Supplementary Information

SI 1 – The R code used to download environmental data layers from the Bio-Oracle database into ascii format for MaxEnt analysis.

SI 2 – The MaxEnt settings used in the models for *S. aurata*, *M. galloprovincialis* and *U. rigida*.

SI 3 – The jackknife testing results for *S. aurata*, *M. galloprovincialis* and *U. rigida*, showing each variables relative importance to the model.

SI 4 – Model response curves for each environmental variable in isolation (Note: scale bars may differ for each variable).

SI 1

#BioOracle Data for GIS and MaxEnt

#Load required packages

```{r}
library(sdmpredictors)
library(raster)
library(sp)
library(rgdal)
```

#Only list datasets that include marine data

```{r}
list_datasets(terrestrial = FALSE, marine = TRUE)
```

#List available layers for use

```{r}
list_layers(terrestrial = FALSE, marine = TRUE)
```

```

#Set geographical projection for selected environmental factors

```{r}

MapProj <- "+proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs"

```

#Set map extent to cover project area

```{r}

euextent <- extent(-11, 2, 36, 61)

```

#Load layers from BioOracle

```{r}

library(leaflet)

curvelmean<-load_layers("BO21_curvelmean_ss")

ph<-load_layers(c("BO_ph"))

sstmean<-load_layers(c("BO_sstmean"))

sstmax<-load_layers(c("BO_sstmax"))

chlomean <- load_layers(c("BO_chlomean"))

salinity <- load_layers(c("BO_salinity"))

```

#Crop environmental data to project extent

```{r}

curvelmeancr <- crop(curvelmean, euextent)

phcr <- crop(ph, euextent)

sstmeancr <- crop(sstmean, euextent)

sstmaxcr <- crop(sstmax, euextent)

chlomeancr <- crop(chlomean, euextent)

salinitycr <- crop(salinity, euextent)

```

#Exclude values outside new extent

```{r}

curvelext <- extend(curvelmeancr, euextent, value = NA)

phext <- extend(phcr, euextent, value = NA)

sstmeanext <- extend(sstmeancr, euextent, value = NA)

sstmaxext <- extend(sstmaxcr, euextent, value = NA)

chlomeanext <- extend(chlomeancr, euextent, value = NA)

salinityext <- extend(salinitycr, euextent, value = NA)

```

#Resample to check layers are the same after changing extent

```{r}

curvelre <- resample(curvelext, bathyext)

phre <- resample(phext, bathyext)

sstmeanre <- resample(sstmeanext, bathyext)

sstmaxre <- resample(sstmaxext, bathyext)

chlomeanre <- resample(chlomeanext, bathyext)

salinityre <- resample(salinityext, bathyext)

```

#Re-extend variables to ensure resampling did not alter extent

```{r}

curvelreex <- extend(curvelre, euextent, value=NA)

phreex <- extend(phre, euextent, value=NA)

sstmeanreex <- extend(sstmeanre, euextent, value=NA)

sstmaxreex <- extend(sstmaxre, euextent, value=NA)

chlomeanreex <- extend(chlomeanre, euextent, value=NA)

salinityreex <- extend(salinityre, euextent, value=NA)

```

#Write cropped data to ASCII files for use in MaxEnt

```{r}

writeRaster(curvelreex, filename = "Current_Velocity.asc", format='ascii', overwrite=TRUE)

writeRaster(phreex, filename = "pH.asc", format='ascii', overwrite=TRUE)

writeRaster(sstmeanreex, filename = "Mean_SST.asc", format='ascii', overwrite=TRUE)

writeRaster(sstmaxreex, filename = "Max_SST.asc", format='ascii', overwrite=TRUE)

writeRaster(chlomeanreex, filename = "Mean_Chlorophyll.asc", format='ascii', overwrite=TRUE)

writeRaster(salinityreex, filename = "Salinity.asc", format='ascii', overwrite=TRUE)

