Habitat Suitability Correlation

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We will now do a subset of simple visual checks for correlation between the environmental inputs of our habitat suitability model. This will be completed by simply leaving one environmental variable out of the overall HSI calculation at a time. If there is a strong correlation between two of the environmental variables, leaving one out will look exactly the same as leaving the other out. For example, if temperature and salinity are highly correlated (which we expect), removing salinity from the HSI model will result in a raster that looks very similar to the resulting raster from removing temperature.

Loading data

```
# Load data
load(paste0('G:/My Drive/Documents_Backup/Modeling/Modeling_RCode/',
            'Raster_Data/ncdf_output.RData'))

# Fix time
time$timestamp <- time$timestamp + lubridate::hours(3)

# Create subset of times to test
timesubs <- seq(1, 2206, by=240)

# Set names of variables
env <- names(env)

# Load SI rasters
for(i in 1:length(env)){
  char <- env[i]
  char_rast <- readRDS(paste0("G:/My Drive/Documents_Backup/Modeling/",
                              "Modeling_RCode/Raster_Data/HSI/",
                              char, "_hsi_rast.RDS"))
  char_rast <- assign(paste0(char, "_si"), char_rast)
}

# Gather SI rasters into list
SI_list <- list(sal_si, tem_si, dox_si, chl_si, tdep_si)
names(SI_list) <- env
```

Remove items sequentially

```
no_sal  <- SI_list[-1]
no_tem  <- SI_list[-2]
no_dox  <- SI_list[-3]
no_chl  <- SI_list[-4]
no_tdep <- SI_list[-5]

# Remove intermediates
rm(sal_si, tem_si, dox_si, chl_si, tdep_si)
```

Calculate leave-one-out HSI results

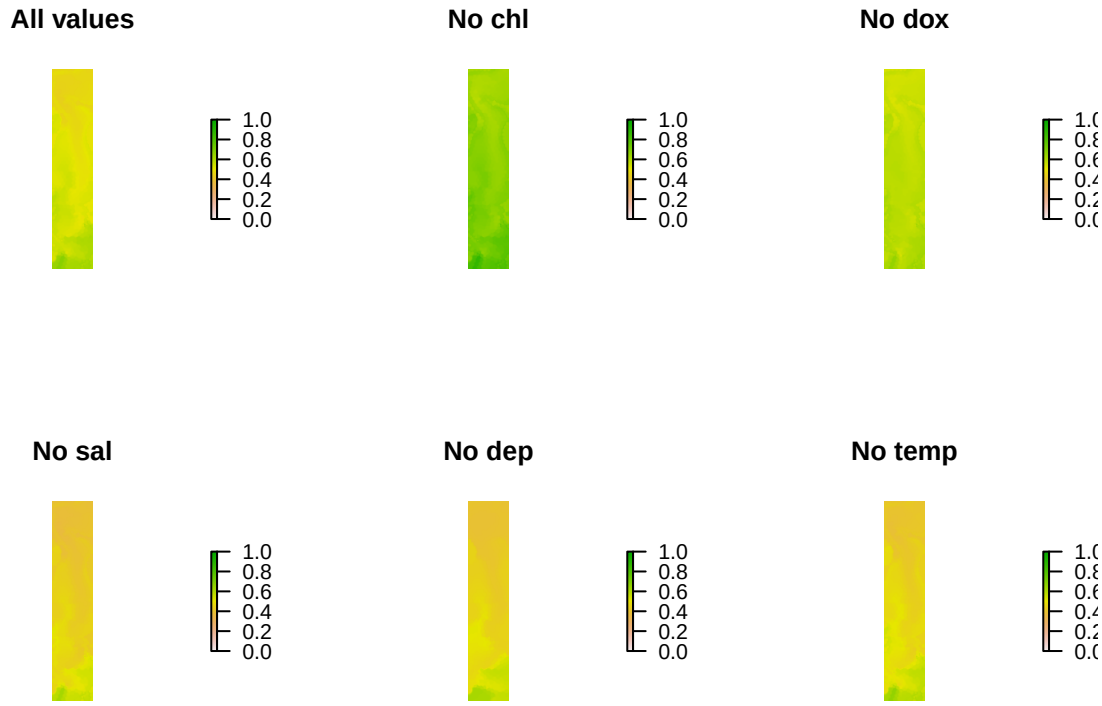
```
# Allocate blank list - all rasters
HSI_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(timesubs)){
  j <- timesubs[i]
  # Overlay all rasters and take geometric mean HSI per cell
  HSI_rast[[i]] <- raster::overlay(SI_list[['sal']][[j]],
                           SI_list[['tem']][[j]],
                           SI_list[['dox']][[j]],
                           SI_list[['chl']][[j]],
                           SI_list[['tdep']][[j]],
                           fun=psych::geometric.mean)
}

# Allocate blank list - no salinity
nosal_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(timesubs)){
  j <- timesubs[i]
  # Overlay all rasters and take geometric mean HSI per cell
  nosal_rast[[i]] <- raster::overlay(#no_sal[['sal']][[j]],
                                     no_sal[['tem']][[j]],
                                     no_sal[['dox']][[j]],
                                     no_sal[['chl']][[j]],
                                     no_sal[['tdep']][[j]],
                                   fun=psych::geometric.mean)
}

# Allocate blank list - no temperature
notem_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(timesubs)){
  j <- timesubs[i]
  # Overlay all rasters and take geometric mean HSI per cell
  notem_rast[[i]] <- raster::overlay(no_tem[['sal']][[j]],
                                     #no_sal[['tem']][[j]],
                                     no_tem[['dox']][[j]],
                                     no_tem[['chl']][[j]],
                                     no_tem[['tdep']][[j]],
                                   fun=psych::geometric.mean)
```

