photobiologyWavebands Version 0.3.3
Catalogue of waveband definitions and BSWF functions

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1 Introduction

```
library(ggplot2)
library(ggspectra)
library(photobiologyWavebands)
```

```
options(photobiology.plot.annotations =
          c("boxes", "labels", "colour.guide", "title"))
```

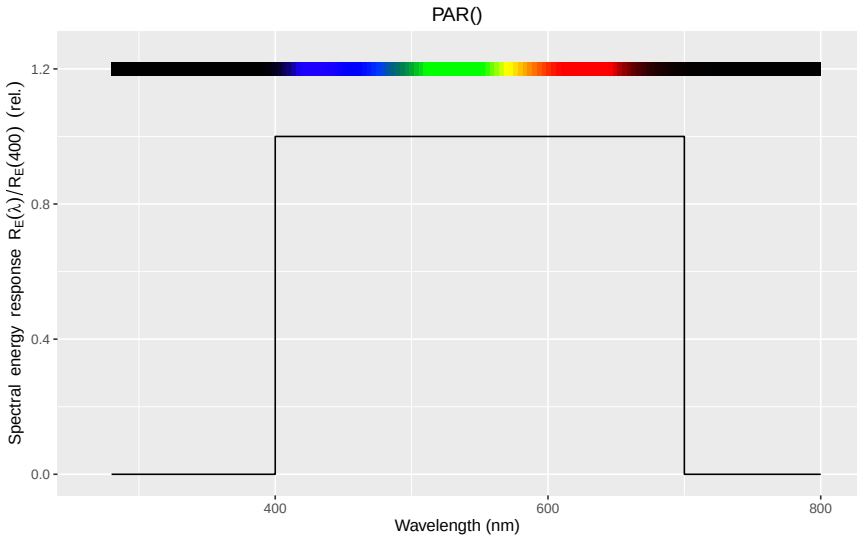
In this vignette we plot some examples of `waveband` constructors defining wavelength ranges, and all constructors for BSWFs, plus the BSWFs function definitions. Many of these constructors have formal arguments that can be used to obtain different 'flavours' of the defintiions as used in the scientific literature. We show only a few of such examples.

The references to the defintions in the literature and further explanations are given in the documentation accesible through R's `help` for each waveband and function definition.

2 Wavebands

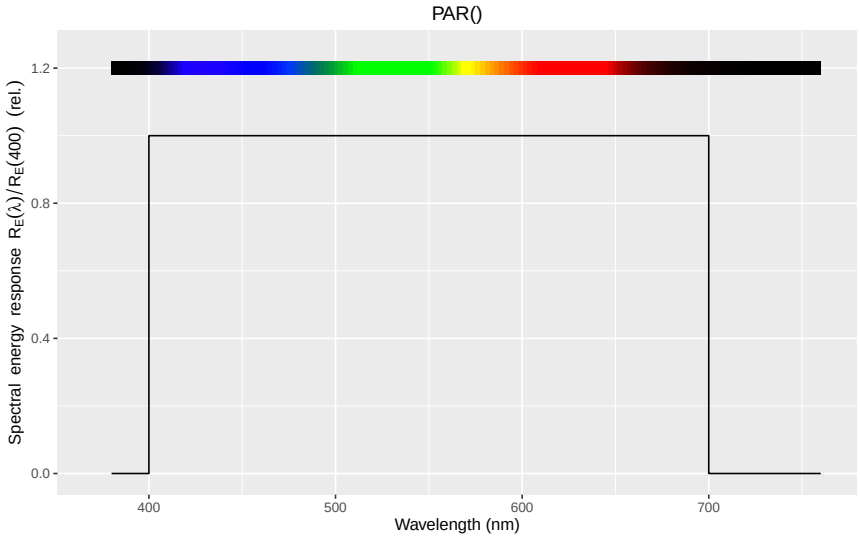
Wavebands can be directly plotted with function plot. Here we guive just a couple of examples, as with the many options plotting all wavebands using different options would be tedious.

```
plot(PAR())
```



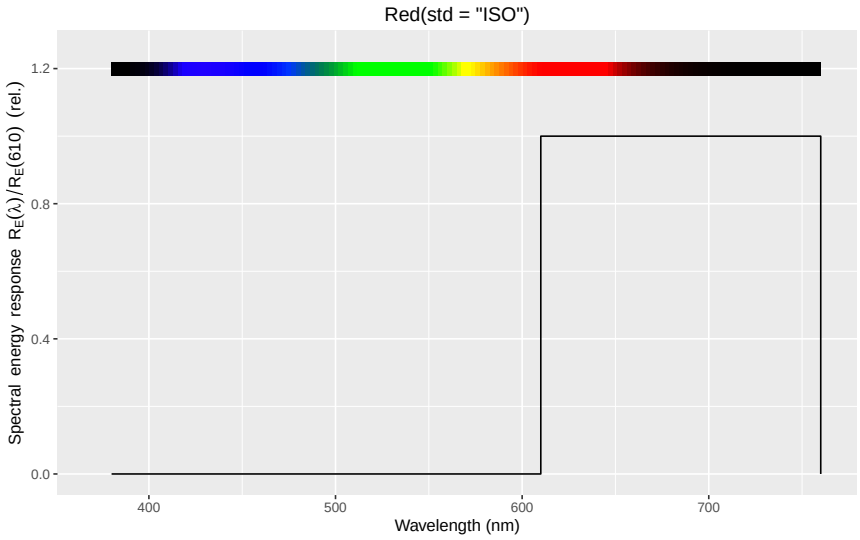
We can limit the plotted wavelengths to a range, even using another waveband object.

```
plot(PAR(), range = VIS())
```

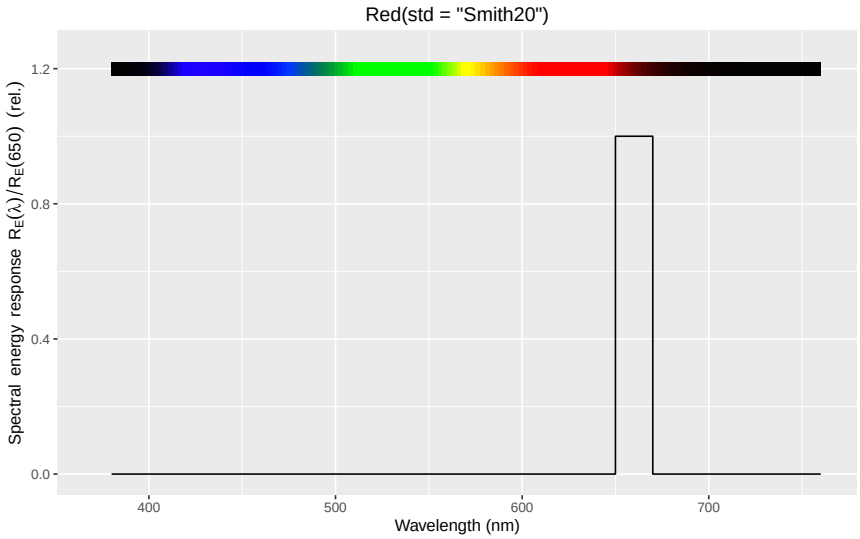


Or plot using a different defintions.

```
plot(Red(std = "ISO"), range = VIS())
```

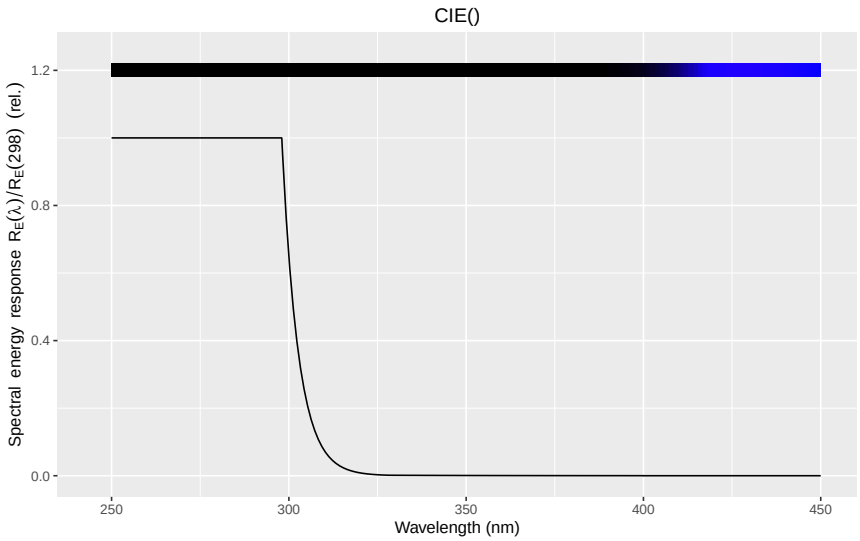



```
plot(Red(std = "Smith20"), range = VIS())
```

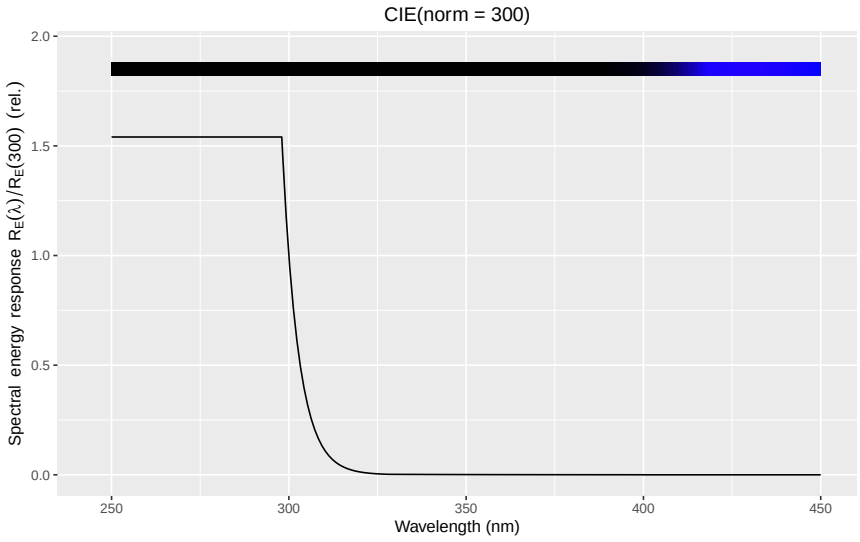


Waveband objetcs defining BSWFs can be similarly plotted. The 'boxes' containing the names of the wavebands show the range of wavelengths used for integration when calculating effective irradiances.