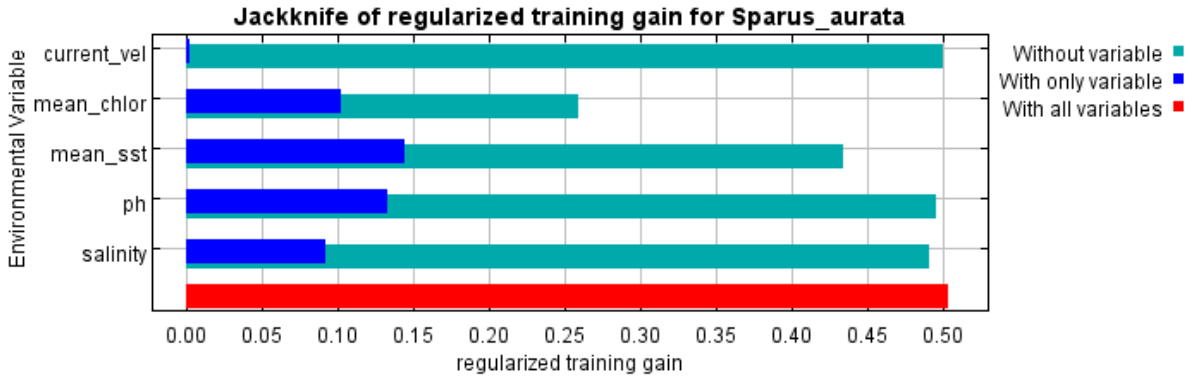
```
```

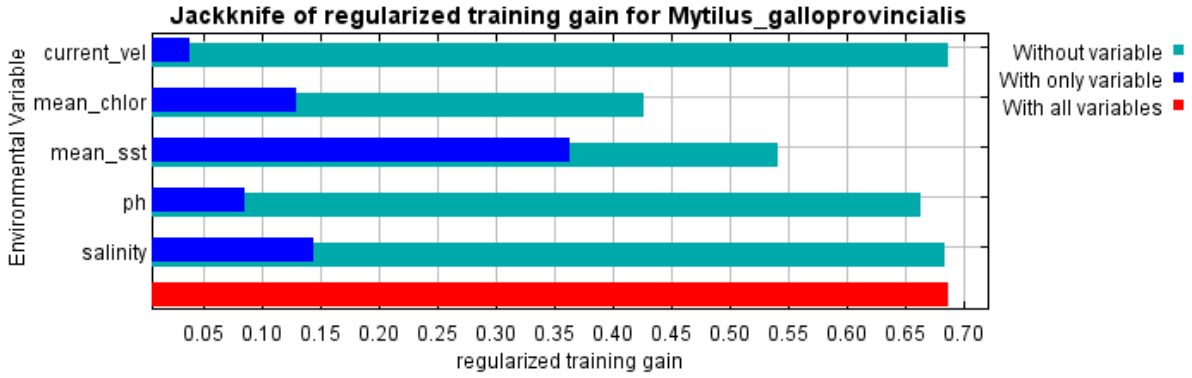
SI 2

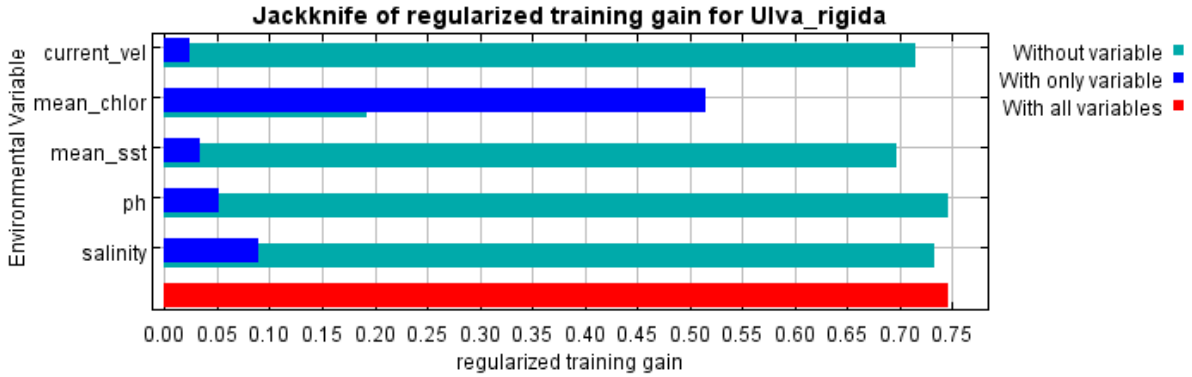
When running the model, the data used spatial jackknifing (geographically structured k-fold crossvalidation). Using the species data, this separates the study area into 3-5 groups, with all groups being used for both calibration and evaluation of the model. To determine the best model for use, comparisons were made using different regularisation multipliers and feature classes to reduce model complexity. Increasing the regularisation multiplier slightly reduces the discriminatory ability of the model, however it significantly reduces omission and commission errors in the model results (Shcheglovitova & Anderson, 2013; Radosavljevic & Anderson, 2014). The models were assessed using three criteria: the Omission Error Rate (OER), AUC and feature class complexity. Models with the lowest OER are selected and, if multiple models have the same OER, the model with the highest AUC is chosen. If the AUC values are the same then the least complex model is used, in this order: 1) Linear 2) Linear and Quadratic 3) Hinge 4) Linear, Quadratic and Hinge 5) Linear, Quadratic, Hinge, Product and Threshold.

Response curves and jackknife tests were performed on the models, with the number of background points used set at 10,000. The model used a logistic output, which produces an output value from 0 – 1. This output can be inferred to be a probability of habitat suitability at each pixel of the study area (Veloz, 2009).

SI 3

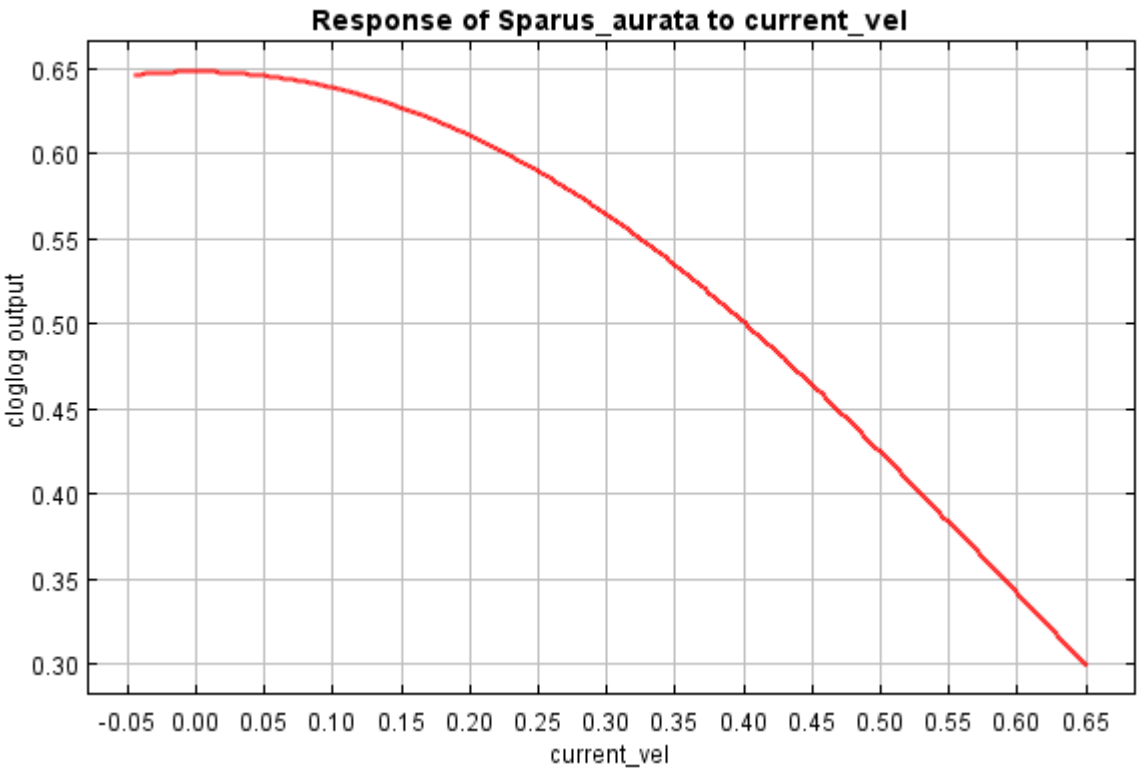

Jackknife of regularized training gain for Sparus_aurata
Environmental Variable
current_vel
mean_chlor
mean_sst
ph
salinity
0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45 0.50
regularized training gain
Without variable
With only variable
With all variables

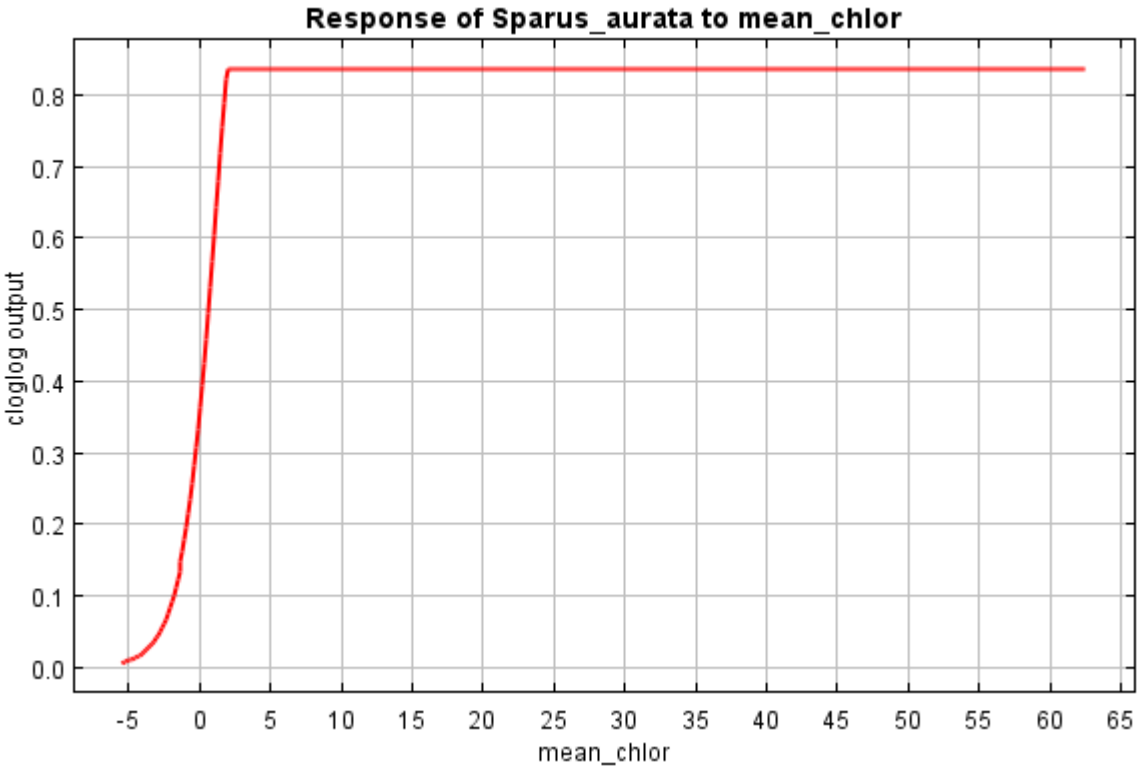

Jackknife of regularized training gain for Mytilus_galloprovincialis
Environmental Variable
current_vel
mean_chlor
mean_sst
ph
salinity
0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60 0.65 0.70
regularized training gain
Without variable
With only variable
With all variables

