

Fitting Threshold Regression Models Using `chngpt`

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In the next two pages we demonstrate the use of the *chngpt* package through two examples from Fong et al. (2017).

1 Logistic regression example

To estimate a logistic regression model with a hinge-type change point in *NAb_SF162L* for the MTCT dataset, we call

```
> fit=chnngptm(formula.1=y~birth, formula.2=~NAb_SF162LS, dat.mtct,  
type="hinge", family="binomial", est.method="smoothapprox", var.type="robust",  
aux.fit=glm(y ~birth + ns(NAb_SF162LS,3), dat.mtct, family="binomial"))
```

The argument *formula.2* gives the threshold variable and the argument *formula.1* gives the rest of the model. The argument *type* conveys the type of threshold effects one wishes to fit, and the argument *est.method* controls the type of search algorithm to use. If the estimation method is grid search and the argument *verbose* is set to 2, the program will output a plot of log likelihoods versus candidate change points (Figure 2a, Fong et al., 2017). The returned *fit* is an object of type *chnngptm*. Calling summary function on the *fit* object produces the following information:

Coefficients:

	OR	p.value	(lower	upper)
(Intercept)	0.7026523	0.341429662	0.3388366	1.4571044
birthVaginal	1.2397649	0.523159883	0.6393632	2.4039809
(NAb_SF162LS-chnngpt)+	0.6712371	0.001332547	0.5270730	0.8548327

Threshold:

26.3%	(lower	upper)
7.373374	5.472271	8.186464

To test whether there is a change point, we call

```
> test=chnngpt.test(formula.null=y~birth, formula.chnngpt=~NAb_SF162LS, dat.mtct,  
type="hinge", family="binomial", main.method="score")
```

The returned *test* is an object of type *htest* and type *chnngpt.test*. When printed, `print.htest` is called and generates a standard output that reports the estimated change point, the test statistic and :

```
Maximal Score Test  
data: dat.mtct  
Maximal statistic = 3.3209, change point = 7.0347, p-value = 0.00284  
alternative hypothesis: two-sided
```

The first line gives the type of test carried out, and it may be maximal likelihood ratio test. In addition, a plot function can be called on the test object to show the score or likelihood ratio statistic as a function of candidate change points.

2 Linear regression example

To estimate a linear regression model with a segmented-type change point in *Girth* for the *trees* dataset, we call

```
> fit=chngpptm(formula.1=Volume~1, formula.2=~Girth, trees,
type="segmented", family="gaussian", est.method="smoothapprox", var.type="bootstrap",
aux.fit=glm(Volume~ns(Girth,df=3), trees, family="gaussian"))
```

The argument *formula.2* gives the threshold variable and the argument *formula.1* gives the rest of the model. The argument *type* conveys the type of threshold effects one wishes to fit, and the argument *est.method* controls the type of search algorithm to use. When the estimation method is grid search and the argument *verbose* is set to 2, the program will output a plot of log likelihoods versus candidate change points (Figure B.1a, Fong et al., 2017). The returned *fit* is an object of type *chngpptm*. Calling summary function on the *fit* object produces the following information:

```
Coefficients:
              Est      p.value  (lower  upper)
(Intercept) -24.614440 NA -39.336944 -17.530558
Girth        3.993966 NA  3.249892  5.370237
(Girth-chngppt)+ 4.266618 NA  2.952945 10.083153

Threshold:
 74.2% (lower  upper)
 16.0   12.9   18.0
```

To test whether there is a change point, we call

```
> test=chngppt.test(formula.null=Volume~1, formula.chngppt=~Girth, trees,
type="segmented", family="gaussian")
```

The returned *test* is an object of type *htest* and type *chngppt.test*. When printed, `print.htest` is called and generates a standard output that reports the estimated change point, the test statistic and :

```
Maximum of Likelihood Ratio Statistics
data: trees
Maximal statistic = 17.694, change point = 15.388, p-value = 0.00014
alternative hypothesis: two-sided
```

The first line gives the type of test carried out, and it is maximal likelihood ratio test here, which is the default. In addition, a plot function can be called on the test object to show the score or likelihood ratio statistic as a function of candidate change points.

References

Fong, Y., Huang, Y., Gilbert, P. and Permar, S. (2017), “chnppt: threshold regression model estimation and inference,” *BMC Bioinformatics*, under revision.