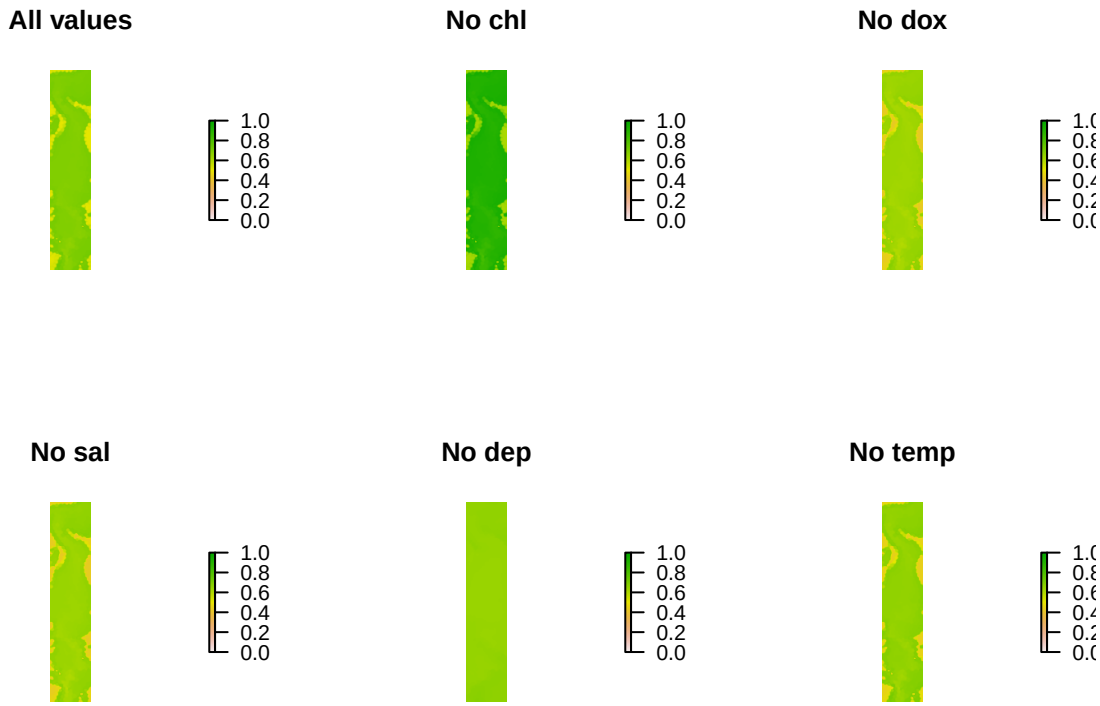
```
}

# Allocate blank list - no dissolved oxygen
nodox_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(timesubs)){
  j <- timesubs[i]
  # Overlay all rasters and take geometric mean HSI per cell
  nodox_rast[[i]] <- raster::overlay(no_dox[['sal']][[j]],
                                     no_dox[['tem']][[j]],
                                     #no_tem[['dox']][[j]],
                                     no_dox[['chl']][[j]],
                                     no_dox[['tdep']][[j]],
                                     fun=psych::geometric.mean)
}

# Allocate blank list - no chlorophyll
nochl_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(timesubs)){
  j <- timesubs[i]
  # Overlay all rasters and take geometric mean HSI per cell
  nochl_rast[[i]] <- raster::overlay(no_chl[['sal']][[j]],
                                     no_chl[['tem']][[j]],
                                     no_chl[['dox']][[j]],
                                     #no_dox[['chl']][[j]],
                                     no_chl[['tdep']][[j]],
                                     fun=psych::geometric.mean)
}

# Allocate blank list - no depth
notdep_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(timesubs)){
  j <- timesubs[i]
  # Overlay all rasters and take geometric mean HSI per cell
  notdep_rast[[i]] <- raster::overlay(no_tdep[['sal']][[j]],
                                     no_tdep[['tem']][[j]],
                                     no_tdep[['dox']][[j]],
                                     no_tdep[['chl']][[j]],
                                     #no_chl[['tdep']][[j]],
                                     fun=psych::geometric.mean)
}
 # Combine all leave-one-out results into list
rastcombine <- list(HSI_rast, nochl_rast, nodox_rast, nosal_rast,
                    notdep_rast, notem_rast)
names(rastcombine) <- c("All values", "No chl", "No dox", "No sal",
                        "No dep", "No temp")
```

