

## Supplementary Information

### The purse-seine fishery for small pelagic fishes off the Madeira Archipelago

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The model specification, results and diagnostic tests of generalised additive models (i.e. GAM plots) describing the influence of the amount of each species in the catch, the fishing location, depth and season on the amount of dead discards, slipping and total discards in the Madeiran purse-seine fishery over the 15-month period investigated. Landings of this fishery are mostly composed of blue jack mackerel *Trachurus picturatus*, Atlantic chub mackerel *Scomber colias*, and small amounts of sardine *Sardina pilchardus*.

```
# Dead discards
```

```
anova(newgam3)
```

Family: gaussian

Link function: identity

Formula:

```
logDD ~ s(logT.pic) + s(logS.col) + s(logS.pil) + Lat * Lon +  
      Depth + Season
```

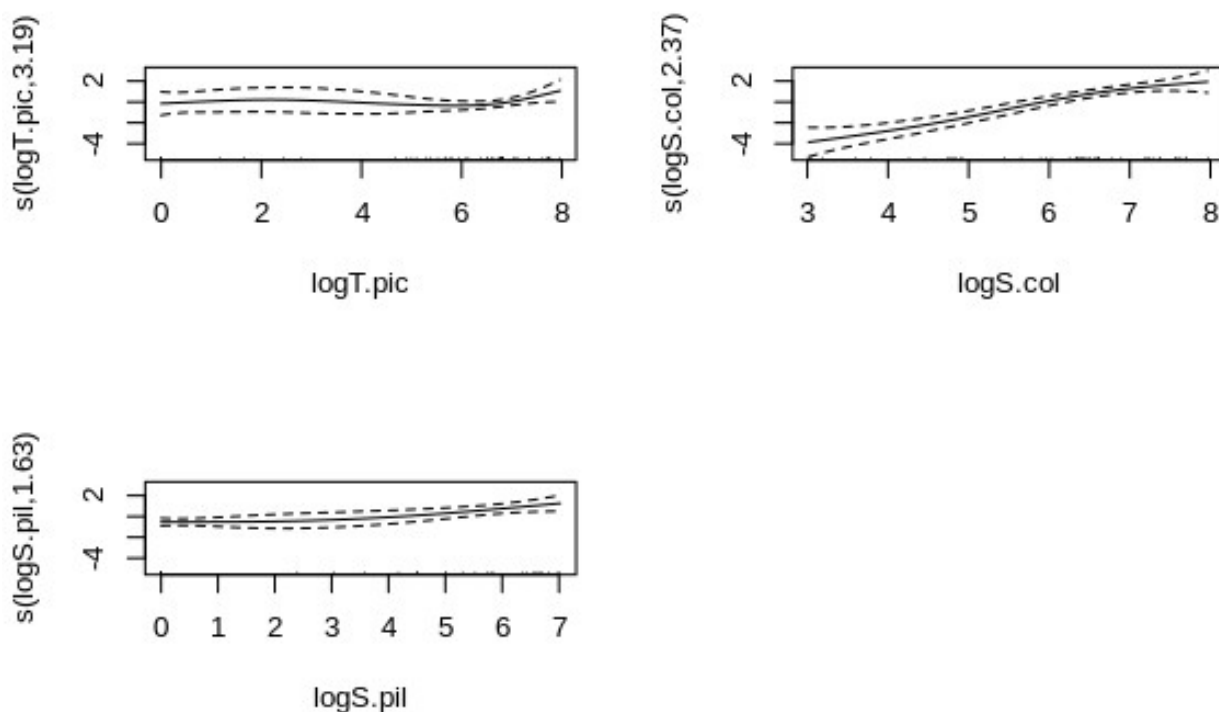
Parametric Terms:

	df	F	p-value
Lat	1 5.824	0.0212	
Lon	1 5.926	0.0202	
Depth	1 2.433	0.1279	
Season	3 0.038	0.9900	
Lat:Lon	1 5.936	0.0201	

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(logT.pic)	3.189	3.863	1.419	0.29783
s(logS.col)	2.371	2.888	24.925	9.44e-10
s(logS.pil)	1.627	1.954	7.366	0.00465

```
plot.gam(newgam3)
```



```
gam.check(newgam3)
```

Method: GCV Optimizer: magic

Smoothing parameter selection converged after 6 iterations.

The RMS GCV score gradient at convergence was 3.054356e-05 .

