

cor

This code creates a correlation matrix to look at relationships between variables. This helps identify specific relationships of interest

[Link:](#)

Getting Started

Libraries

Data

Cleaning

Remove non-numeric variables

```
bo<-  
  bo %>%  
  select(!c(date, ...1))  
  
c2<-  
  c2 %>%  
  select(!c(date, ...1))  
  
rd<-  
  rd %>%  
  select(!c(date, ...1))
```

Make Datasets for normal and non-normal variables

Variables that are normally distributed across all three sites will be in one df. All others will be in another.

```
#BLIND OSO
b_norm<-
  bo %>%
  select(!c(sal, secchi, nn, tdn, don, doc, toc, tn))
b_para<-
  bo %>%
  select(sal, secchi, nn, tdn, don, doc, toc, tn)

#CANALS
c_norm<-
  c2 %>%
  select(!c(sal, secchi, nn, tdn, don, doc, toc, tn))
c_para<-
  c2 %>%
  select(sal, secchi, nn, tdn, don, doc, toc, tn)

#GULF
r_norm<-
  rd %>%
  select(!c(sal, secchi, nn, tdn, don, doc, toc, tn))
r_para<-
  rd %>%
  select(sal, secchi, nn, tdn, don, doc, toc, tn)
```

Log10 Transform non-normally distributed data for Norm df

Distributions can be found in 1_distribution.qmd

```
#BLIND OSO
b_norm<-
  b_norm %>%
  mutate(amm = log10(amm), #Log-transforms data
         din_dip = log10(din_dip),
         dust = log10(dust),
         chl = log10(chl),
         dust_lag = log10(dust_lag))
```

```

#CANALS
c_norm<-
  c_norm %>%
  mutate(orthop = log10(orthop),
         dust = log10(dust),
         dust_lag = log10(dust_lag))

#GULF
r_norm<-
  r_norm %>%
  mutate(dust = log10(dust),
         dust_lag = log10(dust_lag))

```

Correlation Matrix

There are different methods for **correlation analysis** : **Pearson parametric correlation test**, **Spearman** and **Kendall** rank-based **correlation analysis**. The default is [pearson correlation coefficient](#) which measures the linear **dependence** between two variables. [kendall](#) and [spearman](#) correlation methods are non-parametric **rank-based correlation test**.

Compute Correlation Matrix

If your data contain missing values, use the following R code to handle missing values by case-wise deletion.

```
cor(x, method = "pearson", use = "complete.obs")
```

Make Function to Format

Simple function for formatting a **correlation matrix** into a table with 4 columns containing : Column 1 : row names (variable 1 for the correlation test), Column 2 : column names (variable 2 for the correlation test), Column 3 : the **correlation coefficients**, Column 4 : the **p-values** of the correlations

```

flattenCorrMatrix <- function(cormat, pmat) {
  ut <- upper.tri(cormat)
  data.frame(
    row = rownames(cormat)[row(cormat)[ut]],

```

```

column = rownames(cormat)[col(cormat)[ut]],
cor    =(cormat)[ut],
p      = pmat[ut])}

```

Make Matrix

The function `rcorr()` [in **Hmisc** package] can be used to compute the **significance levels** for **pearson** and **spearman correlations**. It returns both the correlation coefficients and the p-value of the correlation for all possible pairs of columns in the data table.

```

bclean<- rcorr(as.matrix(b_norm))
flattenCorrMatrix(bclean$r, bclean$P)

```

	row	column	cor	p
1	copies_mL	chl	0.424384223	1.691235e-01
2	copies_mL	temp	-0.236364771	4.595296e-01
3	chl	temp	-0.334160061	2.884230e-01
4	copies_mL	do_mgl	0.040715966	9.000217e-01
5	chl	do_mgl	0.399047726	1.987862e-01
6	temp	do_mgl	-0.798746187	1.834246e-03
7	copies_mL	do_per	-0.101928025	7.526039e-01
8	chl	do_per	0.333264084	2.897980e-01
9	temp	do_per	-0.739913350	5.938779e-03
10	do_mgl	do_per	0.981998903	1.444345e-08
11	copies_mL	pH	-0.090384104	7.799754e-01
12	chl	pH	0.118857022	7.129402e-01
13	temp	pH	-0.206445779	5.197354e-01
14	do_mgl	pH	0.212156883	5.079865e-01
15	do_per	pH	0.233586970	4.649763e-01
16	copies_mL	amm	0.268597289	3.985937e-01
17	chl	amm	0.101391969	7.538694e-01
18	temp	amm	-0.341512612	2.772798e-01
19	do_mgl	amm	0.312548446	3.226143e-01
20	do_per	amm	0.250623240	4.320520e-01
21	pH	amm	-0.425690164	1.676752e-01
22	copies_mL	orthop	0.482379585	1.122269e-01
23	chl	orthop	0.427723591	1.654355e-01
24	temp	orthop	-0.321965443	3.074536e-01
25	do_mgl	orthop	0.323036048	3.057556e-01
26	do_per	orthop	0.258084418	4.180008e-01
27	pH	orthop	-0.024529552	9.396827e-01