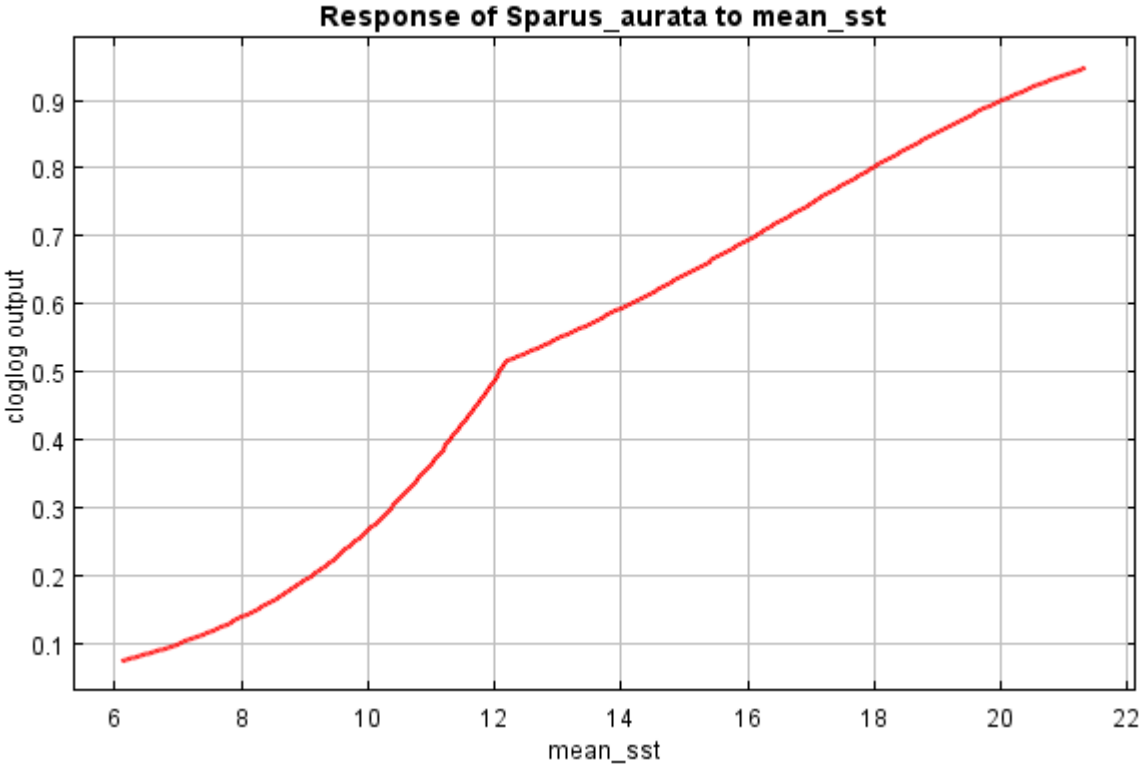

Jackknife of regularized training gain for Ulva_rigida
Environmental Variable
current_vel
mean_chlor
mean_sst
ph
salinity
0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60 0.65 0.70 0.75
regularized training gain
Without variable
With only variable
With all variables

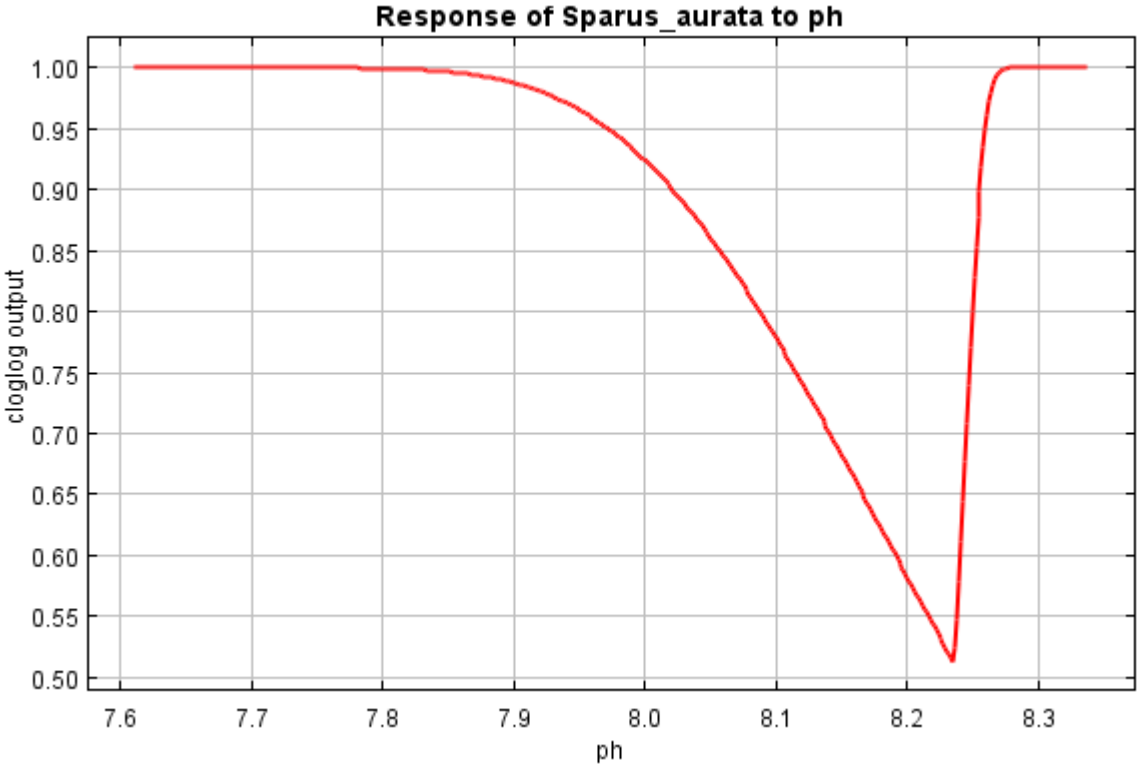
SI 4

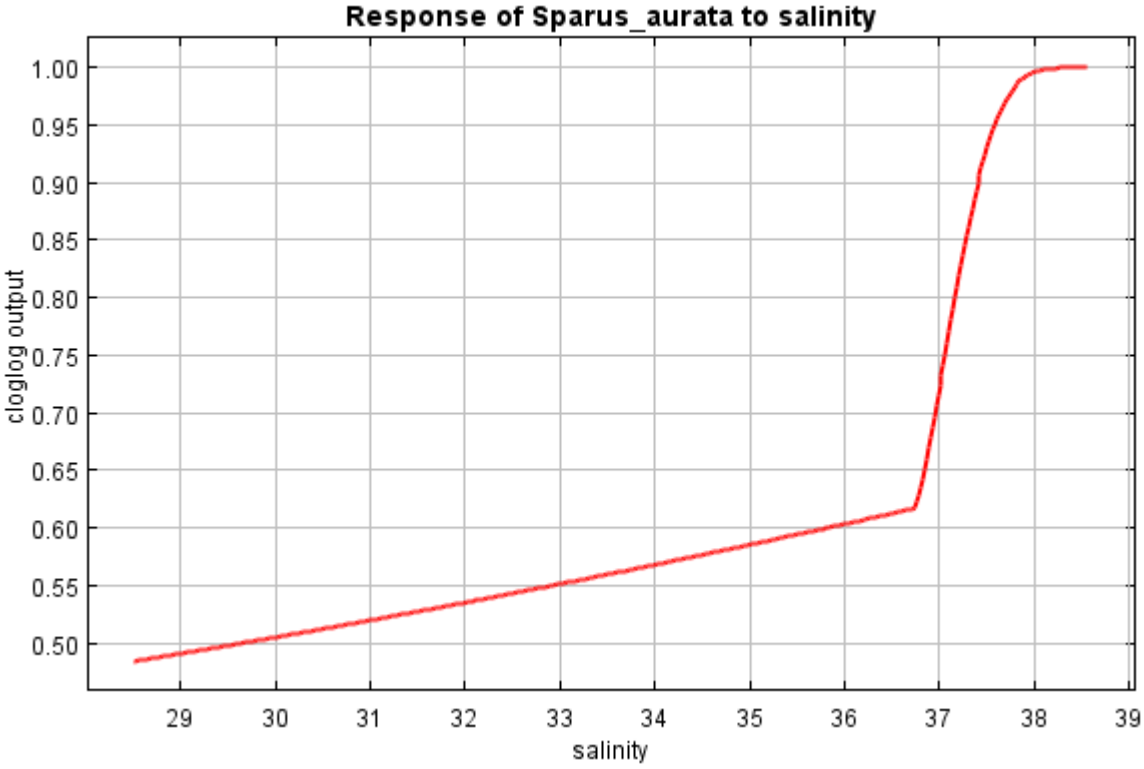
Sparus aurata:

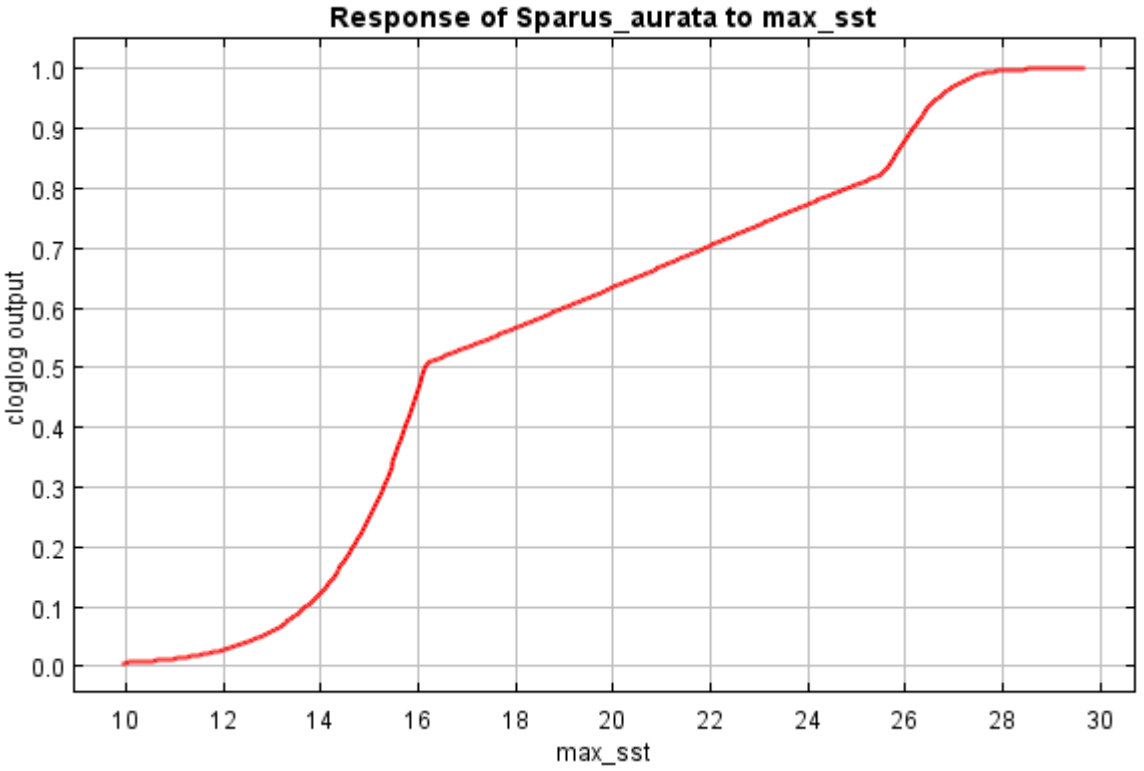




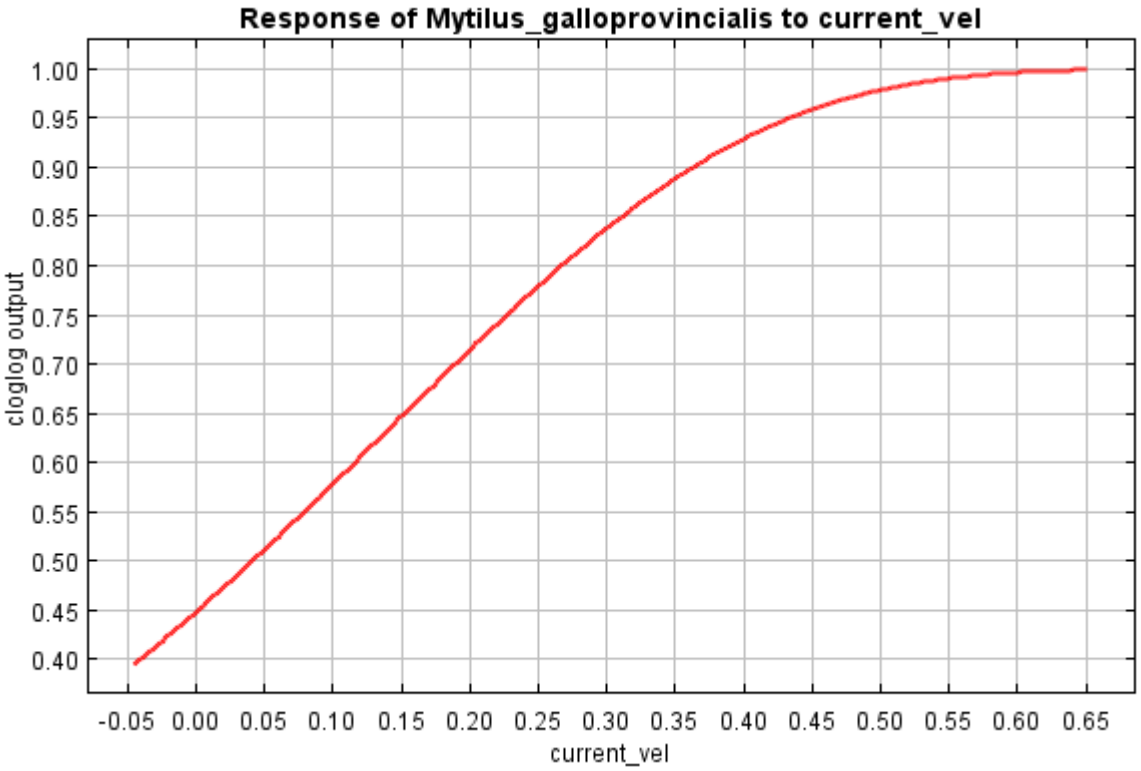

Response of Sparus_aurata to mean_sst
cloglog output
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
6
8
10
12
14
16
18
20
22
mean_sst