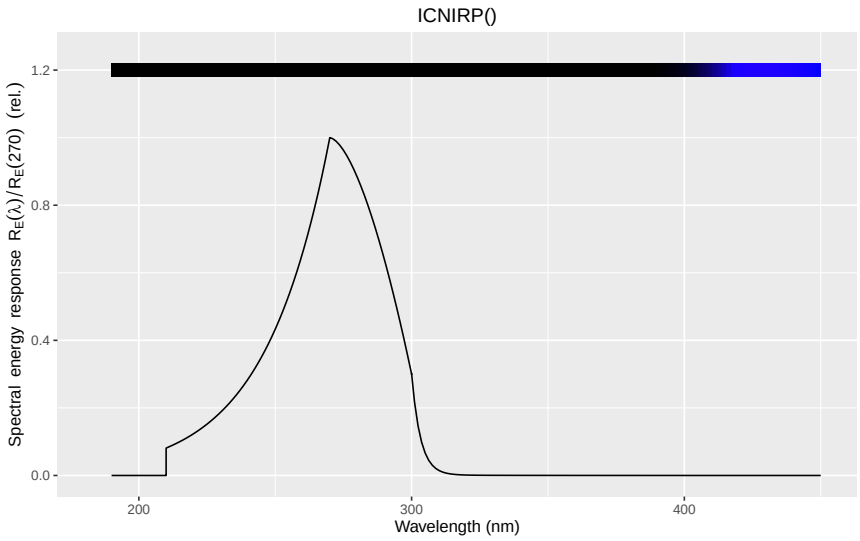
```
plot(CIE(), range=c(250,450))
```



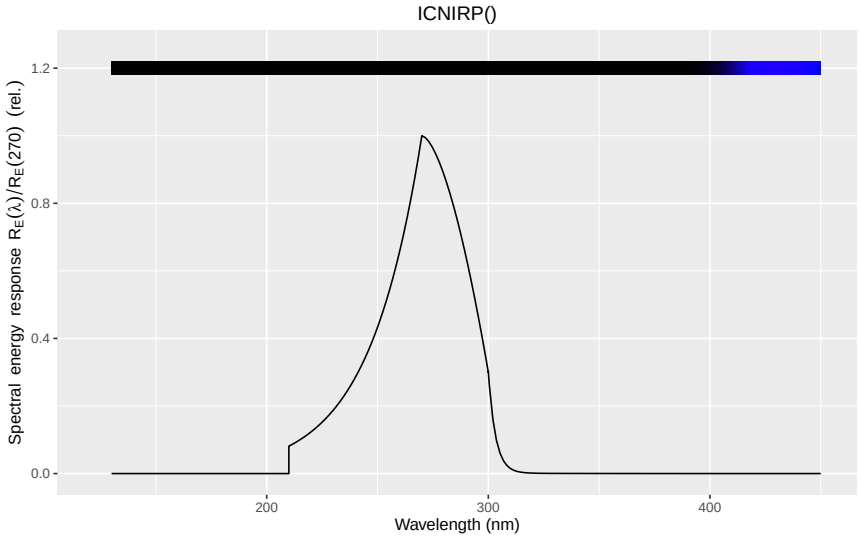

```
plot(CIE(norm = 300), range=c(250,450))
```



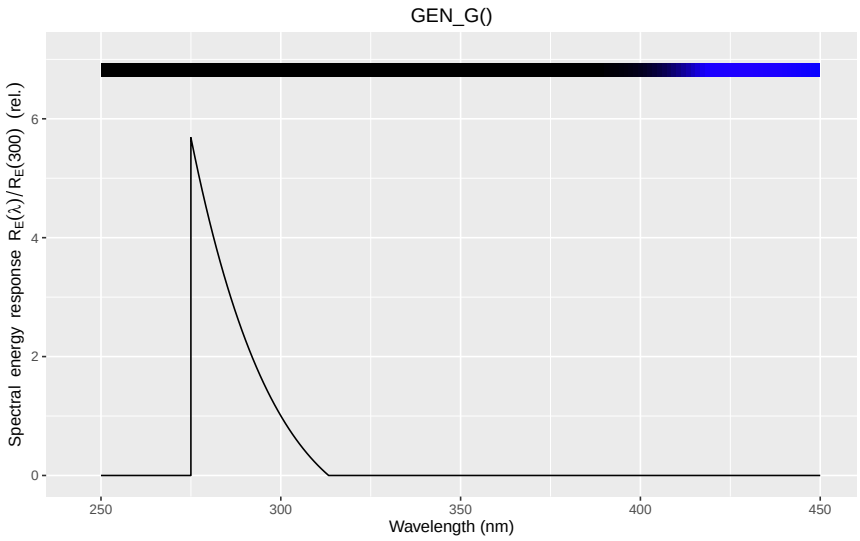
```
plot(ICNIRP(), range=c(190,450))
```



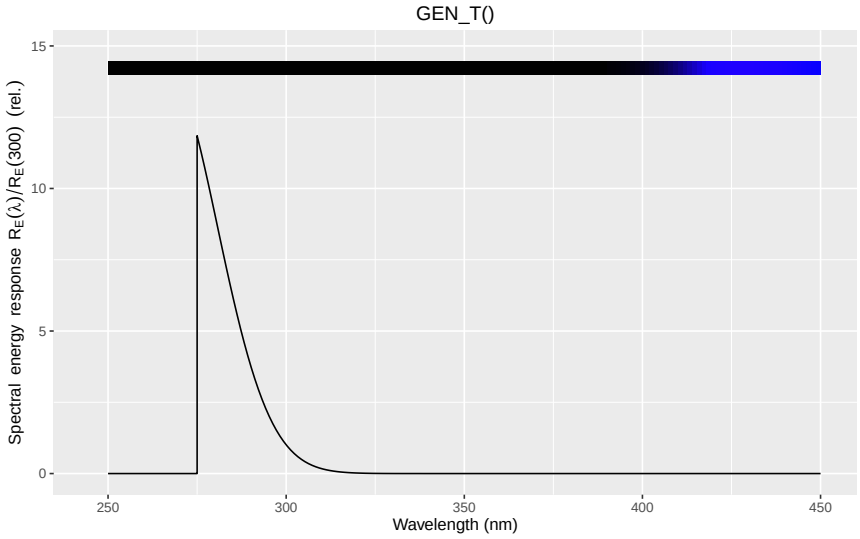

```
plot(ICNIRP(), range=c(130,450))
```