28	amm	orthop	-0.249224323	4.347118e-01
29	copies_mL	sil	-0.152314048	6.365199e-01
30	chl	sil	-0.240499923	4.514774e-01
31	temp	sil	-0.379349806	2.239156e-01
32	do_mgl	sil	0.373777105	2.313547e-01
33	do_per	sil	0.396807301	2.015529e-01
34	pH	sil	-0.218608814	4.948563e-01
35	amm	sil	0.571850831	5.205678e-02
36	orthop	sil	-0.007650716	9.811735e-01
37	copies_mL	din	0.548177280	6.499395e-02
38	chl	din	0.359558395	2.509945e-01
39	temp	din	-0.543618288	6.771861e-02
40	do_mgl	din	0.467503637	1.253957e-01
41	do_per	din	0.329780358	2.951793e-01
42	pH	din	-0.203800072	5.252178e-01
43	amm	din	0.191467249	5.510959e-01
44	orthop	din	0.774072897	3.127218e-03
45	sil	din	0.208555520	5.153816e-01
46	copies_mL	din_dip	0.215717277	5.007219e-01
47	chl	din_dip	0.310276559	3.263321e-01
48	temp	din_dip	-0.716129317	8.801145e-03
49	do_mgl	din_dip	0.493488547	1.030132e-01
50	do_per	din_dip	0.394498473	2.044286e-01
51	pH	din_dip	-0.139062662	6.664474e-01
52	amm	din_dip	0.663275601	1.870811e-02
53	orthop	din_dip	0.028172577	9.307424e-01
54	sil	din_dip	0.509873632	9.036752e-02
55	din	din_dip	0.514231116	8.718991e-02
56	copies_mL	dust	0.368987692	2.378645e-01
57	chl	dust	0.401551076	1.957225e-01
58	temp	dust	-0.504965586	9.403916e-02
59	do_mgl	dust	0.714404445	9.042658e-03
60	do_per	dust	0.626559055	2.925072e-02
61	pH	dust	0.251170708	4.310133e-01
62	amm	dust	0.564496961	5.586262e-02
63	orthop	dust	0.072257076	8.234119e-01
64	sil	dust	0.283264128	3.723002e-01
65	din	dust	0.399525867	1.981988e-01
66	din_dip	dust	0.522786799	8.117270e-02
67	copies_mL	dust_lag	0.698802162	1.145807e-02
68	chl	dust_lag	0.727093796	7.376737e-03
69	temp	dust_lag	-0.593908784	4.173571e-02
70	do_mgl	dust_lag	0.646031933	2.323543e-02

71	do_per	dust_lag	0.550716789	6.350957e-02
72	pH	dust_lag	0.012884387	9.682993e-01
73	amm	dust_lag	0.268809701	3.982063e-01
74	orthop	dust_lag	0.656305678	2.045221e-02
75	sil	dust_lag	0.076670381	8.127900e-01
76	din	dust_lag	0.690183358	1.298173e-02
77	din_dip	dust_lag	0.360213993	2.500682e-01
78	dust	dust_lag	0.622673425	3.057347e-02

```
cclean<- rcorr(as.matrix(c_norm))
flattenCorrMatrix(cclean$r, cclean$P)
```

	row	column	cor	p
1	copies_mL	chl	0.422398495	1.713409e-01
2	copies_mL	temp	0.063173362	8.453586e-01
3	chl	temp	0.652961803	2.132979e-02
4	copies_mL	do_mgl	-0.149524858	6.427796e-01
5	chl	do_mgl	-0.068547700	8.323608e-01
6	temp	do_mgl	-0.453600118	1.385817e-01
7	copies_mL	do_per	-0.128740158	6.900762e-01
8	chl	do_per	-0.028510814	9.299127e-01
9	temp	do_per	-0.416625174	1.778912e-01
10	do_mgl	do_per	0.998276278	1.194600e-13
11	copies_mL	pH	-0.182827097	5.695324e-01
12	chl	pH	0.097087354	7.640515e-01
13	temp	pH	0.079501170	8.059920e-01
14	do_mgl	pH	0.172759583	5.913201e-01
15	do_per	pH	0.158984068	6.216394e-01
16	copies_mL	amm	-0.108144710	7.379693e-01
17	chl	amm	0.326671917	3.000280e-01
18	temp	amm	0.872365160	2.144869e-04
19	do_mgl	amm	-0.601754981	3.844305e-02
20	do_per	amm	-0.578097323	4.896998e-02
21	pH	amm	-0.033534377	9.175976e-01
22	copies_mL	orthop	-0.165890855	6.063666e-01
23	chl	orthop	-0.481702264	1.128057e-01
24	temp	orthop	-0.157001675	6.260488e-01
25	do_mgl	orthop	-0.493694850	1.028470e-01
26	do_per	orthop	-0.505758703	9.343916e-02
27	pH	orthop	-0.102317357	7.516851e-01
28	amm	orthop	0.132858057	6.806183e-01