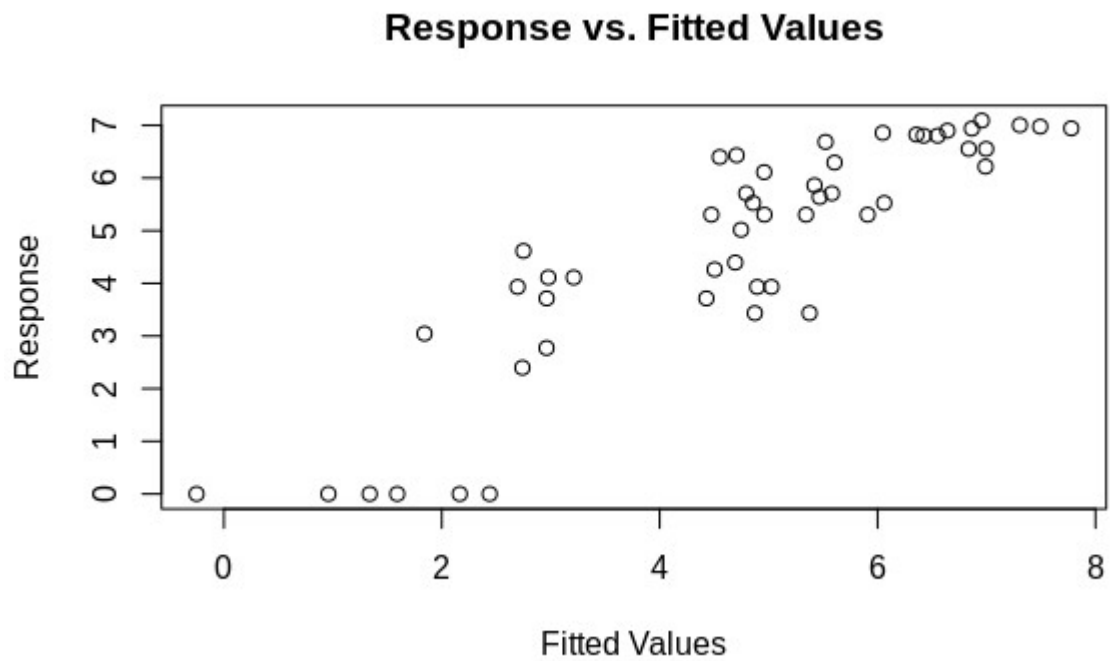
The Hessian was positive definite.

Model rank = 35 / 35

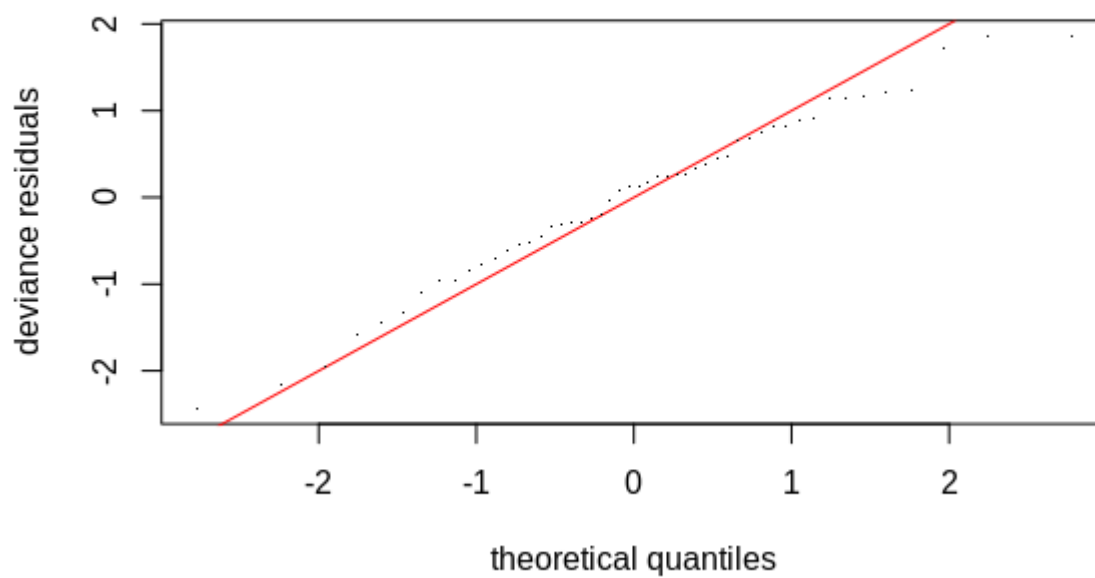
Basis dimension (k) checking results. Low p-value (k-index<1) may

indicate that  $k$  is too low, especially if  $\text{edf}$  is close to  $k'$ .