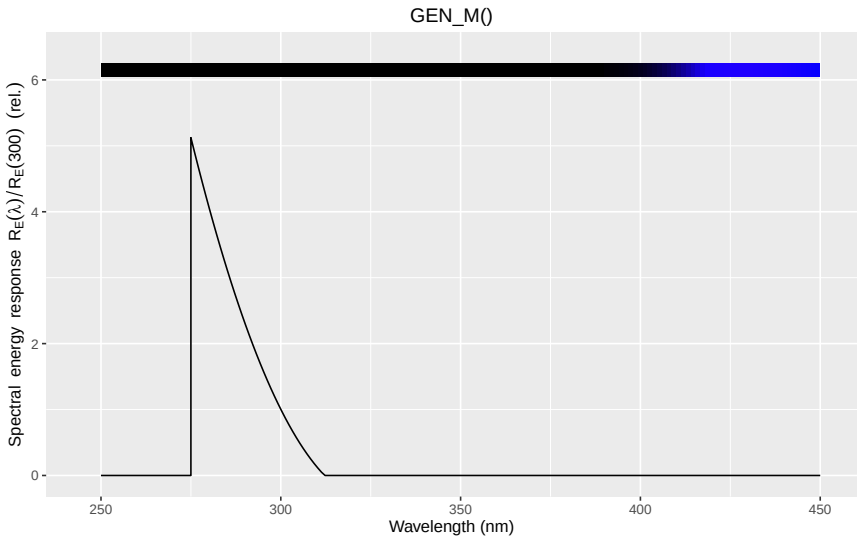
```
plot(GEN_G(), range=c(250,450))
```



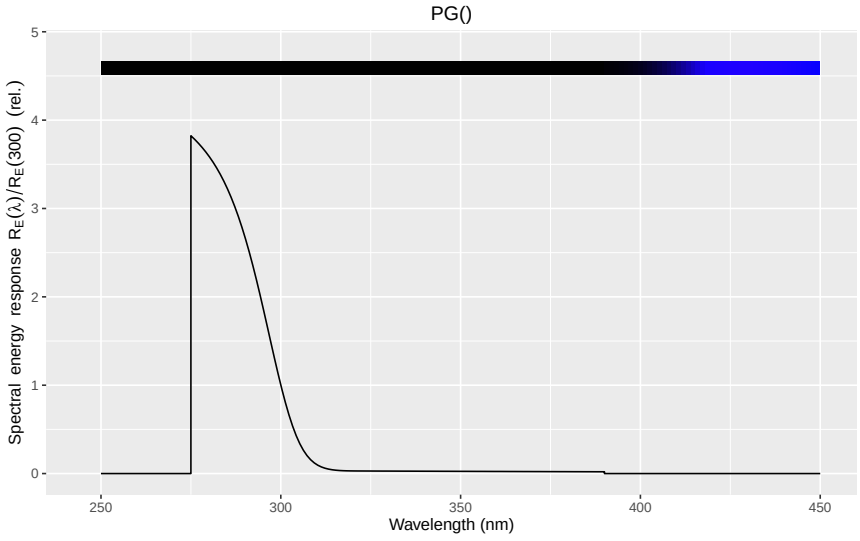

```
plot(GEN_T(), range=c(250,450))
```



```
plot(GEN_M(), range=c(250,450))
```

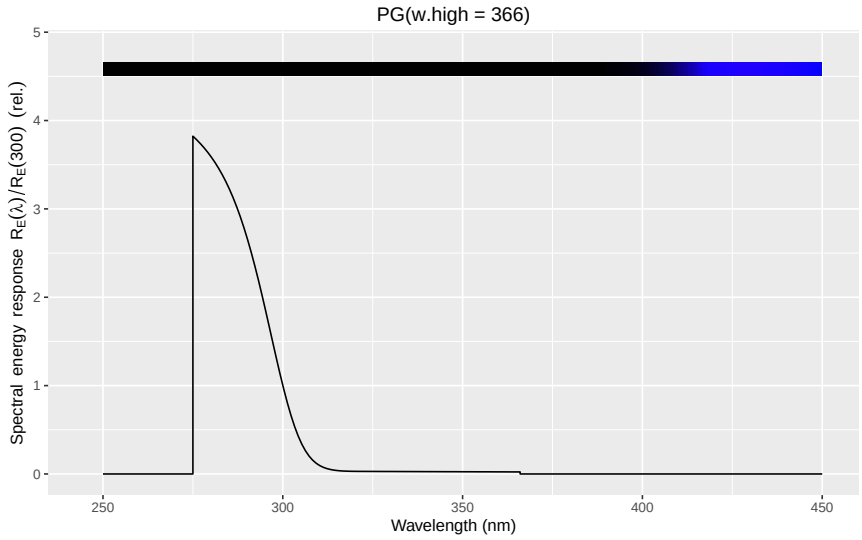



```
plot(PG(), range=c(250,450))
```

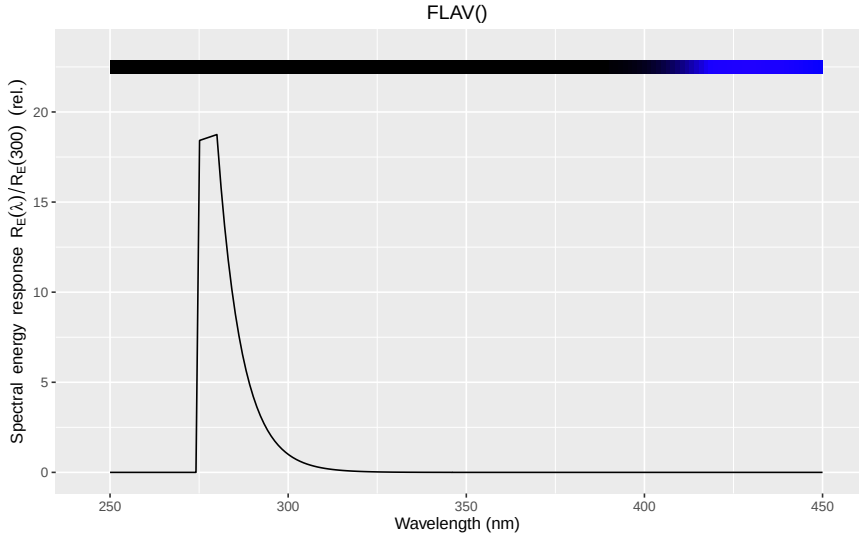


As used in the TUV model.

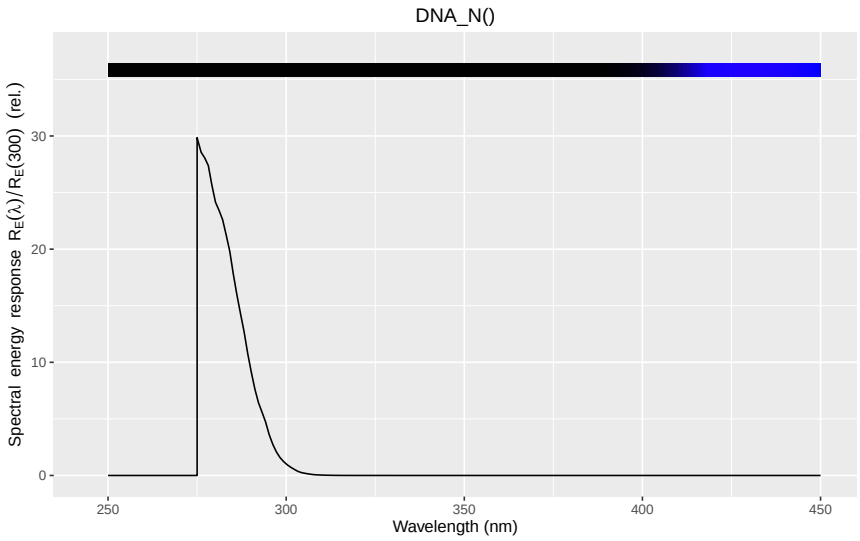
```
plot(PG(w.high = 366), range=c(250,450))
```



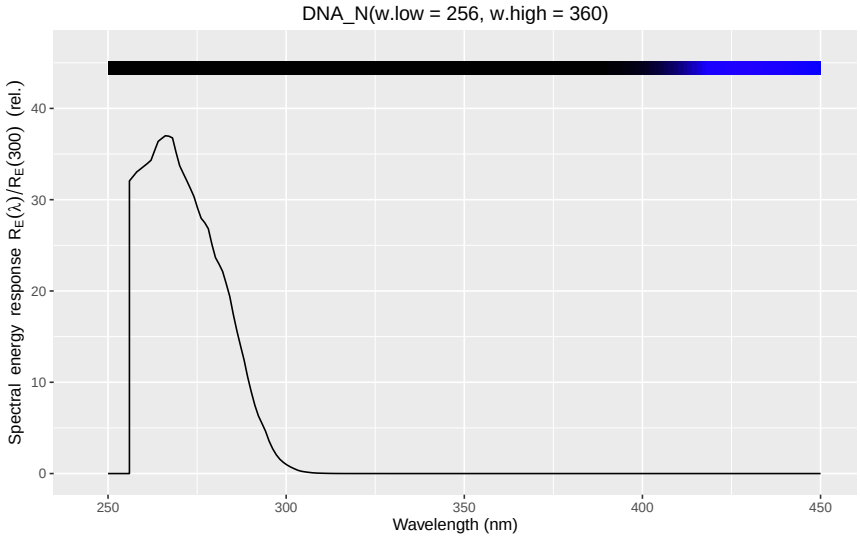

```
plot(FLAV(), range=c(250,450))

## Warning in SWF.q.fun(w.length):  FLAV BSWF is extrapolated for w.length < 280 nm
##  to the value for 280 nm
```