29	copies_mL	sil	-0.121687035	7.063701e-01
30	chl	sil	0.459947218	1.324558e-01
31	temp	sil	0.223780014	4.844441e-01
32	do_mgl	sil	0.563745981	5.626190e-02
33	do_per	sil	0.581788786	4.720759e-02
34	pH	sil	0.132684837	6.810153e-01
35	amm	sil	0.116490441	7.184483e-01
36	orthop	sil	-0.725568926	7.563691e-03
37	copies_mL	din	0.046835143	8.850781e-01
38	chl	din	-0.006894311	9.830346e-01
39	temp	din	0.557600165	5.960457e-02
40	do_mgl	din	-0.872287147	2.151139e-04
41	do_per	din	-0.862859406	3.020937e-04
42	pH	din	-0.116239090	7.190340e-01
43	amm	din	0.752930699	4.705593e-03
44	orthop	din	0.622873031	3.050449e-02
45	sil	din	-0.552619842	6.241273e-02
46	copies_mL	din_dip	0.349732772	2.651184e-01
47	chl	din_dip	0.632909856	2.717830e-02
48	temp	din_dip	0.459549730	1.328341e-01
49	do_mgl	din_dip	-0.070507102	8.276314e-01
50	do_per	din_dip	-0.051842656	8.728746e-01
51	pH	din_dip	0.018141273	9.553750e-01
52	amm	din_dip	0.156697851	6.267255e-01
53	orthop	din_dip	-0.762075382	3.962779e-03
54	sil	din_dip	0.343844269	2.737984e-01
55	din	din_dip	-0.139428555	6.656148e-01
56	copies_mL	dust	0.308382544	3.294492e-01
57	chl	dust	0.380630232	2.222269e-01
58	temp	dust	0.246445675	4.400184e-01
59	do_mgl	dust	-0.525278678	7.947479e-02
60	do_per	dust	-0.508465866	9.141058e-02
61	pH	dust	0.047651181	8.830877e-01
62	amm	dust	0.218564123	4.949467e-01
63	orthop	dust	0.340545296	2.787316e-01
64	sil	dust	-0.411845524	1.834308e-01
65	din	dust	0.508319232	9.151969e-02
66	din_dip	dust	0.126471490	6.953044e-01
67	copies_mL	dust_lag	0.747545414	5.189617e-03
68	chl	dust_lag	0.691939899	1.265970e-02
69	temp	dust_lag	0.110776455	7.317976e-01
70	do_mgl	dust_lag	0.036626502	9.100255e-01
71	do_per	dust_lag	0.069470043	8.301339e-01

```

72      pH dust_lag -0.138028896 6.688017e-01
73      amm dust_lag -0.203933228 5.249413e-01
74      orthop dust_lag -0.218820295 4.944285e-01
75      sil dust_lag 0.072668880 8.224196e-01
76      din dust_lag -0.156602903 6.269371e-01
77      din_dip dust_lag 0.355997752 2.560607e-01
78      dust dust_lag 0.401032196 1.963551e-01

```

```

rclean<- rcorr(as.matrix(r_norm))
flattenCorrMatrix(rclean$r, rclean$P)

```

	row	column	cor	p
1	copies_mL	chl	0.794313377	2.029048e-03
2	copies_mL	temp	-0.694069633	1.227724e-02
3	chl	temp	-0.443563509	1.486370e-01
4	copies_mL	do_mgl	0.053133959	8.697316e-01
5	chl	do_mgl	-0.093135507	7.734296e-01
6	temp	do_mgl	-0.298063032	3.467157e-01
7	copies_mL	do_per	-0.277222477	3.830195e-01
8	chl	do_per	-0.420595307	1.733703e-01
9	temp	do_per	-0.104089537	7.475068e-01
10	do_mgl	do_per	0.849285771	4.728164e-04
11	copies_mL	pH	-0.605752072	3.683882e-02
12	chl	pH	-0.446839506	1.453050e-01
13	temp	pH	0.344394945	2.729798e-01
14	do_mgl	pH	0.181718635	5.719154e-01
15	do_per	pH	0.236204096	4.598438e-01
16	copies_mL	amm	0.818594338	1.131031e-03
17	chl	amm	0.652838885	2.136257e-02
18	temp	amm	-0.754522513	4.569286e-03
19	do_mgl	amm	0.365888141	2.421346e-01
20	do_per	amm	0.018341958	9.548818e-01
21	pH	amm	-0.253018859	4.275157e-01
22	copies_mL	orthop	0.372356247	2.332747e-01
23	chl	orthop	0.268756214	3.983039e-01
24	temp	orthop	-0.232958050	4.662137e-01
25	do_mgl	orthop	-0.259132952	4.160445e-01
26	do_per	orthop	-0.406559303	1.896810e-01
27	pH	orthop	-0.012512767	9.692133e-01
28	amm	orthop	0.145320512	6.522556e-01
29	copies_mL	sil	-0.148270301	6.456022e-01