Plot and visually inspect results

```
for(k in 1:length(timesubs)){
  par(mfrow=c(2,3))
```

```
  for(i in 1:length(rastcombine)){
       raster::plot(rastcombine[[i]][[k]],
         zlim=c(0, 1),
         main=paste0(names(rastcombine[i])),
         axes=F,
         box=F)
  }
}
```

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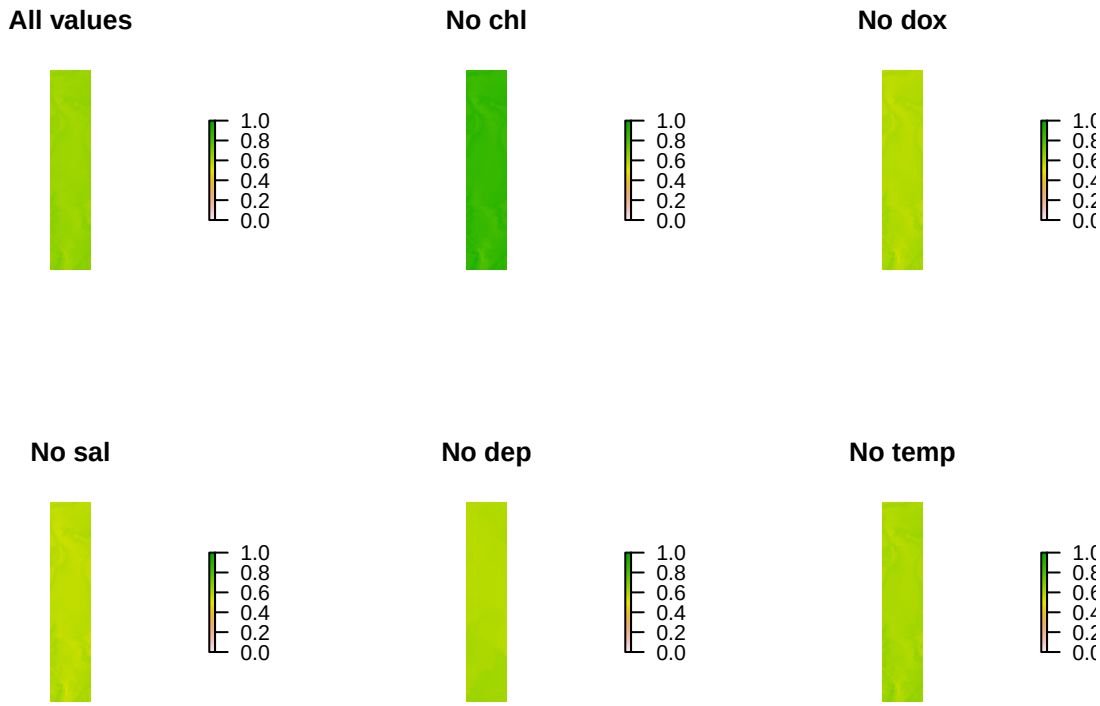
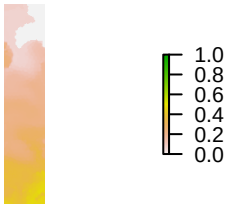
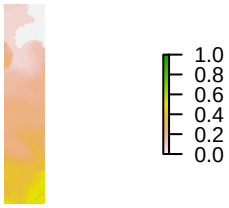
0.8
0.6
0.4
0.2
0.0
No chl
1.0
0.8
0.6
0.4
0.2
0.0
No dox
No sal
1.0
0.8
0.6
0.4
0.2
0.0
No dep
1.0
0.8
0.6
0.4
0.2
0.0
No temp
1.0
0.8
0.6
0.4
0.2
0.0