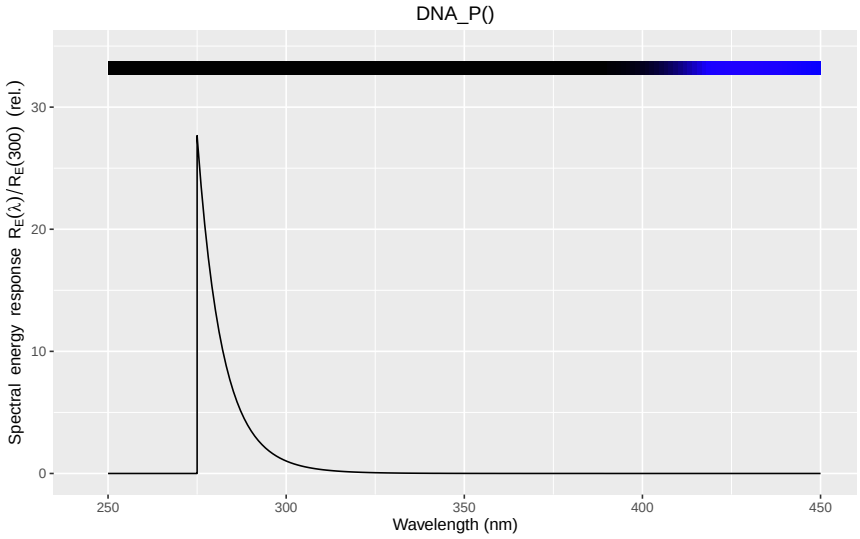
```
plot(DNA_N(), range=c(250,450))
```



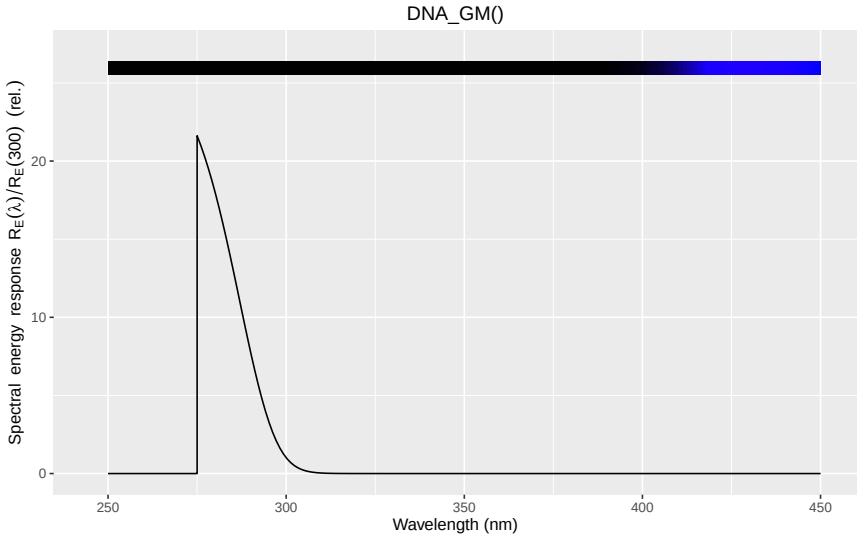

```
plot(DNA_N(w.low = 256, w.high = 360), range=c(250,450))
```



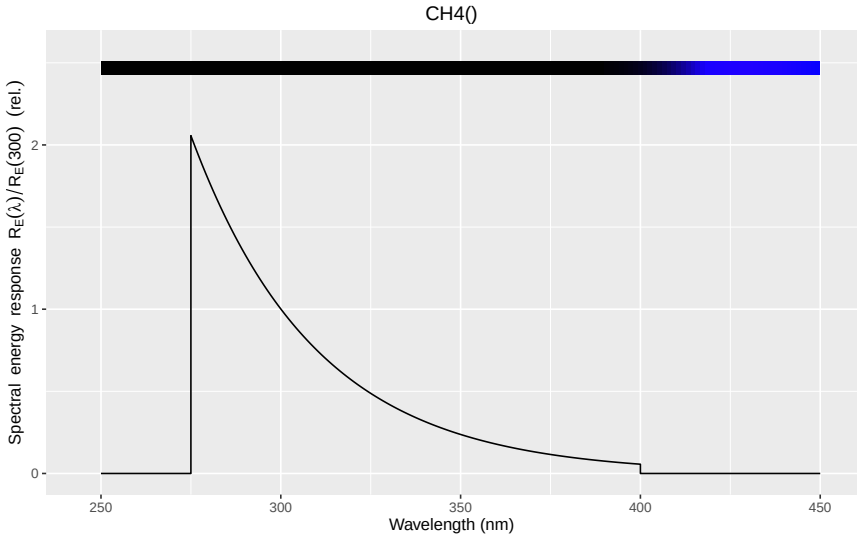
```
plot(DNA_P(), range=c(250,450))
```




```
plot(DNA_GM(), range=c(250,450))
```



```
plot(CH4(), range=c(250,450))
```



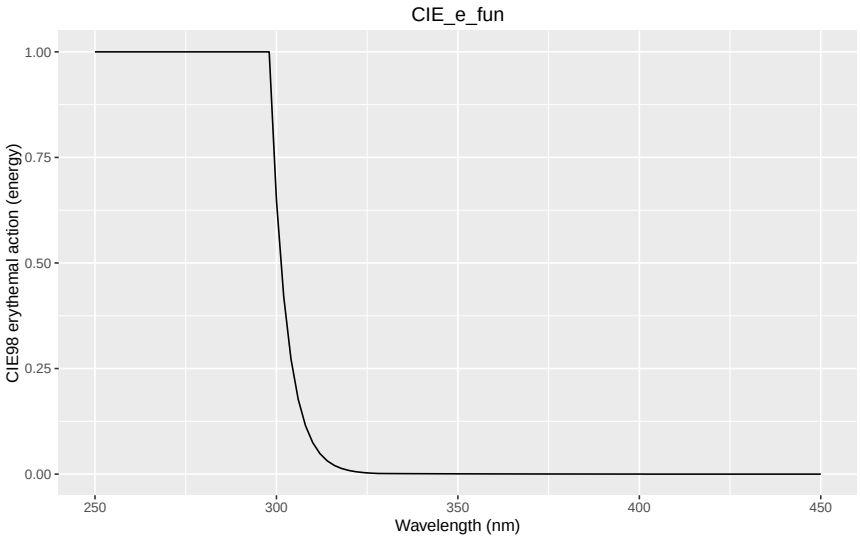
3 The BSWF functions

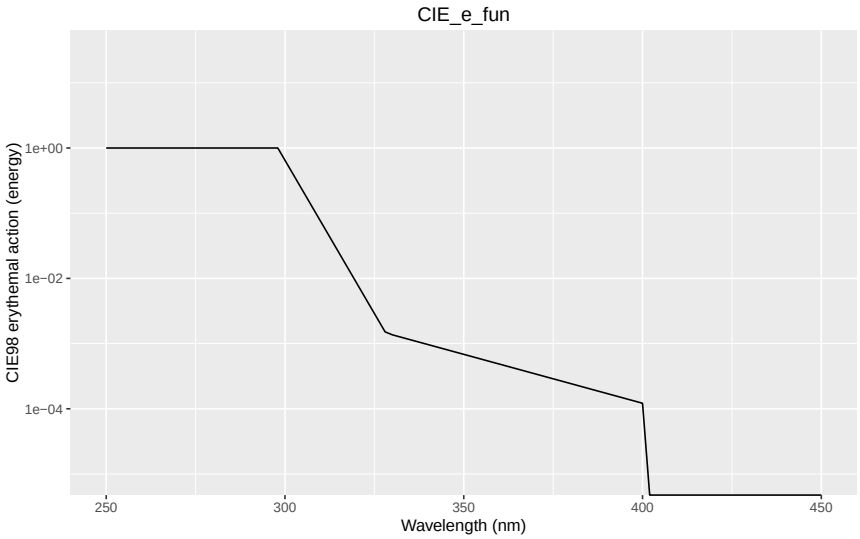
We define a function that takes as argument the function to be plotted, so as to simplify later code.

```
my.plotter <- function(bwfs.fun, w.low=250, w.high=450, ylab="Action"){
  fig_linear <- ggplot(data.frame(x = c(w.low, w.high)), aes(x)) +
  stat_function(fun = bwfs.fun) +
  labs(x="Wavelength (nm)", y=ylab, title= deparse(substitute(bwfs.fun)))
fig_log <- fig_linear + scale_y_log10(limits=c(1e-5,30))
print(fig_linear)
print(fig_log)
}
```

3.1 CIE 1998, erythemal

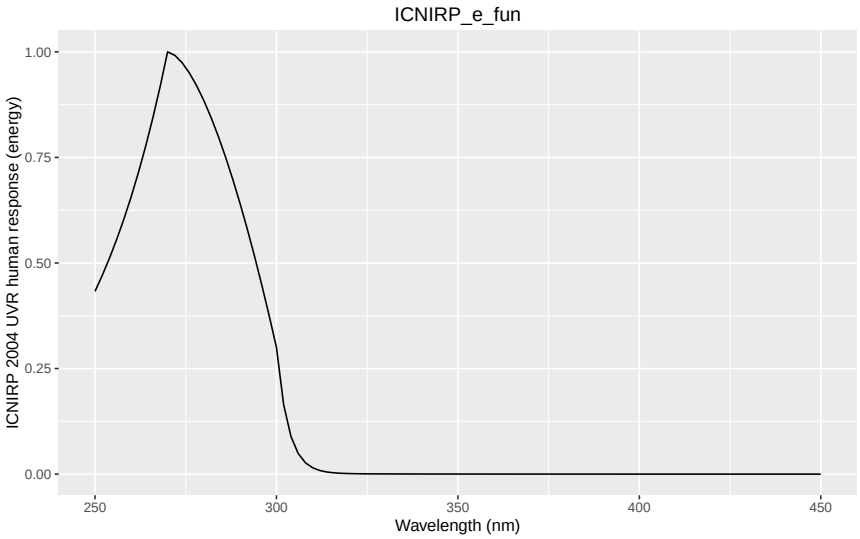
```
my.plotter(CIE_e_fun, ylab="CIE98 erythemal action (energy)")
```