	$k'$	$\text{edf}$	$k$ -index	p-value
<code>s(logT.pic)</code>	9.00	3.19	1.11	0.76
<code>s(logS.col)</code>	9.00	2.37	1.28	0.97
<code>s(logS.pil)</code>	9.00	1.63	1.01	0.49



`qq.gam(newgam3)`



```
# Slipping
```

```
anova(newgam2)
```

Family: gaussian

Link function: identity

Formula:

```
logS ~ s(logT.pic) + s(logS.col) + s(logS.pil) + Lat * Lon +  
      Depth + Season
```

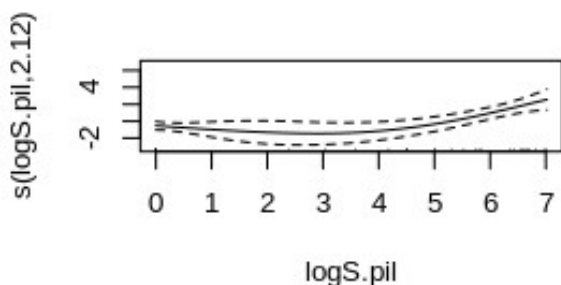
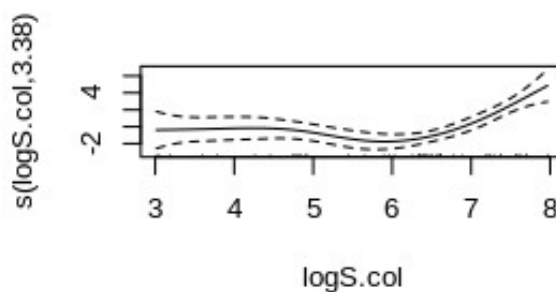
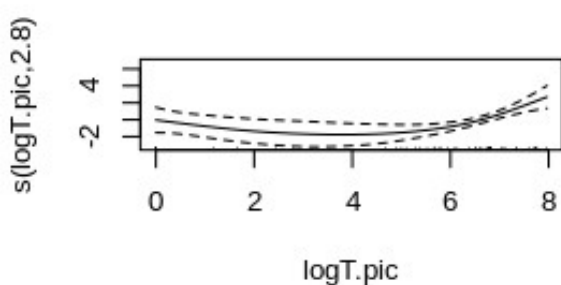
Parametric Terms:

	df	F	p-value
Lat	1 0.038	0.84750	
Lon	1 0.039	0.84443	
Depth	1 1.092	0.30348	
Season	3 5.581	0.00321	
Lat:Lon	1 0.041	0.84108	

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(logT.pic)	2.804	3.416	5.851	0.001941
s(logS.col)	3.384	4.102	10.682	4.89e-06
s(logS.pil)	2.116	2.498	8.053	0.000615

```
plot.gam(newgam2)
```



```
gam.check(newgam2)
```

Method: GCV Optimizer: magic

Smoothing parameter selection converged after 6 iterations.

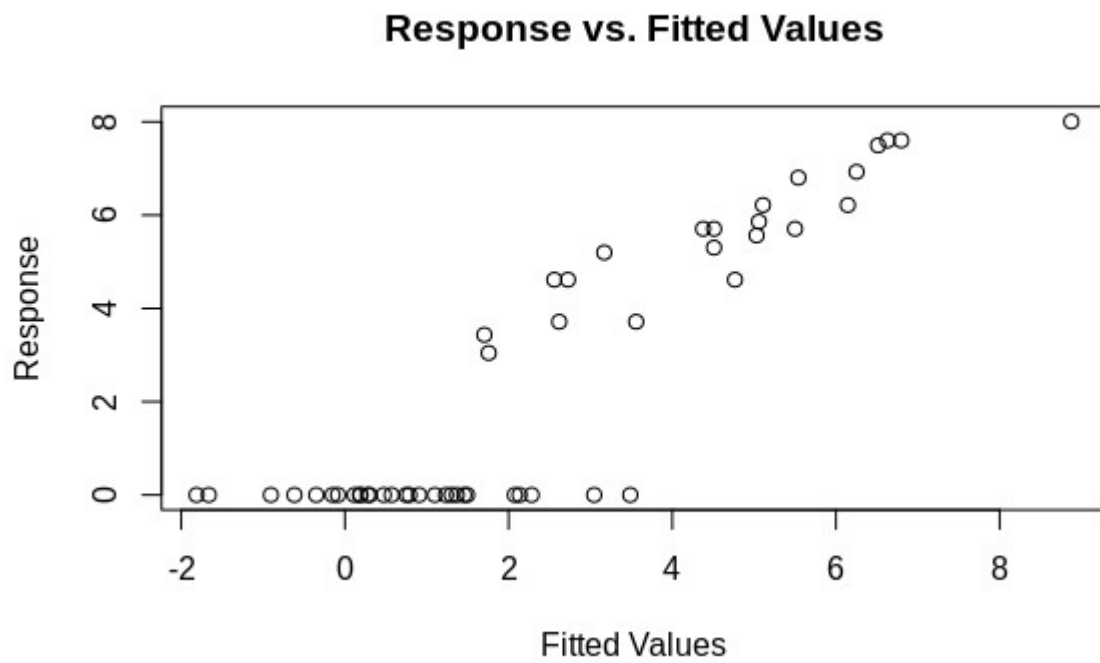
The RMS GCV score gradient at convergence was 9.026201e-07 .