All values
1.0
0.8
0.6
0.4
0.2
0.0
No chl
1.0
0.8
0.6
0.4
0.2
0.0
No dox
No sal
1.0
0.8
0.6
0.4
0.2
0.0
No dep
1.0
0.8
0.6
0.4
0.2
0.0
No temp
1.0
0.8
0.6
0.4
0.2
0.0

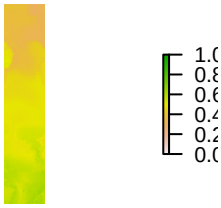
All values



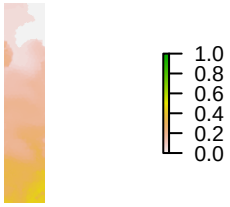
No chl



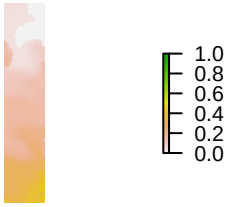
No dox



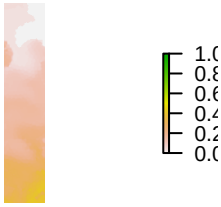
No sal

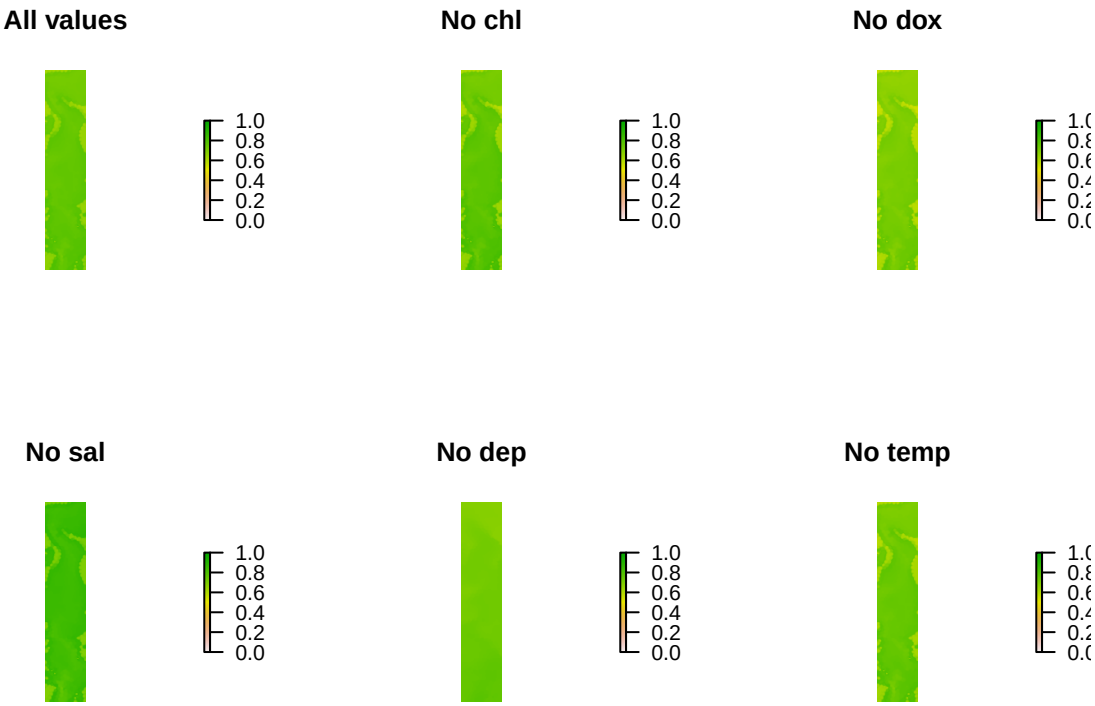


No dep



No temp




All values
1.0
0.8
0.6
0.4
0.2
0.0
No chl
1.0
0.8
0.6
0.4
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0.0
No dox
No sal
1.0
0.8
0.6
0.4
0.2
0.0
No dep
1.0
0.8
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No temp
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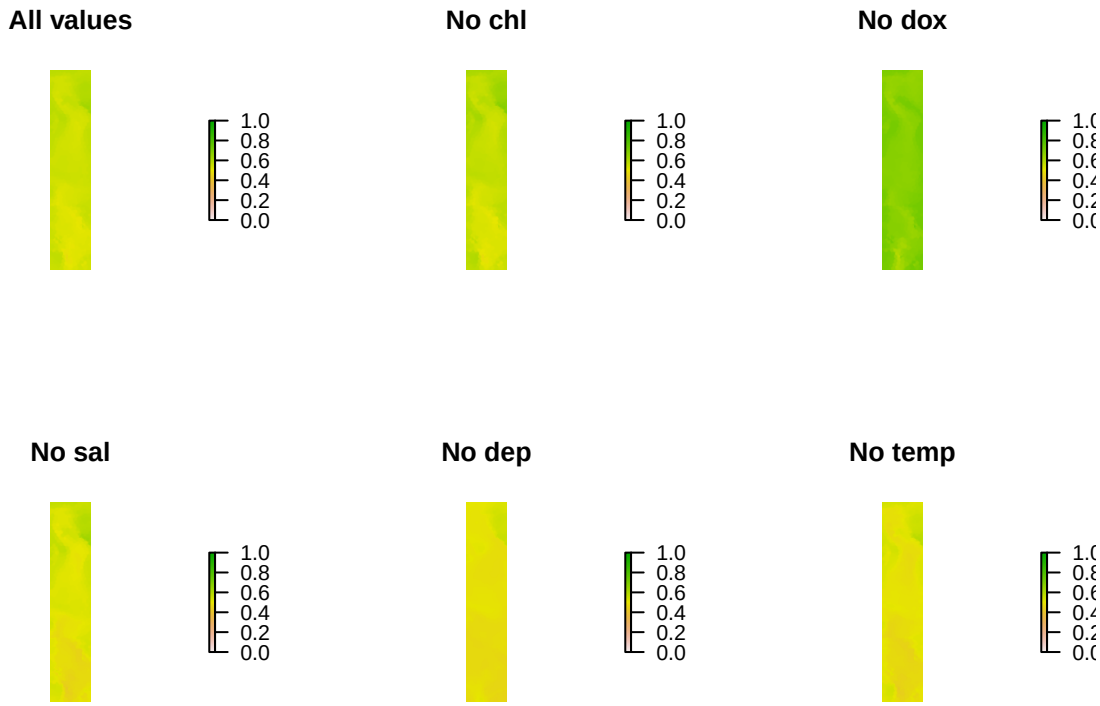
All values