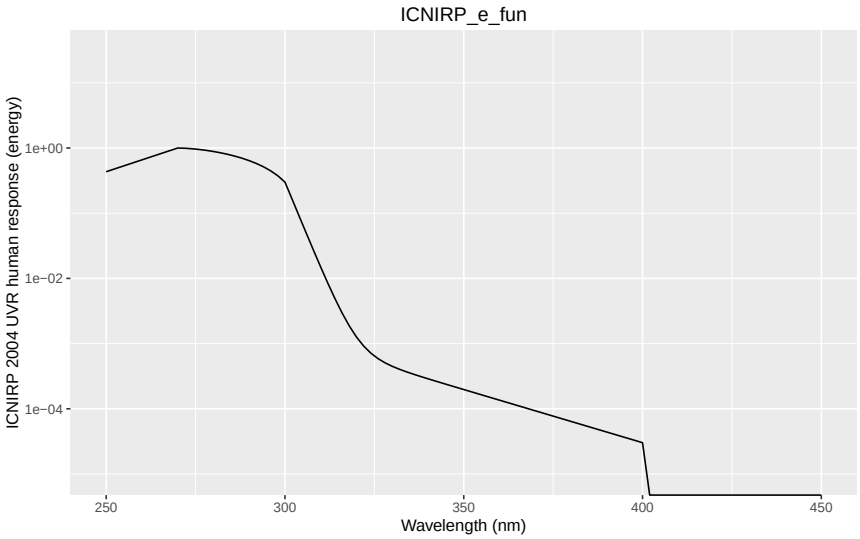




3.2 ICNIRP 2004

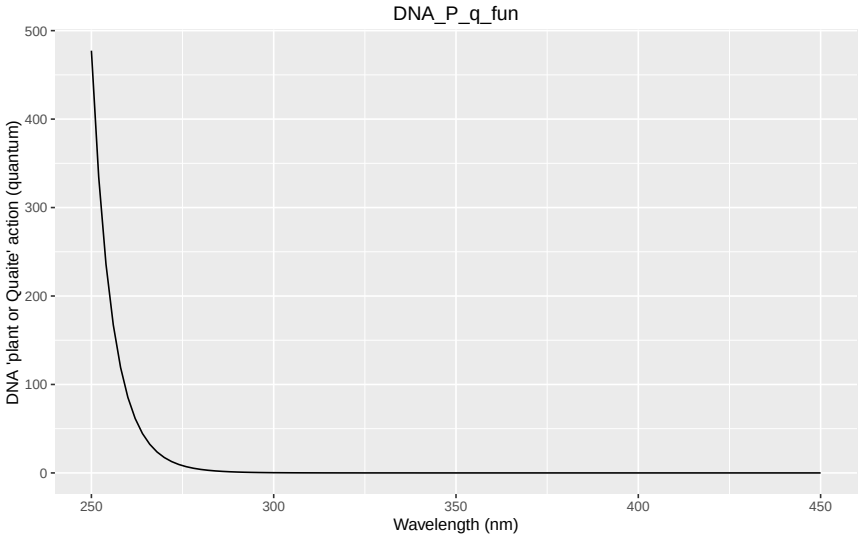
```
my.plotter(ICNIRP_e_fun, ylab="ICNIRP 2004 UVR human response (energy)")
```

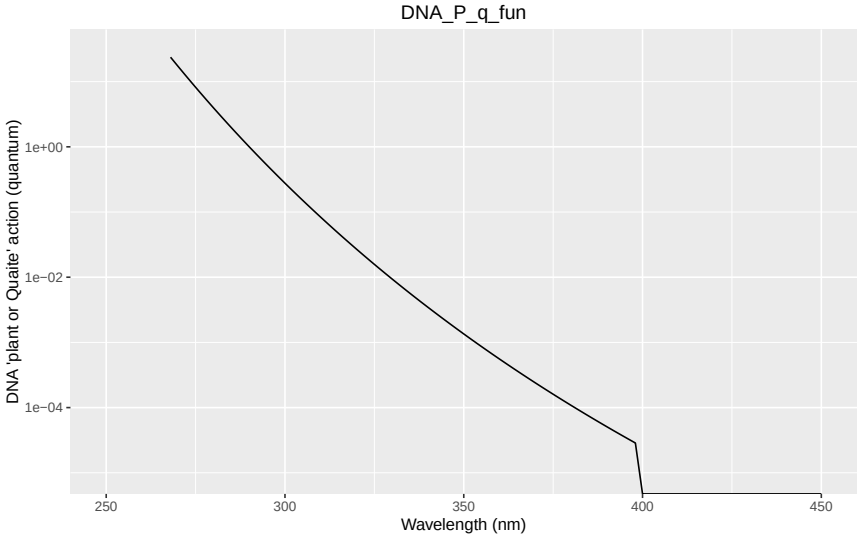




3.3 DNA 'Plant', Quaite

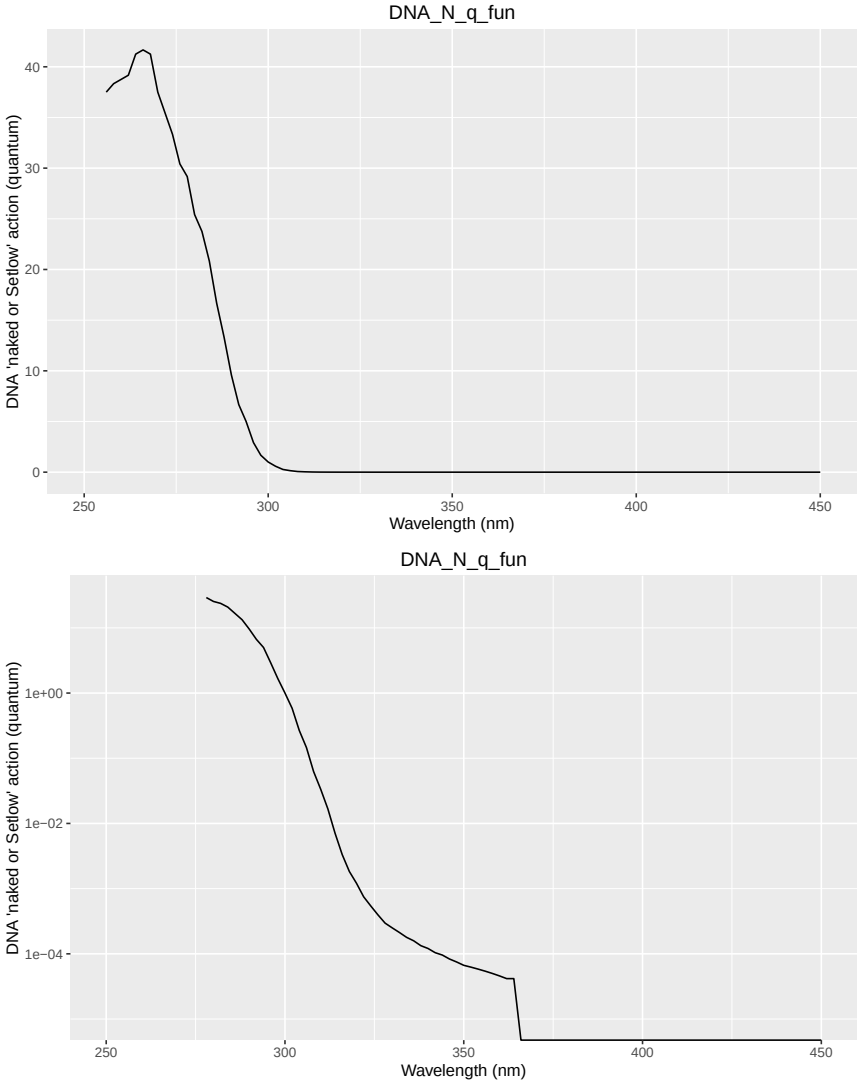
```
my.plotter(DNA_P_q_fun, ylab="DNA 'plant or Quaite' action (quantum)")

## Warning:  Removed 9 rows containing missing values (geom_path).
```