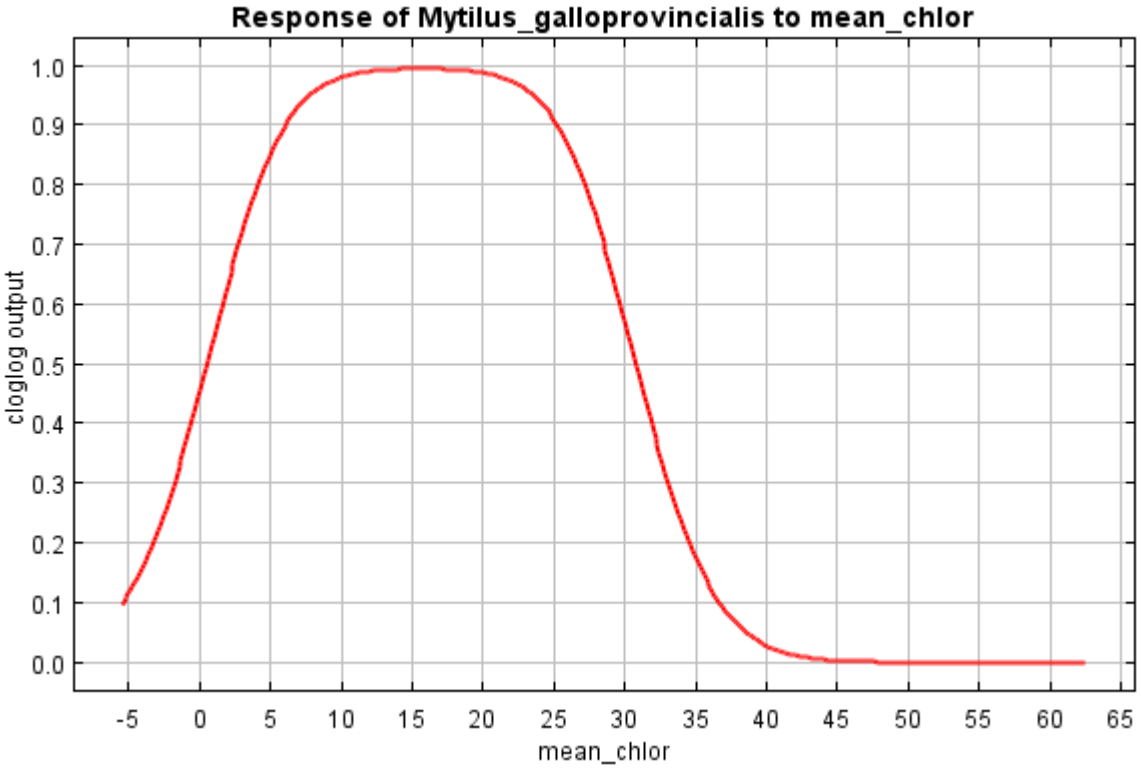

Response of Sparus_aurata to ph
cloglog output
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
7.6
7.7
7.8
7.9
8.0
8.1
8.2
8.3
ph

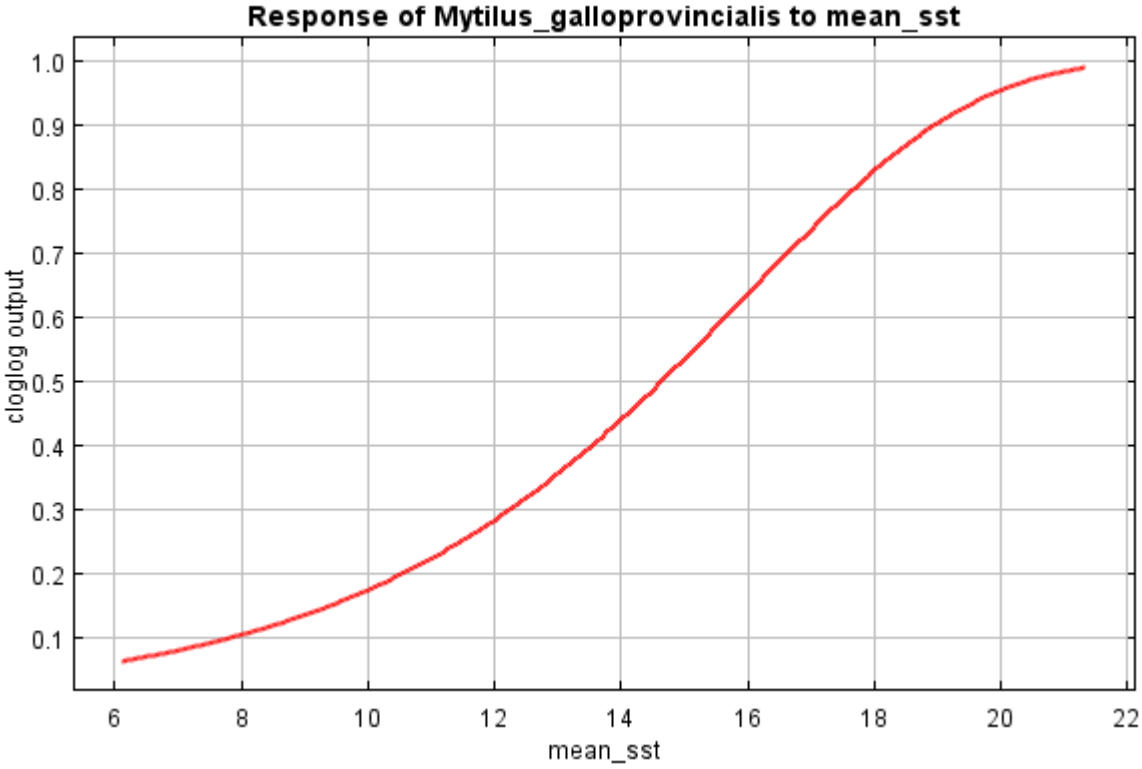

Response of Sparus_aurata to salinity
cloglog output
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
29
30
31
32
33
34
35
36
37
38
39
salinity

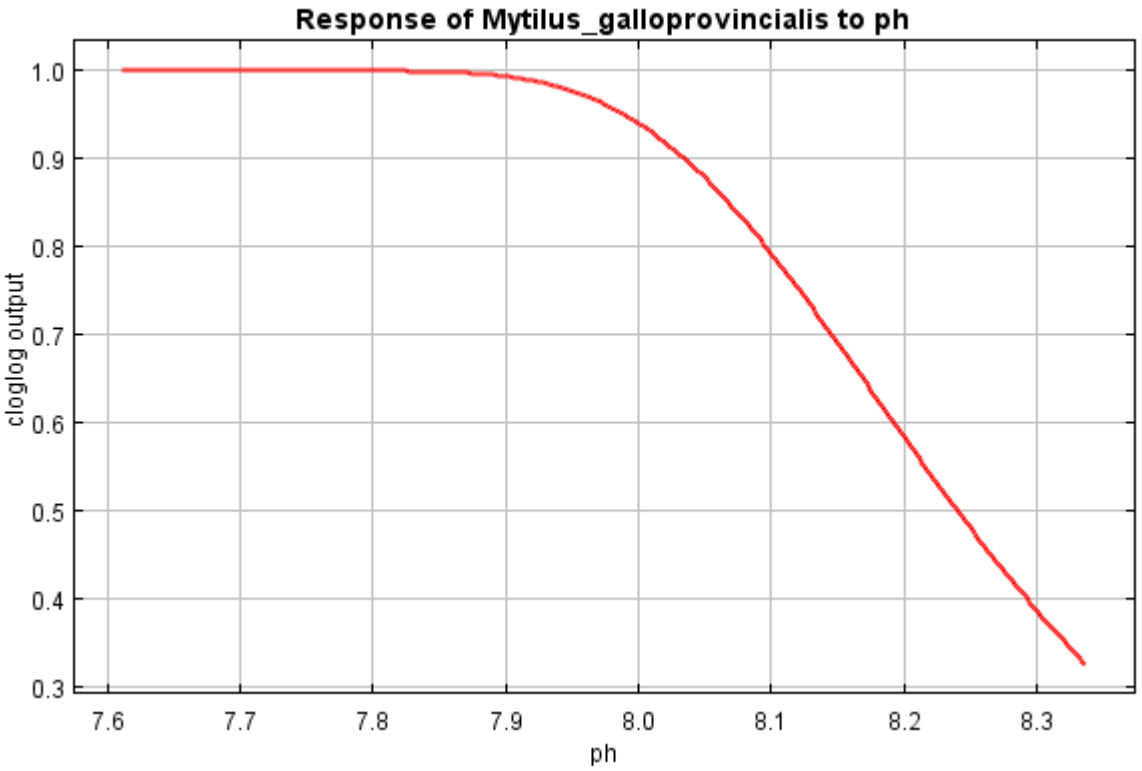

Response of Sparus_aurata to max_sst
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
10
12
14
16
18
20
22
24
26
28
30
max_sst