30	chl	sil	0.029808950	9.267289e-01
31	temp	sil	0.436241090	1.562603e-01
32	do_mgl	sil	-0.694381992	1.222187e-02
33	do_per	sil	-0.562797731	5.676890e-02
34	pH	sil	-0.423805935	1.697674e-01
35	amm	sil	-0.473660911	1.198284e-01
36	orthop	sil	-0.001857214	9.954295e-01
37	copies_mL	din	0.824224135	9.758559e-04
38	chl	din	0.662898086	1.879968e-02
39	temp	din	-0.754324335	4.586092e-03
40	do_mgl	din	0.359004781	2.517783e-01
41	do_per	din	0.008917153	9.780578e-01
42	pH	din	-0.230646797	4.707741e-01
43	amm	din	0.997424631	8.884005e-13
44	orthop	din	0.201101449	5.308352e-01
45	sil	din	-0.483244657	1.114905e-01
46	copies_mL	din_dip	0.689745678	1.306290e-02
47	chl	din_dip	0.568365081	5.383735e-02
48	temp	din_dip	-0.661399605	1.916640e-02
49	do_mgl	din_dip	0.523777956	8.049442e-02
50	do_per	din_dip	0.216684979	4.987554e-01
51	pH	din_dip	-0.235818220	4.605989e-01
52	amm	din_dip	0.942026284	4.677072e-06
53	orthop	din_dip	-0.173125530	5.905225e-01
54	sil	din_dip	-0.517084122	8.515090e-02
55	din	din_dip	0.922943116	1.878016e-05
56	copies_mL	dust	0.609074501	3.554219e-02
57	chl	dust	0.396820491	2.015366e-01
58	temp	dust	-0.825081966	9.537341e-04
59	do_mgl	dust	0.088367808	7.847807e-01
60	do_per	dust	-0.028003720	9.311566e-01
61	pH	dust	-0.461536881	1.309496e-01
62	amm	dust	0.486749576	1.085398e-01
63	orthop	dust	0.540027877	6.991911e-02
64	sil	dust	-0.064970788	8.410074e-01
65	din	dust	0.507091907	9.243639e-02
66	din_dip	dust	0.297131770	3.482972e-01
67	copies_mL	dust_lag	0.666513887	1.793597e-02
68	chl	dust_lag	0.620290805	3.140552e-02
69	temp	dust_lag	-0.507661770	9.200999e-02
70	do_mgl	dust_lag	-0.227706899	4.766046e-01
71	do_per	dust_lag	-0.390328132	2.096861e-01
72	pH	dust_lag	-0.837690963	6.709882e-04

```

73      amm dust_lag 0.350879809 2.634464e-01
74    orthop dust_lag 0.099840923 7.575342e-01
75      sil dust_lag 0.425220100 1.681956e-01
76      din dust_lag 0.332242196 2.913707e-01
77    din_dip dust_lag 0.287296281 3.652342e-01
78      dust dust_lag 0.622673425 3.057347e-02

```

Extract cor and p values

```

b_p_values<-
  as.data.frame(bclean$P)

```

Visualize with corrplot() function

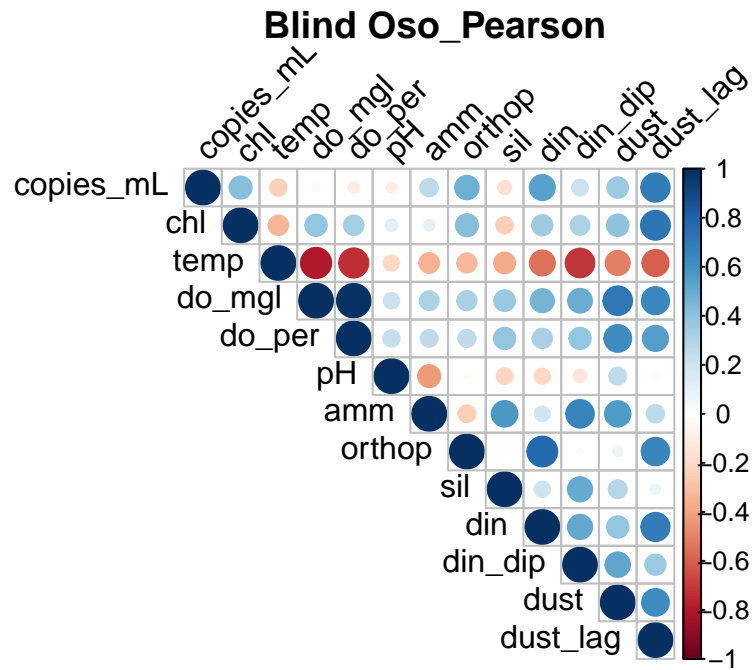
The function `corrplot()` takes the **correlation matrix** as the first argument. The second argument (`type="upper"`) is used to display only the upper triangular of the **correlation matrix**.