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0.8
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No chl
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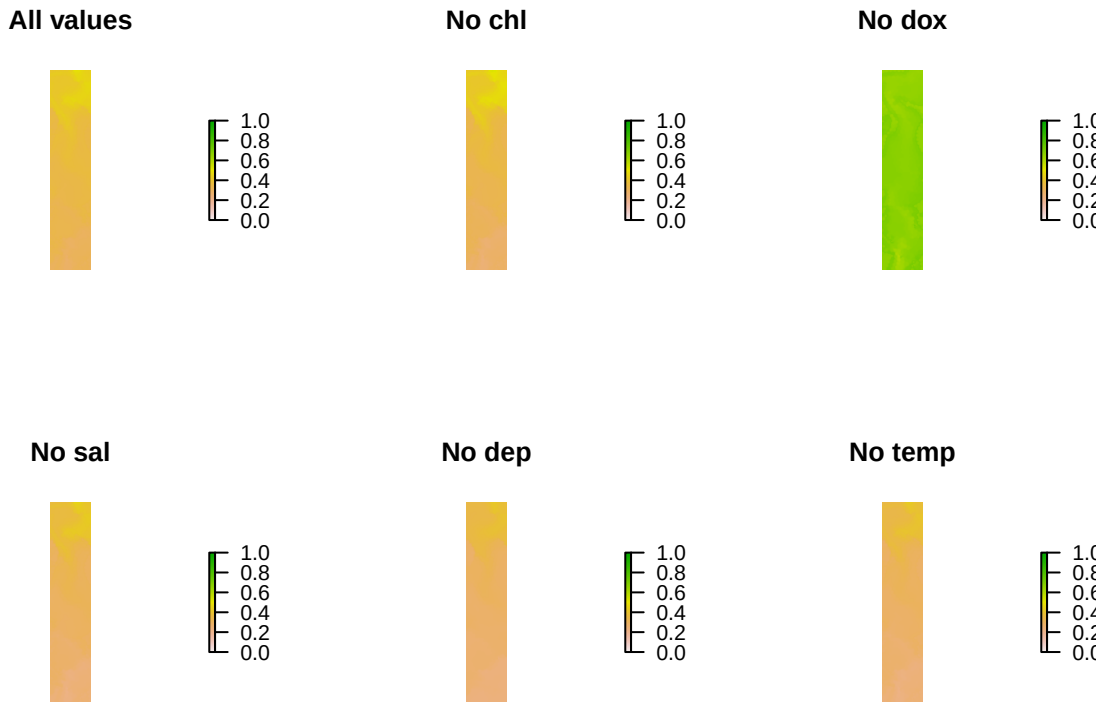
All values
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0.8
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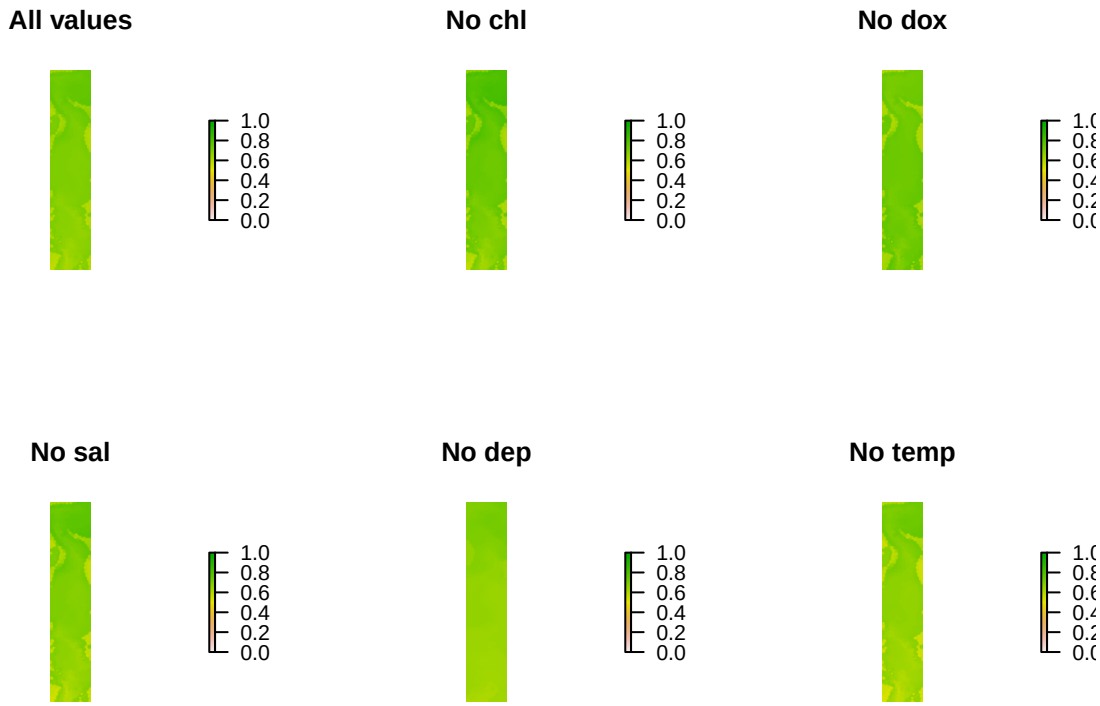
No temp