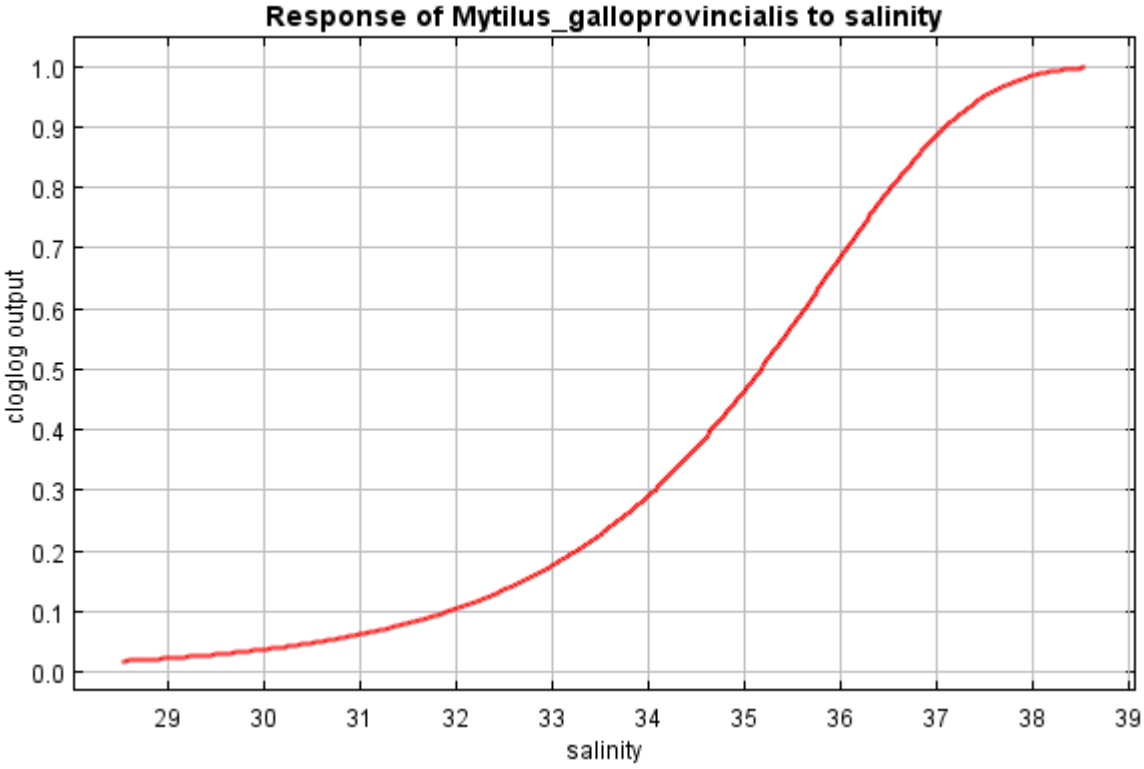
Mytilus galloprovincialis:

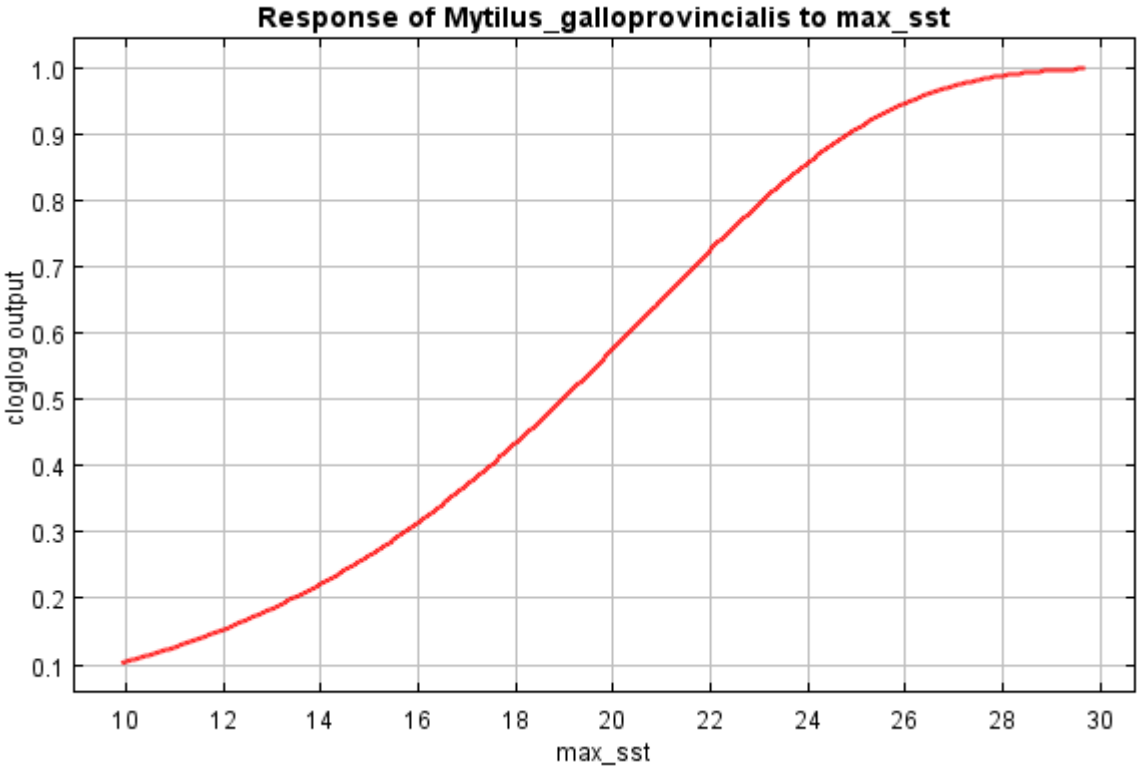




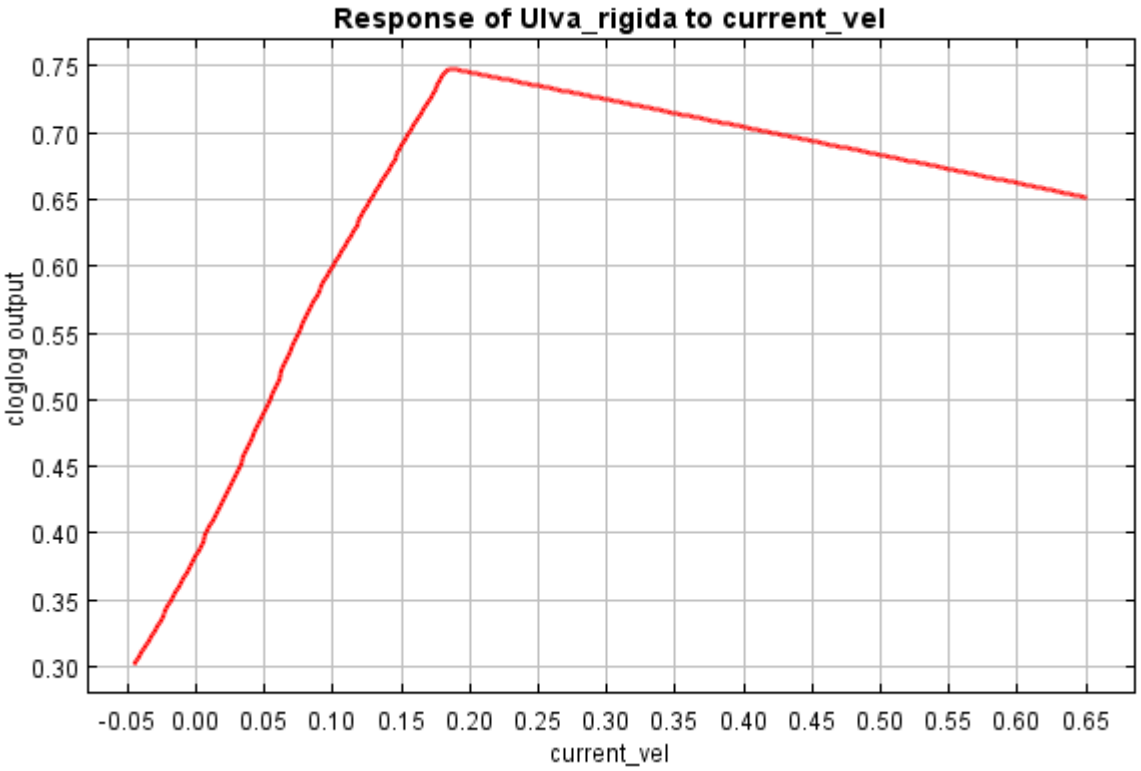

Response of Mytilus_galloprovincialis to mean_sst
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
6
8
10
12
14
16
18
20
22
mean_sst

