0067831	0.0010753	0.00060130	0.0034942	0.0002339	0.00040770	0.0028139	-0.0025005	-0.0036506

Krill Slopes 1hr Summary Table

Code

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.0056	-0.0018	-0.00200	0.0049160	0.00140	0.0027	
CUR	0.0113	0.0024	0.00100	0.0051190	0.00260	0.0051	
TMP	0.0048	-0.0025	-0.00370	0.0057160	0.00120	0.0024	

Krill Slopes (70min cutoff) Summary Table

Code

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.00317323	-0.00049765	-0.000041590	0.00290097160	0.000793310	0.00155488	
CUR	0.00229879	-0.00030711	-0.000025710	0.00241889190	0.000527380	0.00103366	
TMP	0.00281395	0.00023391	0.000407710	0.00384843160	0.000703490	0.00137884	

Krill Slopes (80min cutoff) Summary Table

Code

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.00406553	0.00057855	0.001429920	0.00205228160	0.001016380	0.00199211	
CUR	0.00328389	-0.00100720	-0.000688250	0.00367781190	0.000753380	0.00147662	
TMP	0.00349420	0.00107532	0.000601280	0.00515613160	0.000873550	0.00171216	

Krill Slopes (all points) Summary Table

Code

Treatment	sd	mean	median	IQR	n	se	ci
CHG	0.00426562	-0.00810690	-0.007795660	0.00723800160	0.001066400	0.00209015	
CUR	0.00667489	-0.01033117	-0.009889890	0.00920864190	0.001531330	0.00300140	
TMP	0.00678308	-0.00975257	-0.008601520	0.00947900160	0.001695770	0.00332371	

Krill Slopes (1hr cutoff) Mixed Effects Model

Code

Version Check
 Libraries
 1.) Setting Working Directory
 2.) DF Creation
 3.) dateTIme objects
 4.) Observation naming
 6.) DO Corrections
 6.a) DO table & DO correction Plot Check
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 15.b) Krill Sparkle Function (1hr Trial dataframe)
 16.) Plots Following Filtering
 17.) Analysis, Respirometry - outliers removed (investigating krillslopes)
 18.) Merging ks... and krillslopes...
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 20.1a) Analysis, Respirometry - Creating Slope Functions & Linear Models 80% cutoff
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 21.) Analysis, Respirometry - Correcting the Slope for Blanks
 21. Summary Statistics on the Unfiltered Dataframe dSlopes
 21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff
 21.c) Summary Statistics on the Unfiltered Dataframe dSlopes
 21.d) Analysis, Respirometry - Correcting the Slope for Blanks - 70% cutoff

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.lhr
##
## REML criterion at convergence: -329.1
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -1.68638 -0.47569  0.00437  0.51632  2.75955
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS   (Intercept) 3.441e-05 0.005866
##   Residual           4.178e-05 0.006464
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  0.002713  0.003173  8.789085  0.855   0.415
## TreatmentCHG -0.004016  0.004212 14.743842 -0.953   0.356
## TreatmentTMP -0.005214  0.005467  6.253781 -0.954   0.376
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TrtCHG -0.616
## TreatmentTMP -0.580  0.357
```

Krill Slopes (80min cutoff) Mixed Effects Model

Code

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.80
##
## REML criterion at convergence: -395.3
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -3.4943 -0.5586  0.1519  0.5739  1.4604
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS   (Intercept) 2.347e-07 0.0004845
##   Residual           1.287e-05 0.0035869
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) -0.0010254 0.0008642  5.6876601 -1.187   0.283
## TreatmentCHG  0.0016000 0.0012697  7.5087302  1.260   0.245
## TreatmentTMP  0.0021007 0.0012916  3.8400048  1.626   0.182
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TrtCHG -0.677
## TreatmentTMP -0.669  0.453
```

Krill Slopes (70min cutoff) Mixed Effects Model

Code

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
## Data: ksSlopes.70
##
## REML criterion at convergence: -431.4
##
## Scaled residuals:
##   Min     1Q  Median     3Q    Max
## -3.1536 -0.5207  0.1268  0.5546  1.5776
##
## Random effects:
##   Groups   Name        Variance Std.Dev.
##   MOATS   (Intercept) 3.331e-06 0.001825
##   Residual           5.069e-06 0.002251
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|)
## (Intercept) -3.734e-04 1.025e-03 9.401e+00 -0.364   0.724
## TreatmentCHG -1.416e-05 1.384e-03 1.437e+01 -0.010   0.992
## TreatmentTMP  6.073e-04 1.742e-03 6.715e+00  0.349   0.738
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TrtCHG -0.628
## TreatmentTMP -0.589  0.370
```

Code

Version Check

Libraries

1.) Setting Working Directory

2.) DF Creation

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7.) Initial Dataframe dRESPmsr Plots, 80% DO, Oxygen Per Vial, Actual DOmg/L

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20.1c) Analysis, Respirometry - Creating Slope Functions & Linear Models 1hr cutoff

21.) Analysis, Respirometry - Correcting the Slope for Blanks

21. Summary Statistics on the Unfiltered Dataframe dSlopes

21.b) Analysis, Respirometry - Correcting the Slope for Blanks - 80% cutoff

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```

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: CorrSlope ~ Treatment + (1 | MOATS)
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##
## REML criterion at convergence: -345.4
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## Random effects:
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##   Residual            3.677e-05 0.006064
## Number of obs: 51, groups: MOATS, 9
##
## Fixed effects:
##   Estimate Std. Error      df t value Pr(>|t|)    
## (Intercept) -0.0103312 0.0013912 48.0000000 -7.426 1.64e-09 ***
## TreatmentCHG 0.0022243 0.0020576 48.0000000  1.081  0.285    
## TreatmentTMP 0.0005786 0.0020576 48.0000000  0.281  0.780    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##   (Intr) TrtCHG
## TrtCHG -0.676
## TreatmentTMP -0.676  0.457
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see ?isSingular

```

Code

END OF SCRIPT | END OF DOCUMENT