# Using GAMs to assess effect of biomarkers on treatment effect (2)

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# Previously...

Aims:

- To determine a biomarker threshold to divide patients into those who do and do not recieve treatment.
- Use proportional hazards model with a nonlinear function of the biomarker to find treatment effect as a function of the biomarker.

$$\log(rac{h_i(t)}{h_0(t)})=eta$$
 treat $_i+f_{treat_i}( ext{biomarker}_i)$ 

► *f* is a thin plate regression spline with wiggliness penalty. Target Product Profile (TPP):

- The TPP is the minimum level of efficacy required.
- Example: The drug must reduce the treatment vs. control hazard ratio to 75%

## General Procedure

## Finding the biomarker threshold

Once the model has been fitted, the curve must be integrated to find the mean value of the log hazard ratio above a given threshold.

$$I(c) = \int_c \log(HR), \quad c* = I^{-1}(TPP)$$



### Type one error inflation

 Type one error is inflated when the same data is used to select a biomarker and test for efficacy.

#### Permutation Test:

- If treatment and control are from the same group (with regards to the effect of the biomarker) then reassigning labels should have no effect.
- Relabel the observations repeatedly e.g. treatment or control. and carrying out the analyses as before.

- Obtain *p*-value from the permutation distribution.
- If significant, then the biomarker threshold may be used.

## Simulated Example



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The TPP is log(0.75)

## Histogram of permutation test

**Biomarker Threshold distribution** 



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#### Possible next steps:

- Look at alternatives to the permutation test for the type one error rate.
- Run simulations to check that the type one error rate is controlled.
- Use other models than proportional hazards.
- Consider Biomarkers which change in time.
- Look at possible confidence intervals for the cutoff point.

Account for model selection uncertainty.