Just Normal Data

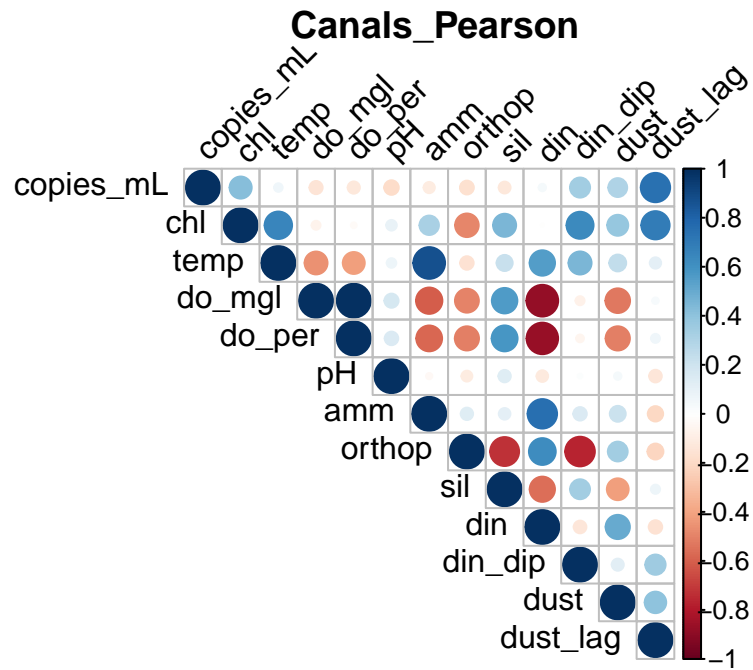
```

#Normal Data
corrplot(b, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Blind Oso_Pearson", mar=c(0,0,1,0)) #Adds and lowers title

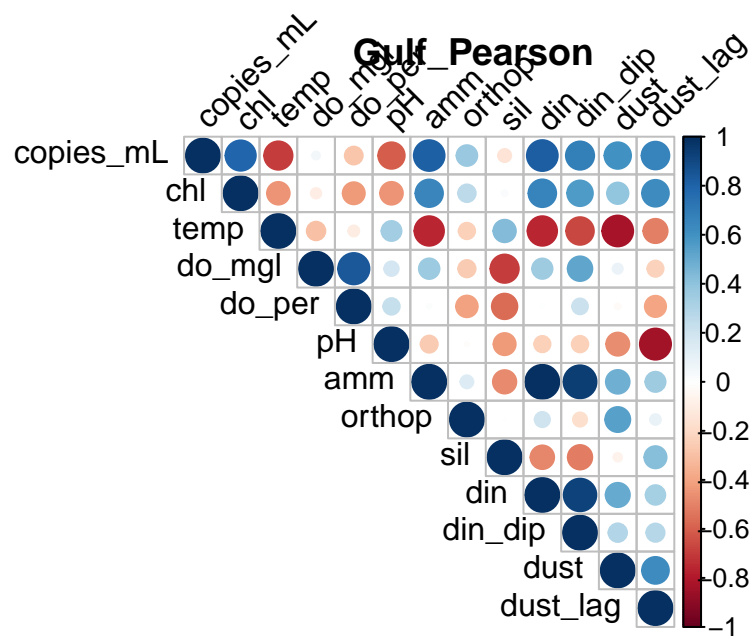
```



```
corrplot(c, type = "upper",
  tl.col = "black", tl.srt = 45,
  title = "Canals_Pearson", mar=c(0,0,1,0))
```

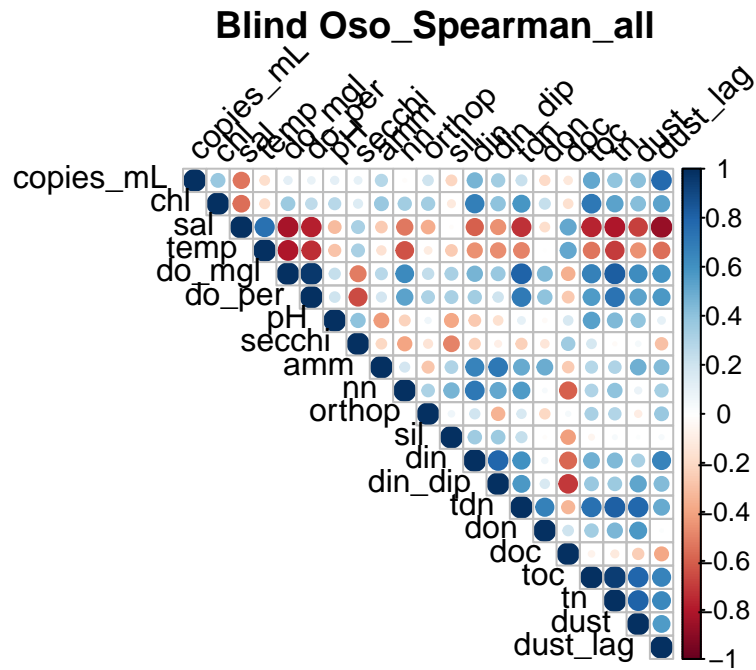


```
corrplot(r, type = "upper",
  tl.col = "black", tl.srt = 45, mar=c(0,0,1,0))
title(main = "Gulf_Pearson")
```