The Hessian was positive definite.

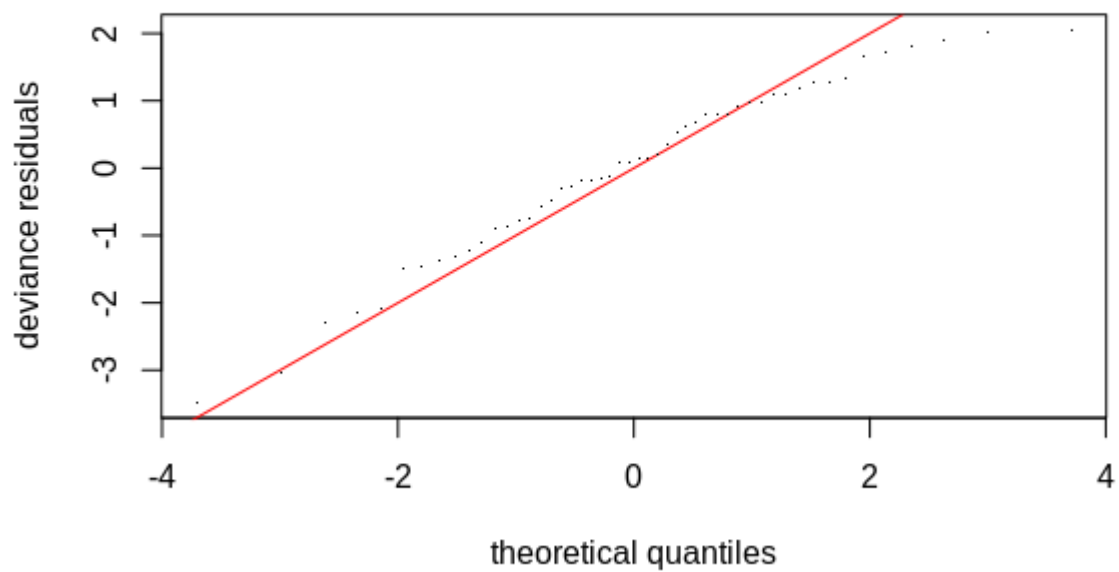
Model rank = 35 / 35

Basis dimension (k) checking results. Low p-value (k-index<1) may indicate that k is too low, especially if edf is close to k'.

	k'	edf	k-index	p-value
s(logT.pic)	9.00	2.80	1.10	0.71
s(logS.col)	9.00	3.38	1.04	0.53
s(logS.pil)	9.00	2.12	1.19	0.88



`qq.gam(newgam2)`



```
# Total discards
```

```
anova(newgam1)
```

Family: gaussian

Link function: identity

Formula:

```
logDiscards ~ s(logT.pic) + s(logS.col) + s(logS.pil) + Lat *  
              Lon + Depth + Season
```