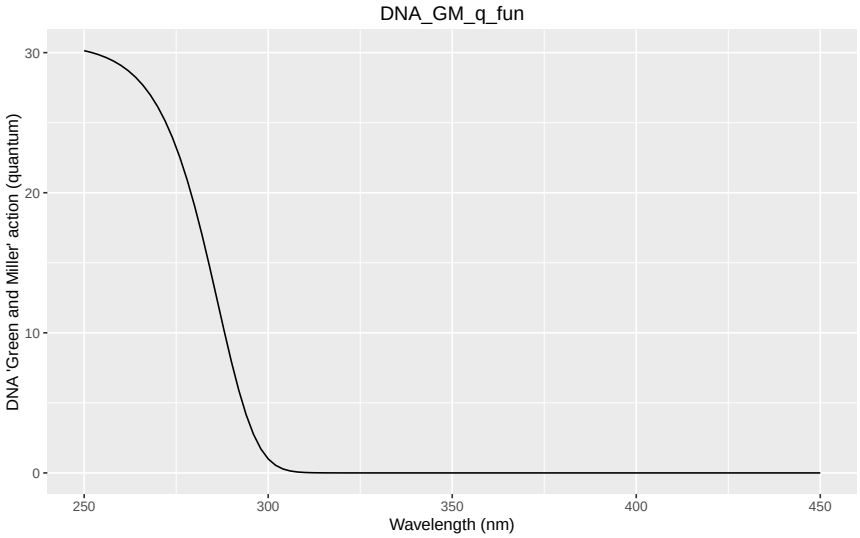
3.4 DNA ‘naked’, Setlow

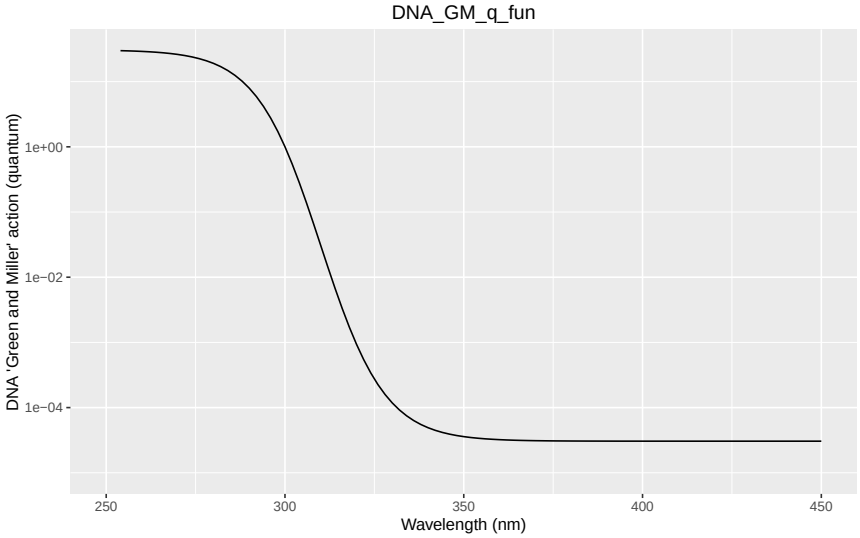
```
my.plotter(DNA_N_q_fun, ylab="DNA 'naked or Setlow' action (quantum)")

## Warning:  Removed 3 rows containing missing values (geom_path).
## Warning:  Removed 14 rows containing missing values (geom_path).
```



3.5 DNA 'Green & Miller', ≈Setlow

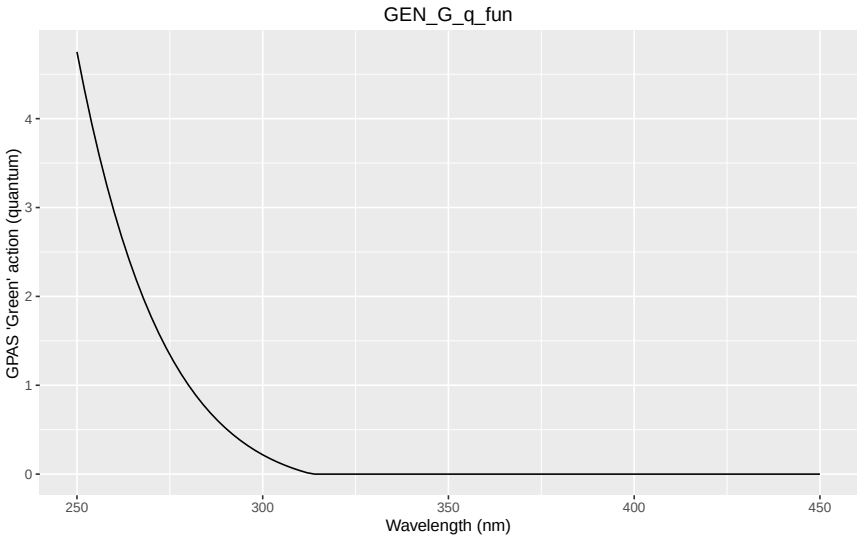
```
my.plotter(DNA_GM_q_fun, ylab="DNA 'Green and Miller' action (quantum)")

## Warning:  Removed 2 rows containing missing values (geom_path).
```

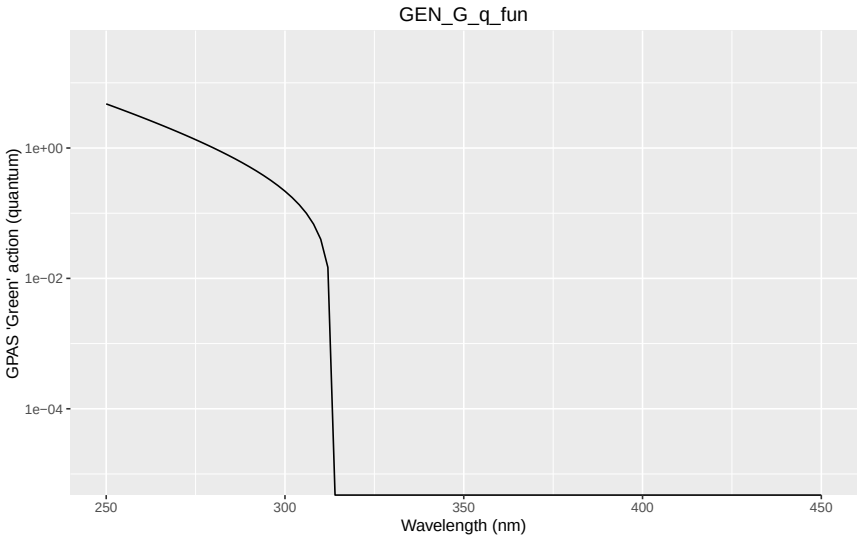




3.6 GPAS 'Green', Caldwell

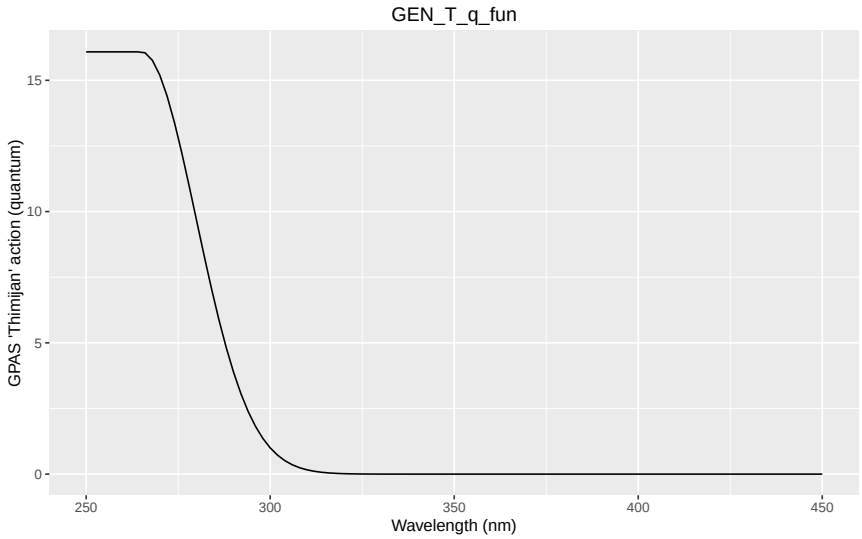
```
my.plotter(GEN_G_q_fun, ylab="GPAS 'Green' action (quantum)")
```