All values
1.0
0.8
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No chl
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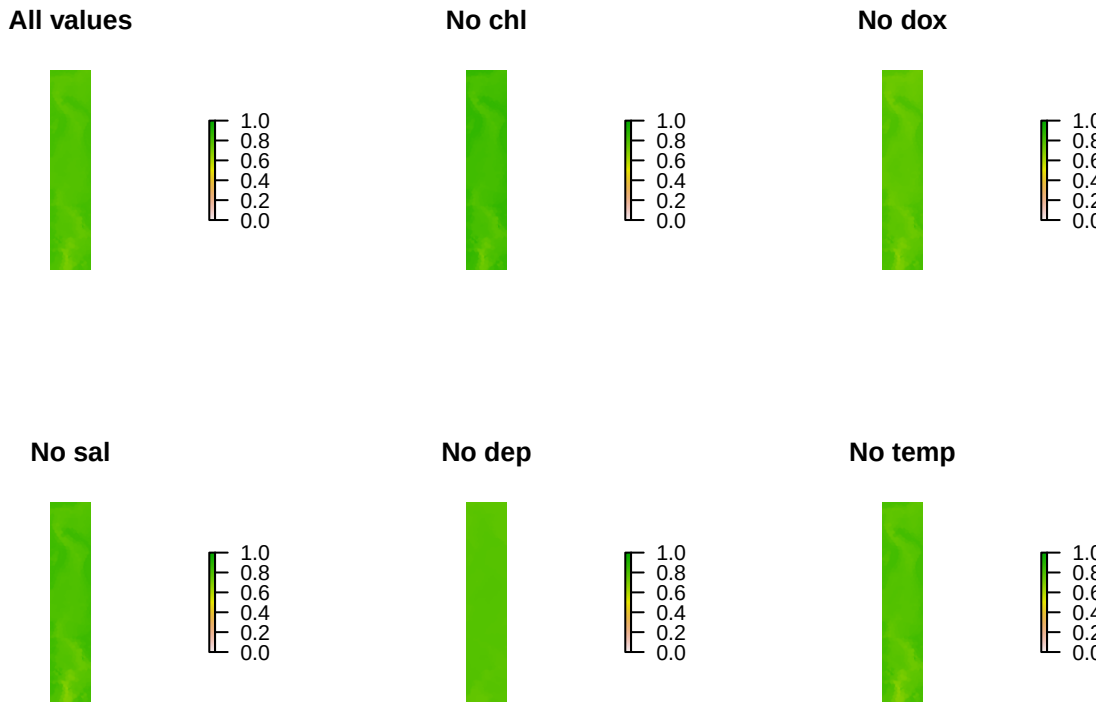
All values
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0.8
0.6
0.4
0.2
0.0
No chl
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No dox
No sal
1.0
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No temp
1.0
0.8
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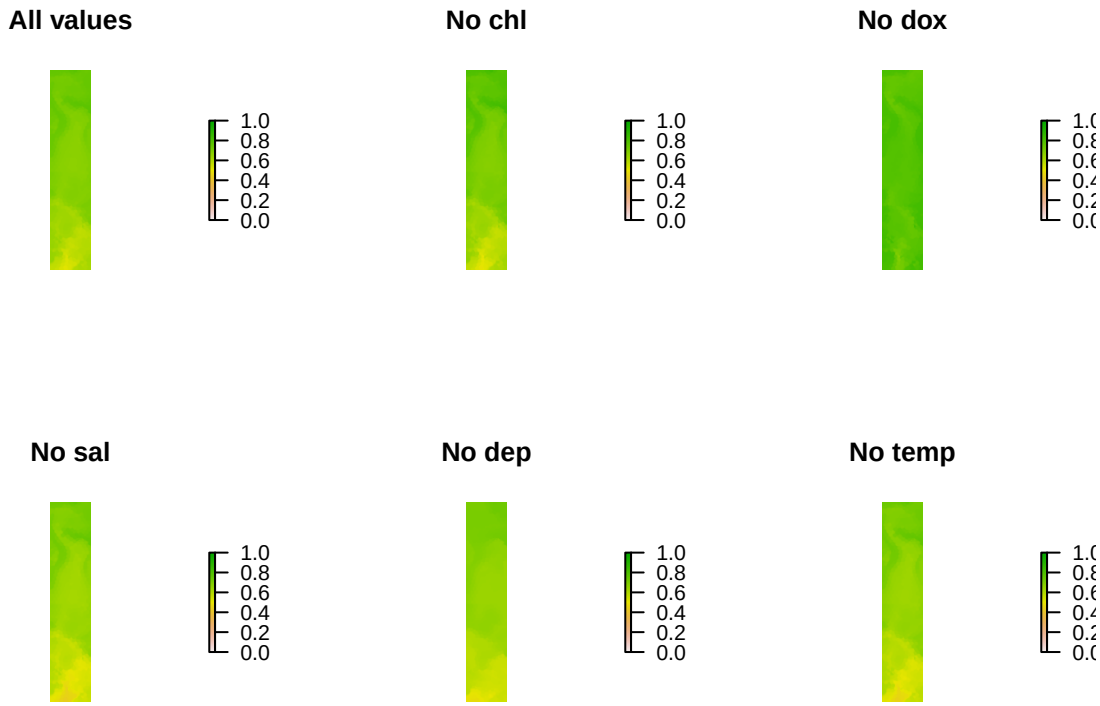
All values
1.0
0.8
0.6
0.4
0.2
0.0
No chl
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No dox
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No dep
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No temp
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Results