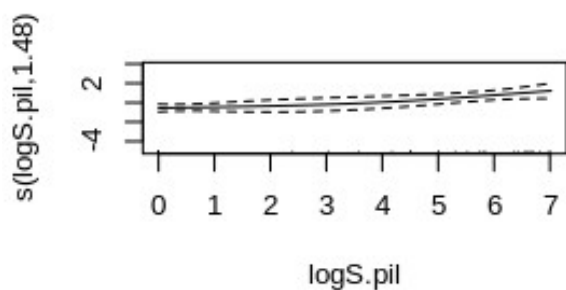
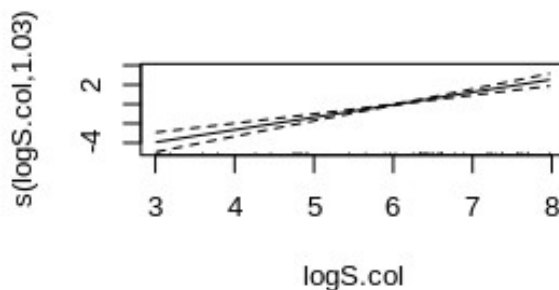
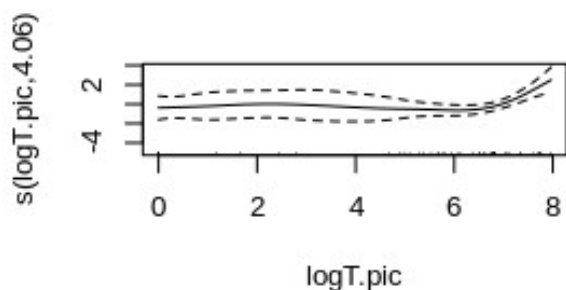
Parametric Terms:

	df	F	p-value
Lat	1 3.100	0.0869	
Lon	1 3.201	0.0822	
Depth	1 3.833	0.0582	
Season	3 0.404	0.7509	
Lat:Lon	1 3.203	0.0821	

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(logT.pic)	4.064	4.863	3.303	0.0146
s(logS.col)	1.031	1.060	58.582	2.91e-10
s(logS.pil)	1.477	1.770	7.333	0.0106

```
plot.gam(newgam1)
```



```
gam.check(newgam1)
```

Method: GCV Optimizer: magic

Smoothing parameter selection converged after 12 iterations.

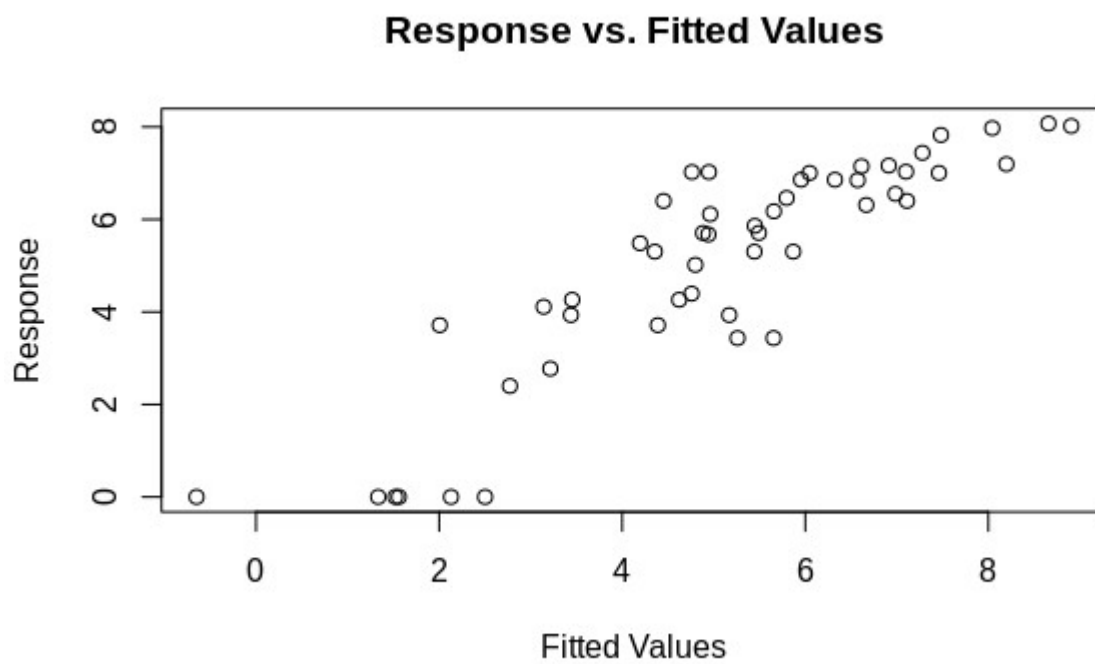
The RMS GCV score gradient at convergence was 7.790831e-07 .

The Hessian was positive definite.

Model rank = 35 / 35

Basis dimension (k) checking results. Low p-value (k-index<1) may indicate that k is too low, especially if edf is close to k'.

	k'	edf	k-index	p-value
s(logT.pic)	9.00	4.06	1.05	0.63
s(logS.col)	9.00	1.03	1.27	0.94
s(logS.pil)	9.00	1.48	1.03	0.54



`qq.gam(newgam1)`