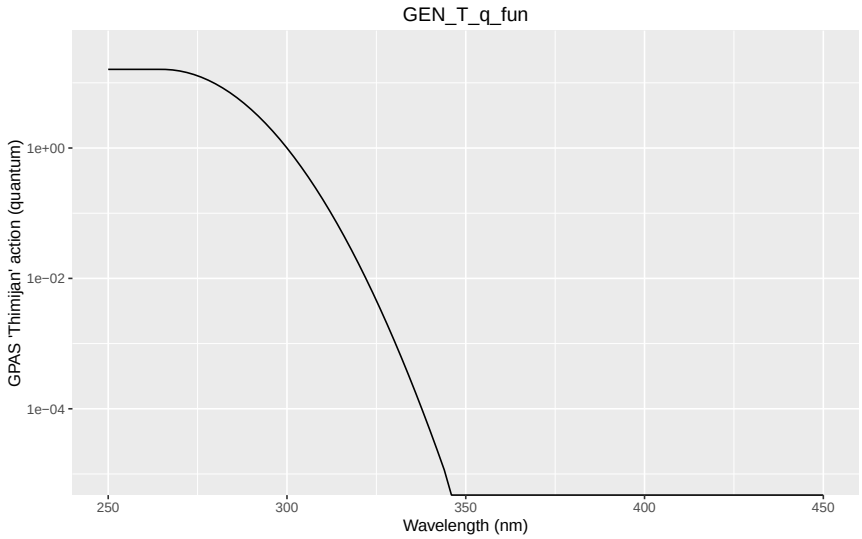




3.7 GPAS 'Thimijan', Caldwell

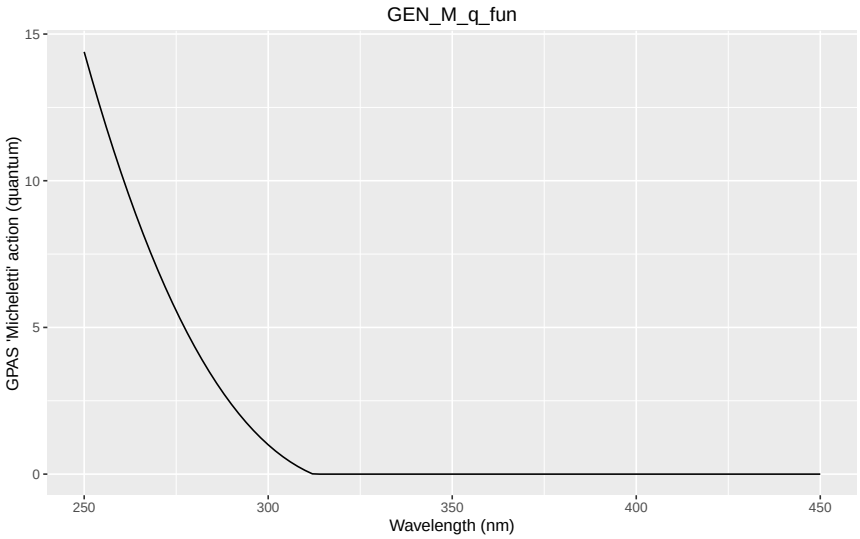
```
my.plotter(GEN_T_q_fun, ylab="GPAS 'Thimijan' action (quantum)")
```

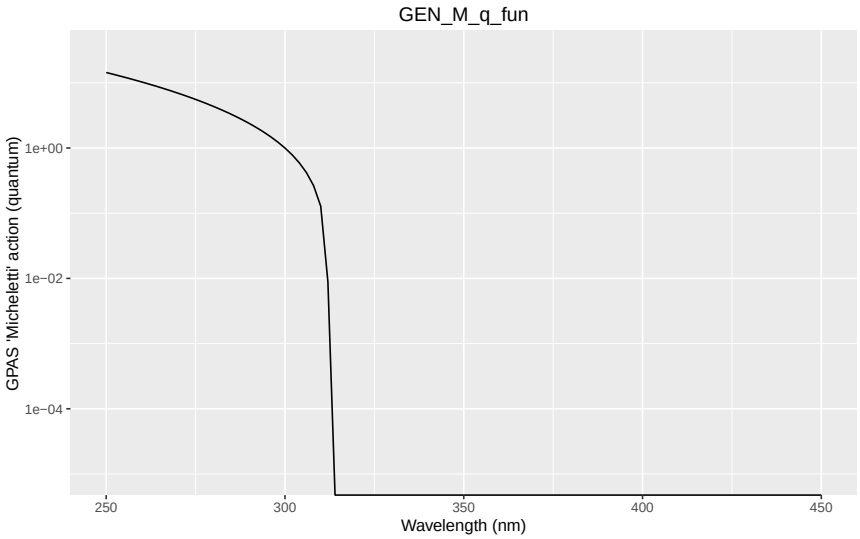




3.8 GPAS ‘Micheletti’, Caldwell

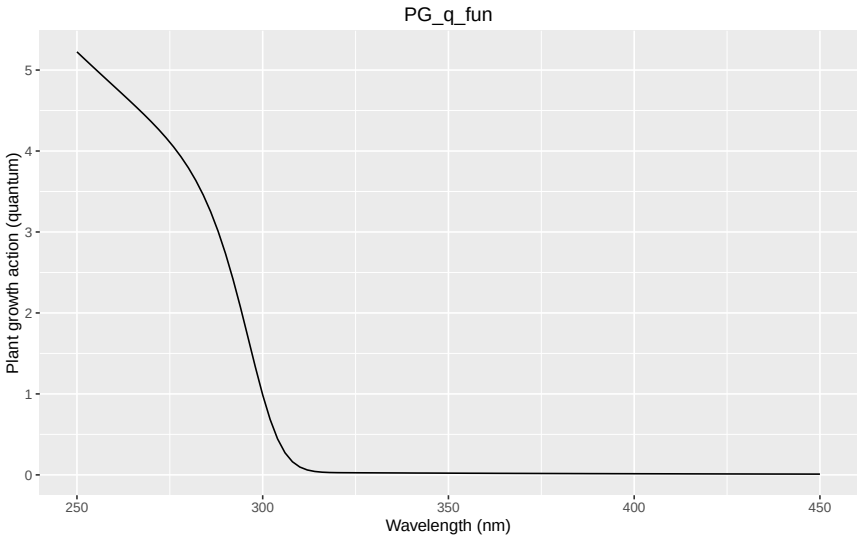
```
my.plotter(GEN_M_q_fun, ylab="GPAS 'Micheletti' action (quantum)")
```

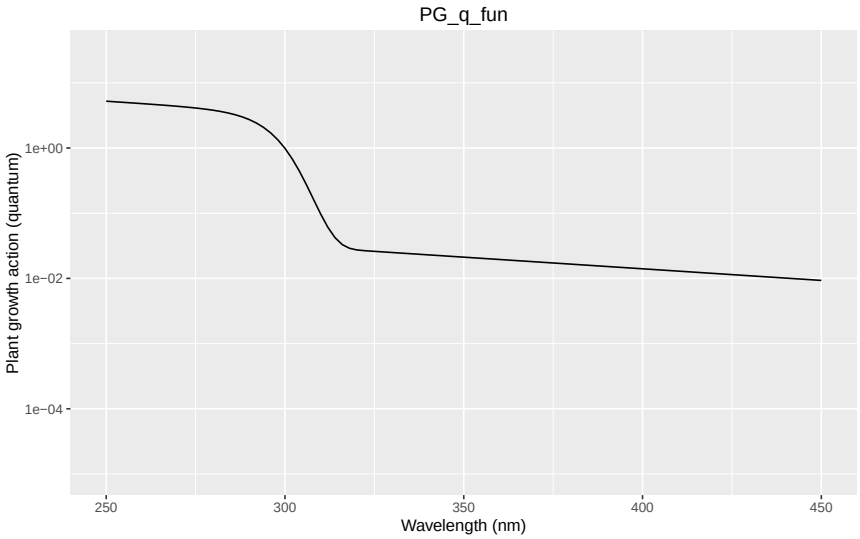




3.9 PG 'Plant Growth', Flint & Caldwell

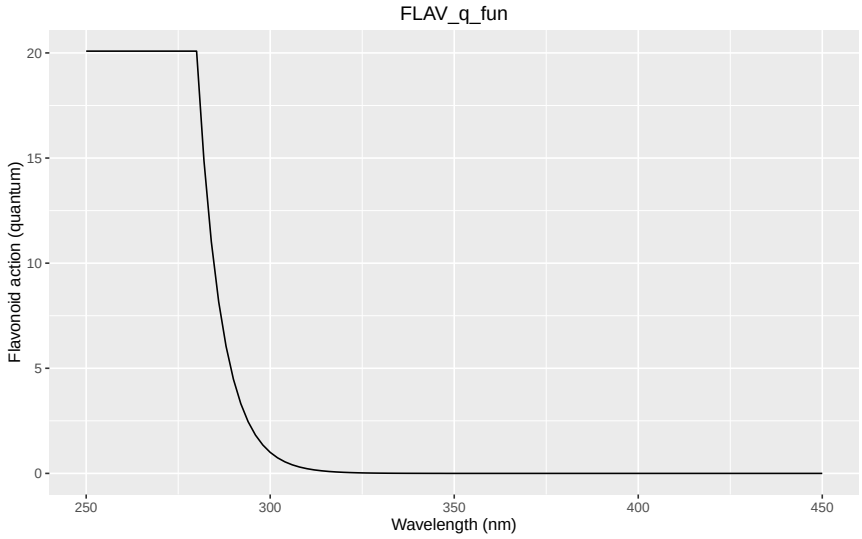
```
my.plotter(PG_q_fun, ylab="Plant growth action (quantum)")
```