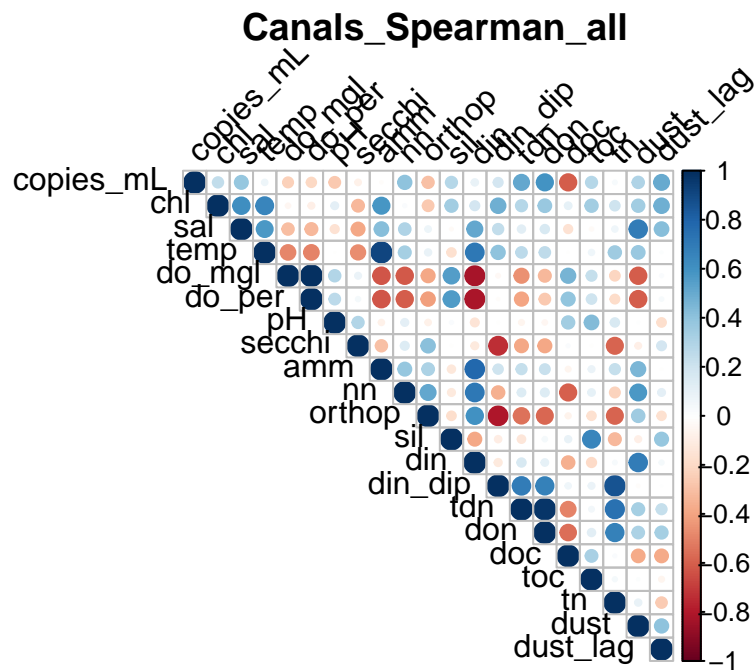


All Spearman

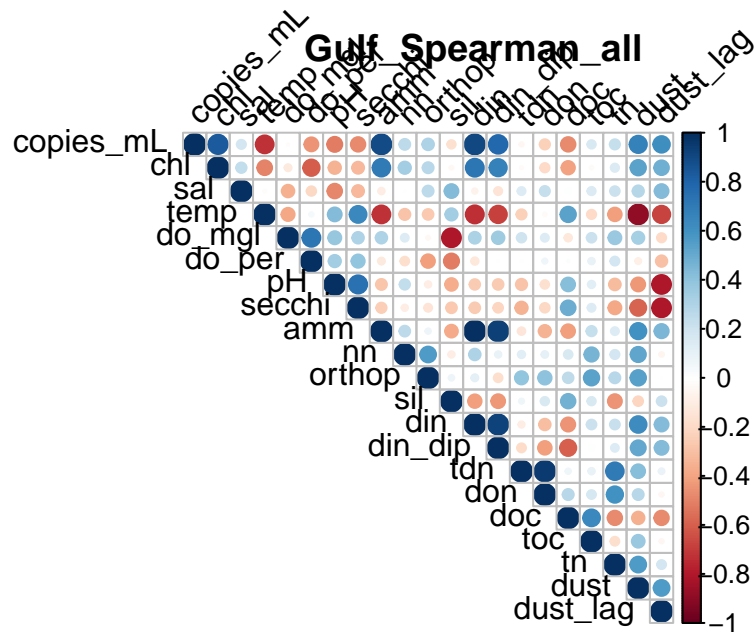
```
#Non-Parametric Data
corrplot(b2, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Blind Oso_Spearman_all", mar=c(0,0,1,0)) #Adds and lowers title
```



```
corrplot(c22, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Canals_Spearman_all", mar=c(0,0,1,0))
```



```
corrplot(r2, type = "upper",
         tl.col = "black", tl.srt = 45, mar=c(0,0,1,0))
title(main = "Gulf_Spearman_all" )
```