This subset of ten timestamps shows that dissolved oxygen is often the "limiting factor" in habitat suitability. The raster that has no dissolved oxygen input usually has the highest average HSI. Chlorophyll is also a frequent limiting factor, though low chlorophyll values have less of an ability to "tank" the overall HSI as compared to dissolved oxygen. Depth is an important limitation at low tides, and in all other rasters you can see a faint outline of the "shoulders" of the river where the water rapidly shallows out to less than 1m and therefore becomes highly unsuitable.

Temperature and salinity have much less of an impact on HSI. This shouldn't be surprising– they're usually a reflection of large-scale processes like tides and seasonal warming. The overall range of temperature and salinity both within a single timestep and over the entire sampling season are limited compared to the other environmental inputs. From this subset, it also appears as though they are highly correlated. One should therefore be removed from the HSI model, as we are essentially "double-counting" the importance of the tidal process in structuring menhaden movement and schooling. Removing salinity would make more sense than removing temperature. The range of salinity in this modeled time period is not likely wide enough to cause noticeable physiological or behavioral changes in menhaden. The range of temperature, on the other hand, is wide enough to cause these changes.

We will now save the HSI model without salinity.

```
# Allocate blank list - no salinity
nosal_rast <-  vector(mode="list", length=length(timesubs))
# Loop through SI rasters to create HSI
for(i in 1:length(SI_list[[1]])){
  # Overlay all rasters and take geometric mean HSI per cell
  nosal_rast[[i]] <- raster::overlay(#no_sal[['sal']][[i]],
                                     no_sal[['tem']][[i]],
                                     no_sal[['dox']][[i]],
                                     no_sal[['chl']][[i]],
                                     no_sal[['tdep']][[i]],
                                    fun=psych::geometric.mean)
  print(i)
}

# Save results
setwd("G:/My Drive/Documents_Backup/Modeling/Modeling_RCode/Raster_Data/HSI/results/")
saveRDS(no_sal, file='HSI_nosal_rast_results.rds')
```

Conclusion

These rasters are the final result of the pre-processing. We can now feed these results into the individual-based model of juvenile menhaden movement in which the menhaden sense and respond to their surrounding environment. A selection of HSI rasters will be animated in a GIF to visualize spatio-temporal suitability trends.