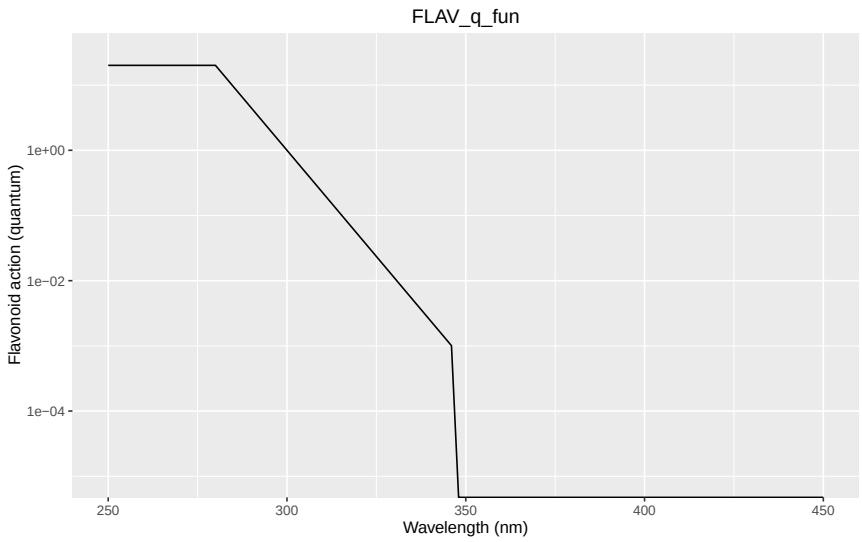




3.10 Flavonoid, Ibdah

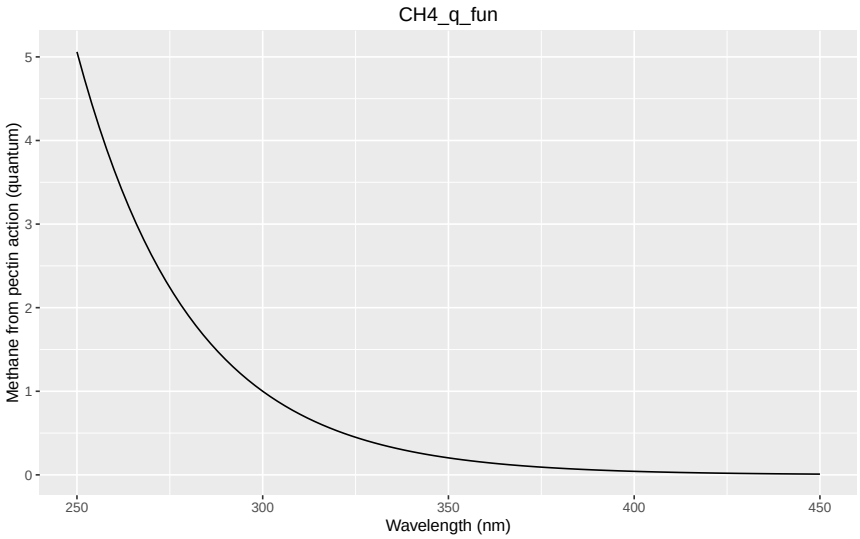
```
my.plotter(FLAV_q_fun, ylab="Flavonoid action (quantum)")

## Warning in (function (w.length) :  FLAV BSWF is extrapolated for w.length < 280
nm
##  to the value for 280 nm
## Warning in (function (w.length) :  FLAV BSWF is extrapolated for w.length < 280
nm
##  to the value for 280 nm
```

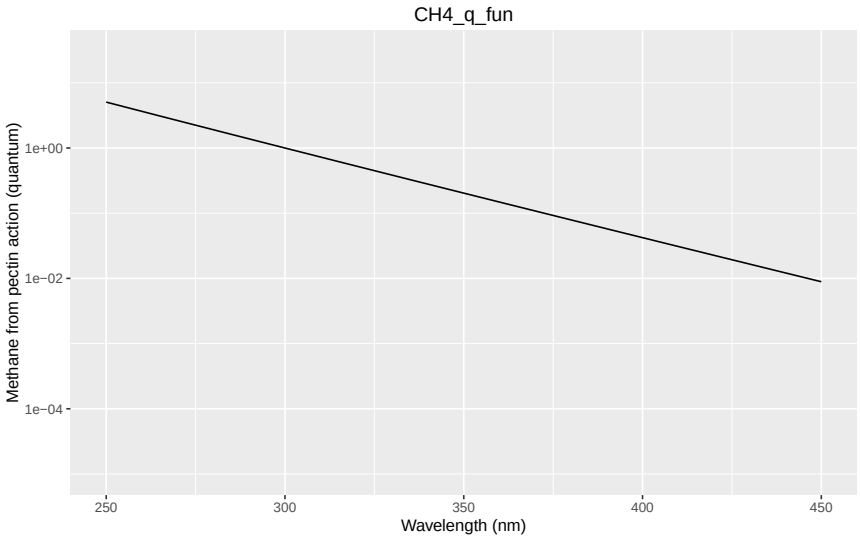




3.11 Methane, McLeod

```
my.plotter(CH4_q_fun, ylab="Methane from pectin action (quantum)")
```

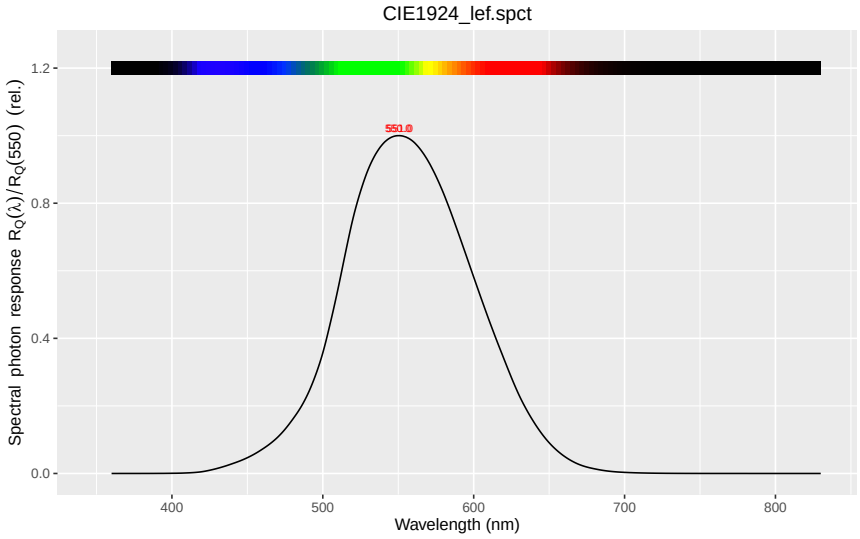




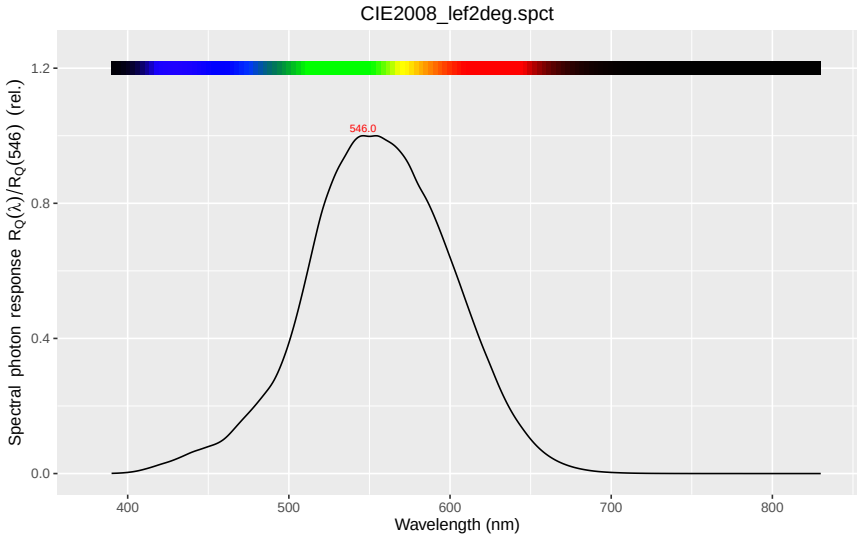
4 Luminous efficiency curves

```
options(photobiology.plot.annotations =
          c("peaks", "colour.guide", "title"))
options(photobiology.radiation.unit = "photon")
```

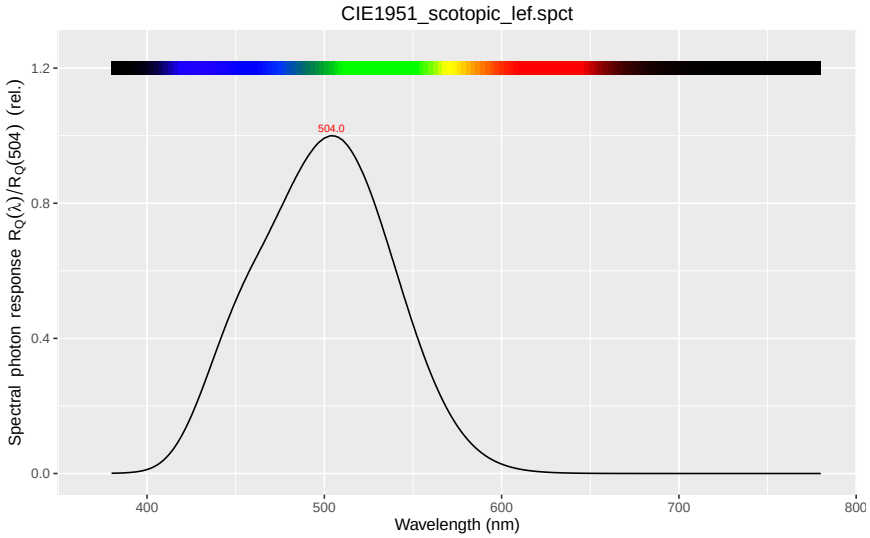
```
plot(CIE1924_lef.spct)
```




```
plot(CIE2008_lef2deg.spct)
```




```
plot(CIE1951_scotopic_lef.spct)
```


CIE1951_scotopic_lef.spct
504.0
1.2
0.8
0.4
0.0
Spectral photon response $R_Q(\lambda)/R_Q(504)$ (rel.)
400
500
600
700
800
Wavelength (nm)