Everything

```
par(mfrow=c(3,3))
#Normal Data
corrplot(b, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Blind Oso_Pearson", mar=c(0,0,1,0)) #Adds and lowers title

corrplot(c, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Canals_Pearson", mar=c(0,0,1,0))

corrplot(r, type = "upper",
         tl.col = "black", tl.srt = 45, mar=c(0,0,1,0))
title(main = "Gulf_Pearson")

#Non-Parametric Data
corrplot(b1, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Blind Oso_Spearman", mar=c(0,0,1,0)) #Adds and lowers title
```



```

corrplot(c1, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Canals_Spearman", mar=c(0,0,1,0))

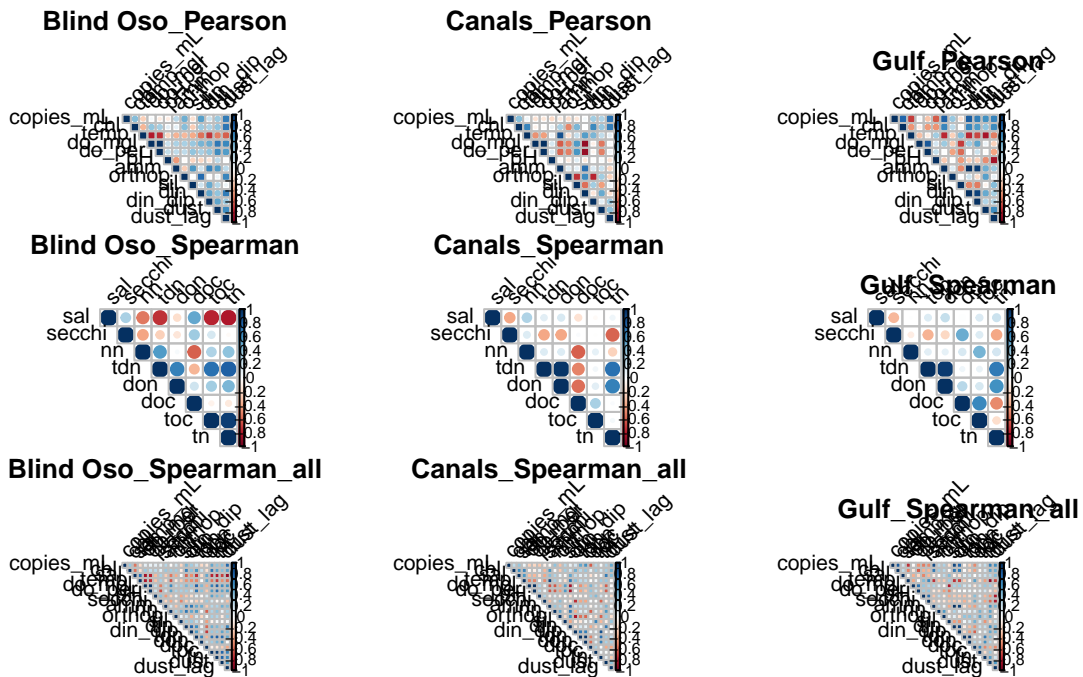
corrplot(r1, type = "upper",
         tl.col = "black", tl.srt = 45, mar=c(0,0,1,0))
         title(main = "Gulf_Spearman" )

#Non-Parametric Data
corrplot(b2, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Blind_Oso_Spearman_all", mar=c(0,0,1,0)) #Adds and lowers title

corrplot(c22, type = "upper",
         tl.col = "black", tl.srt = 45,
         title = "Canals_Spearman_all", mar=c(0,0,1,0))

corrplot(r2, type = "upper",
         tl.col = "black", tl.srt = 45, mar=c(0,0,1,0))
         title(main = "Gulf_Spearman_all" )

```



It's also possible to **combine correlogram with the significance test**. We'll use the result *res.cor2* generated in the previous section with **rcorr()** function [in **Hmisc** package]:

```
# Insignificant correlation are crossed
#corrplot(bclean$r, type="upper", order="hclust",
          # p.mat = bclean$P, sig.level = 0.05, insig = "blank")

#corrplot(cclean$r, type="upper", order="hclust",
          # p.mat = cclean$P, sig.level = 0.05, insig = "blank")

#corrplot(rclean$r, type="upper", order="hclust",
          #p.mat = rclean$P, sig.level = 0.05, insig = "blank")
```

Correlation Tables

Load in data again to bypass earlier code

Rename COpies -> T0tal Vib

```
bo<-
  bo %>%
  rename("Vibrio" = "copies_mL")

c2<-
  c2 %>%
  rename("Vibrio" = "copies_mL")

rd<-
  rd %>%
  rename("Vibrio" = "copies_mL")
```

Create Species Dataframes and Site-Species Dataframes

```
#SPECIES DF
vc<-
  sp %>%
  filter(type %in% "V. cholerae") %>%
```

```

    rename("Vc" = "copies_mL")
vp<-
  sp %>%
  filter(type %in% "V. parahaemolyticus") %>%
  rename("Vp" = "copies_mL")
vv<-
  sp %>%
  filter(type %in% "V. vulnificus") %>%
  rename("Vv" = "copies_mL")

#SITE_SPECIES DF
b_vc <-
  vc %>%
  filter(site %in% "Blind Oso") %>%
  select(Vc, date)
b_vv <-
  vv %>%
  filter(site %in% "Blind Oso") %>%
  select(Vv, date)
b_vp <-
  vp %>%
  filter(site %in% "Blind Oso") %>%
  select(Vp, date)

c_vc <-
  vc %>%
  filter(site %in% "Canals") %>%
  select(Vc, date)
c_vv <-
  vv %>%
  filter(site %in% "Canals") %>%
  select(Vv, date)
c_vp <-
  vp %>%
  filter(site %in% "Canals") %>%
  select(Vp, date)

r_vc <-
  vc %>%
  filter(site %in% "Gulf") %>%
  select(Vc, date)

```

```

r_vv <-
  vv %>%
  filter(site %in% "Gulf") %>%
  select(Vv, date)
r_vp <-
  vp %>%
  filter(site %in% "Gulf") %>%
  select(Vp, date)

```

Combine Species with Site Masters

```

b_list<- list(b_vc, b_vv, b_vp, bo)
c_list<- list(c_vc, c_vv, c_vp, c2)
r_list<- list(r_vc, r_vv, r_vp, rd)

bo<-
  b_list %>% reduce(full_join, by = 'date') %>%
  select(!c(date, ...1, Vp))

c2<-
  c_list %>% reduce(full_join, by = 'date') %>%
  select(!c(date, ...1))

rd<-
  r_list %>% reduce(full_join, by = 'date') %>%
  select(!c(date, ...1))