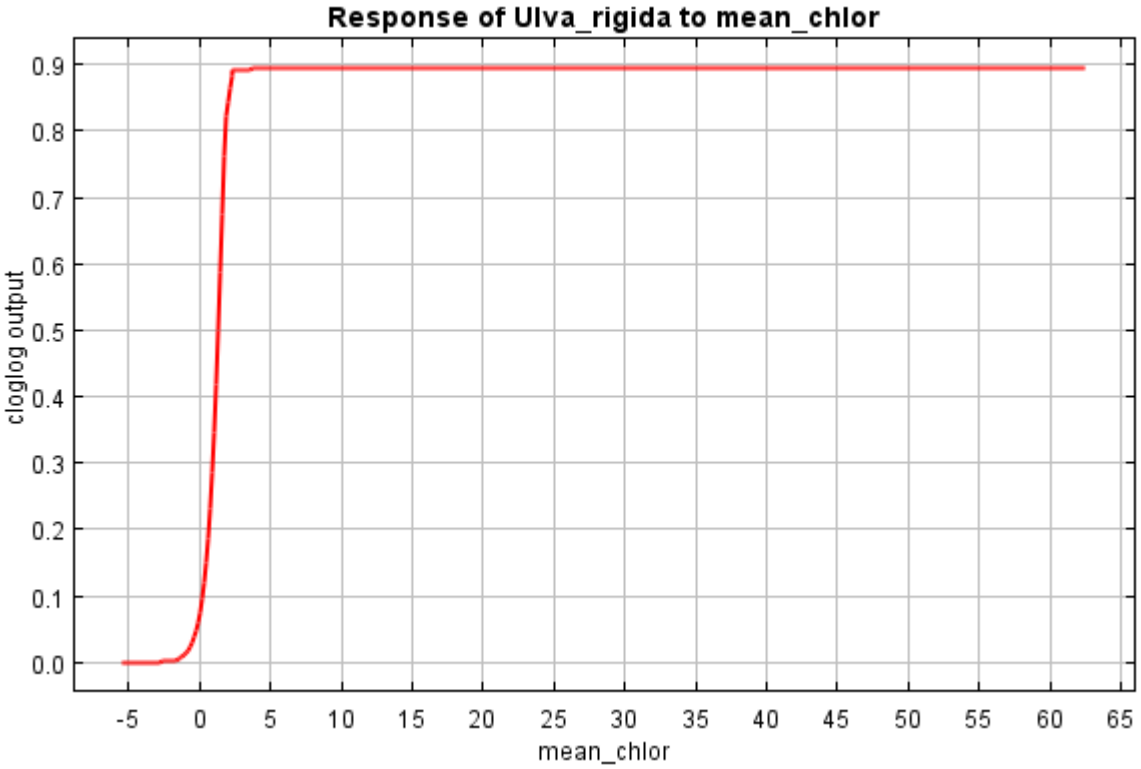

Response of Mytilus_galloprovincialis to ph
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
7.6
7.7
7.8
7.9
8.0
8.1
8.2
8.3
ph

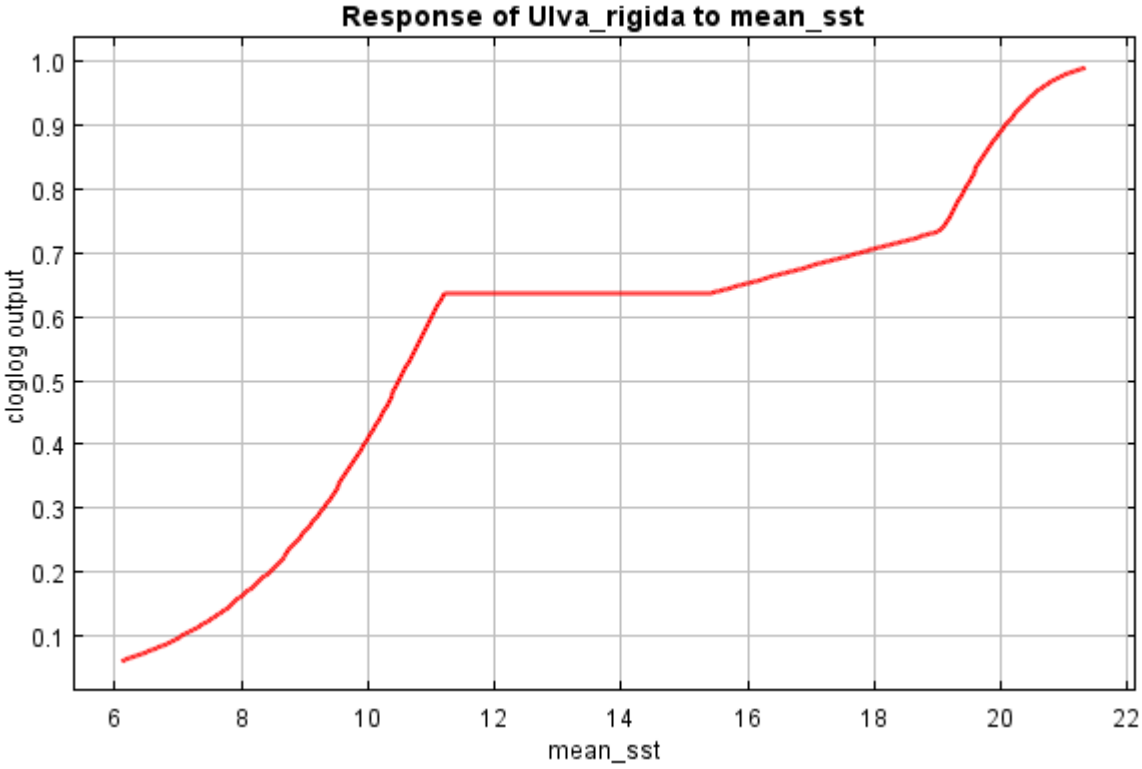

Response of Mytilus_galloprovincialis to salinity
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
29
30
31
32
33
34
35
36
37
38
39
salinity