```

This is using Spearman's for all

Make Correlation Function

$p^* = < 0.05$

$** = < 0.01$

$*** = < 0.001$

```

bo_table<-
  kable(as.data.frame(correlation_matrix(bo, type = "spearman", digits = 2)) %>%
  select(1:4) %>%
  filter(!row_number() %in% c(1:4)),

```

Table 1: Blind Oso: Correlations between Environmental and Biological Variables using Spearman's Rank correlations

	Vc	Vv	Vibrio	chl
sal	-0.52	-0.78**	-0.41	-0.63*
temp	-0.61*	-0.67*	-0.24	-0.30
do_mgl	0.64*	0.83***	0.04	0.43
do_per	0.55	0.78**	-0.10	0.38
pH	-0.16	0.04	-0.09	0.21
secchi	-0.24	-0.37	-0.27	-0.24
amm	0.69*	0.71**	0.19	-0.09
nn	0.61*	0.45	0.55	0.30
orthop	0.12	0.24	0.48	0.45
sil	0.51	0.53	-0.15	-0.26
din	0.62*	0.47	0.55	0.29
din_dip	0.63*	0.66*	-0.05	0.02
tdn	0.81**	0.90***	0.29	0.41
don	0.37	0.64*	-0.20	0.21
doc	-0.10	0.01	-0.18	0.19
toc	0.29	0.64*	0.31	0.80**
tn	0.65*	0.89***	0.37	0.65*
dust	0.77**	0.91***	0.27	0.35
dust_lag	0.42	0.69*	0.65*	0.76**

```

caption = "Blind Oso: Correlations between Environmental and Biological Variables using

c2_table<-
kable(as.data.frame(correlation_matrix(c2, type = "spearman", digits = 2)) %>%
select(1:5) %>%
  filter(!row_number() %in% c(1:5)),
caption = "Canals: Correlations between Environmental and Biological Variables using Spear

rd_table<-
kable(as.data.frame(correlation_matrix(rd, type = "spearman", digits = 2)) %>%
select(1:5) %>%
  filter(!row_number() %in% c(1:5)),
caption = "Gulf: Correlations between Environmental and Biological Variables using Spear

bo_table

```

Table 2: Canals: Correlations between Environmental and Biological Variables using Spearman's Rank correlations

	Vc	Vv	Vp	Vibrio	chl
sal	-0.30	0.27	0.33	0.38	0.64*
temp	0.18	-0.27	0.04	0.06	0.65*
do_mgl	-0.26	0.21	0.17	-0.15	-0.07
do_per	-0.27	0.18	0.18	-0.13	-0.03
pH	-0.01	0.38	-0.02	-0.18	0.10
secchi	0.28	0.06	-0.52	-0.02	-0.34
amm	0.14	-0.34	-0.09	-0.11	0.33
nn	-0.12	0.20	-0.11	0.21	-0.42
orthop	-0.13	0.18	-0.14	0.11	-0.48
sil	0.08	-0.24	0.06	-0.12	0.46
din	0.04	-0.15	-0.15	0.05	-0.01
din_dip	0.13	-0.15	0.14	0.35	0.63*
tdn	0.18	-0.35	0.06	0.43	0.39
don	0.17	-0.32	0.10	0.41	0.39
doc	-0.14	0.48	-0.08	-0.33	-0.05
toc	-0.21	0.33	-0.23	0.03	0.16
tn	-0.13	0.01	0.10	0.16	0.39
dust	-0.25	0.35	0.38	0.31	0.32
dust_lag	-0.08	-0.25	-0.16	0.78**	0.76**

c2_table

rd_table

Table 3: Gulf: Correlations between Environmental and Biological Variables using Spearman's Rank correlations

	Vc	Vv	Vp	Vibrio	chl
sal	0.43	0.20	-0.34	0.23	0.32
temp	-0.30	-0.07	0.28	-0.69*	-0.44
do_mgl	-0.25	0.10	-0.16	0.05	-0.09
do_per	-0.37	0.11	0.01	-0.28	-0.42
pH	-0.48	0.40	0.43	-0.61*	-0.45
secchi	-0.45	0.26	0.58*	-0.58*	-0.39
amm	0.08	0.11	-0.08	0.82**	0.65*
nn	-0.20	-0.09	0.26	0.26	0.29
orthop	-0.01	-0.04	0.32	0.37	0.27
sil	0.30	-0.19	0.04	-0.15	0.03
din	0.06	0.10	-0.05	0.82***	0.66*
din_dip	0.08	0.15	-0.20	0.69*	0.57
tdn	-0.13	-0.43	-0.11	0.06	-0.07
don	-0.14	-0.44	-0.09	-0.12	-0.22
doc	-0.36	0.30	0.73**	-0.46	-0.43
toc	-0.26	0.11	0.54	0.18	-0.04
tn	0.01	-0.42	-0.34	0.33	0.06
dust	0.29	-0.25	-0.05	0.54	0.26
dust_lag	0.77**	-0.16	-0.47	0.65*	0.68*