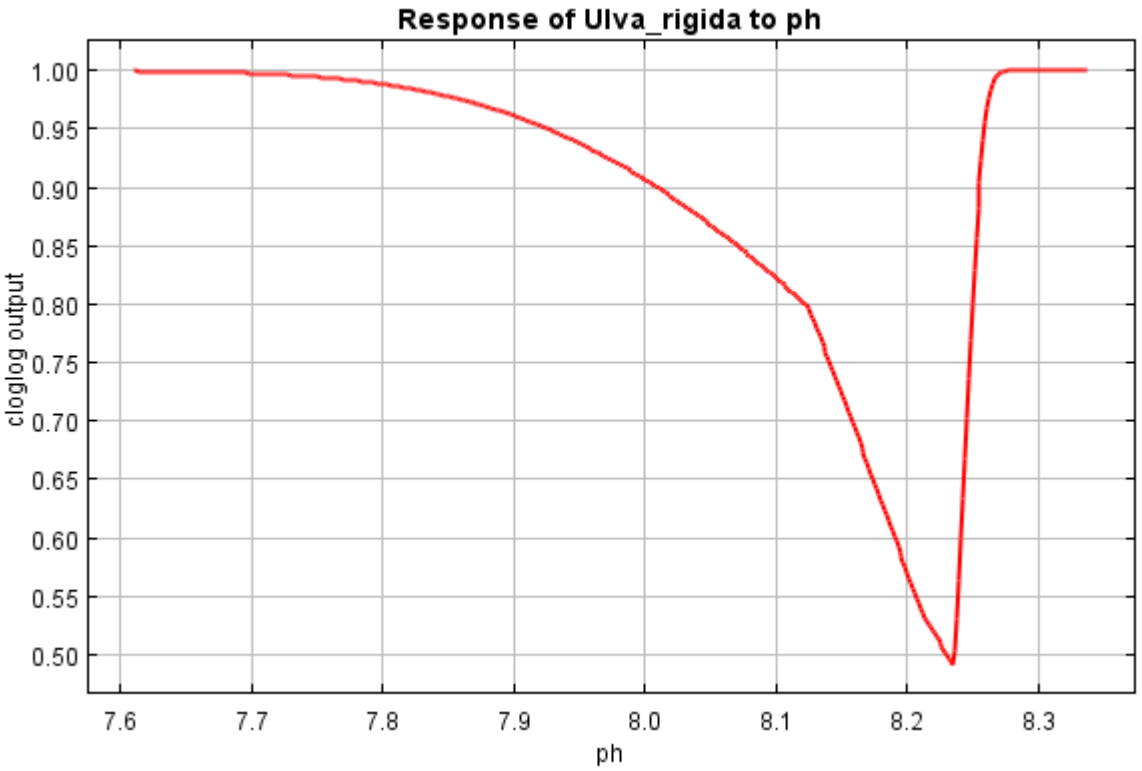

Response of Mytilus_galloprovincialis to max_sst
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
10
12
14
16
18
20
22
24
26
28
30
max_sst

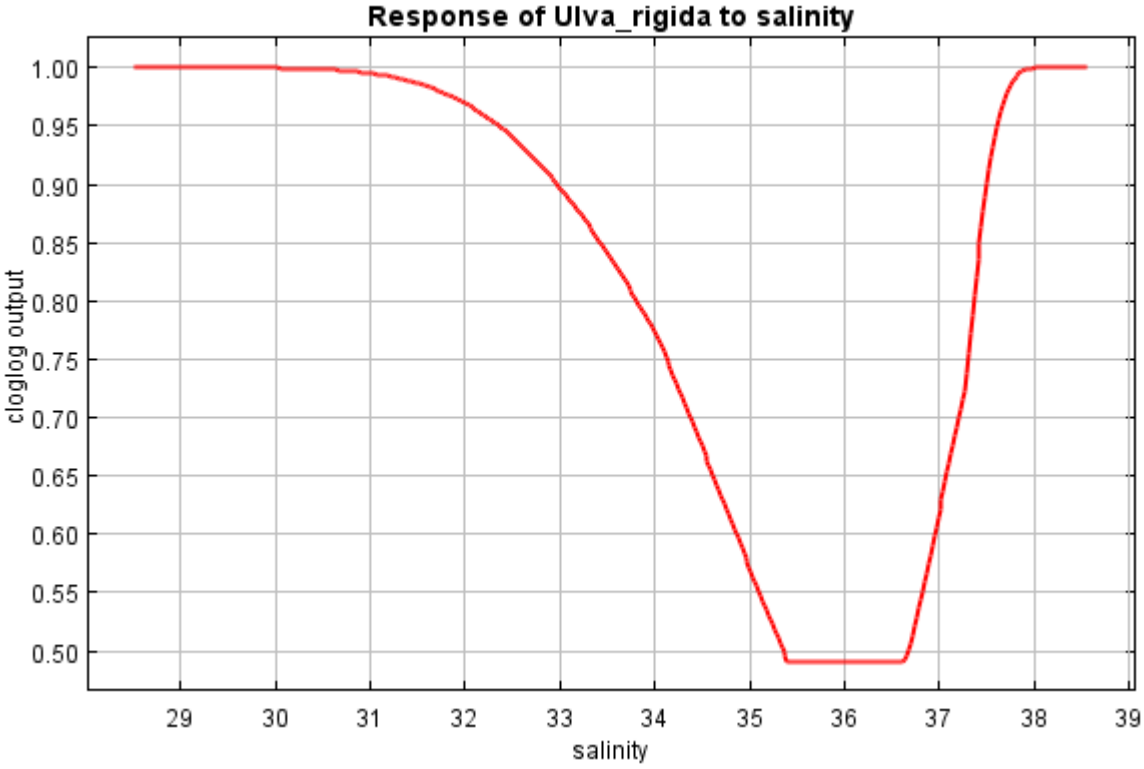
Ulva rigida:

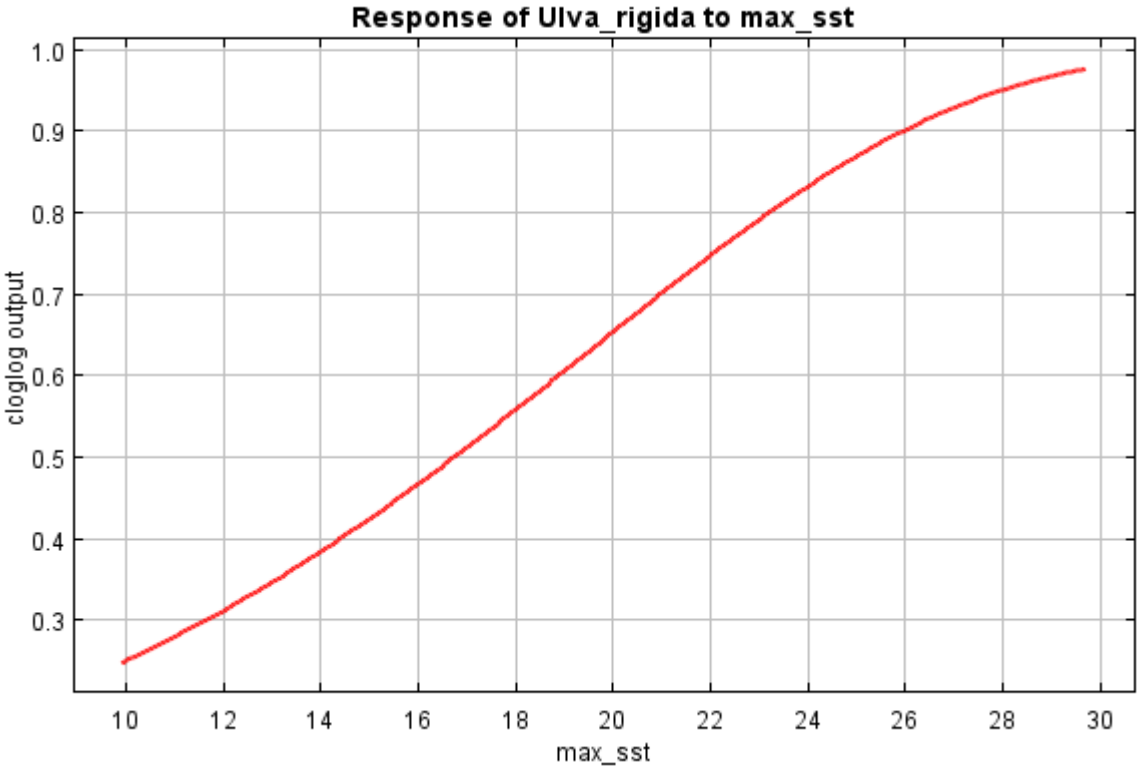

Response of Ulva_rigida to current_vel
cloglog output
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
-0.05 0.00 0.05 0.10 0.15 0.20 0.25 0.30 0.35 0.40 0.45 0.50 0.55 0.60 0.65
current_vel


Response of Ulva_rigida to mean_chlor
cloglog output
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
-5 0 5 10 15 20 25 30 35 40 45 50 55 60 65
mean_chlor


Response of Ulva_rigida to mean_sst
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
6
8
10
12
14
16
18
20
22
mean_sst


Response of Ulva_rigida to ph
cloglog output
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
7.6
7.7
7.8
7.9
8.0
8.1
8.2
8.3
ph


Response of Ulva_rigida to salinity
cloglog output
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
29
30
31
32
33
34
35
36
37
38
39
salinity


Response of Ulva_rigida to max_sst
cloglog output
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
10
12
14
16
18
20
22
24
26
28
30
max_sst