

photobiologyPlants Version 0.4.1

Plots of the data

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1 Set up

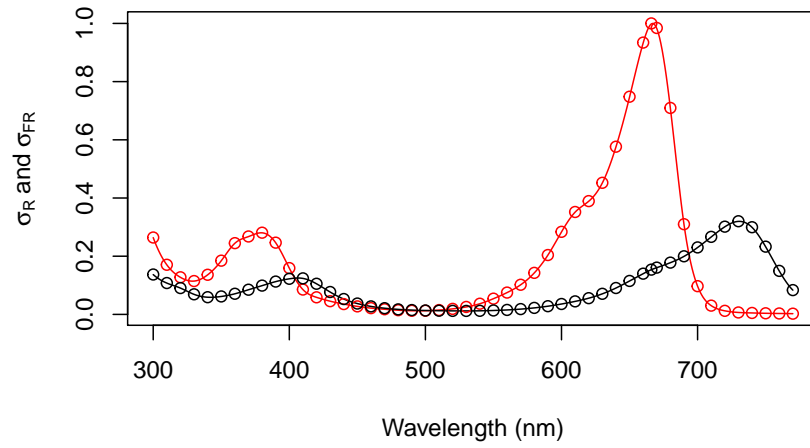
```
library(ggplot2)
library(ggspectra)
library(photobiologyPlants)
library(photobiology)
```

```
# options(photobiology.filter.qty = "absorbance")
options(photobiology.plot.annotations =
  c("boxes", "labels", "colour.guide", "title"))
options(photobiology.radiation.unit = "photon")
```

2 Phytochrome

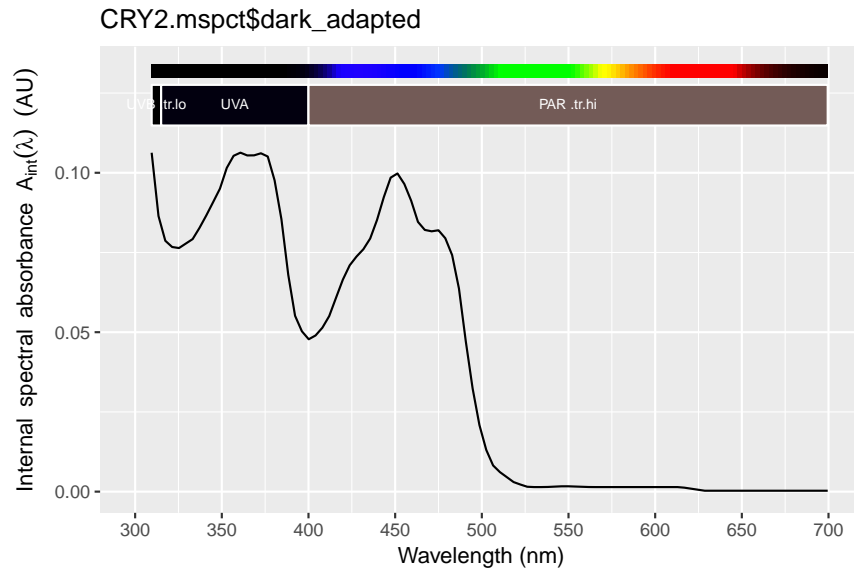
3 Test of interpolation

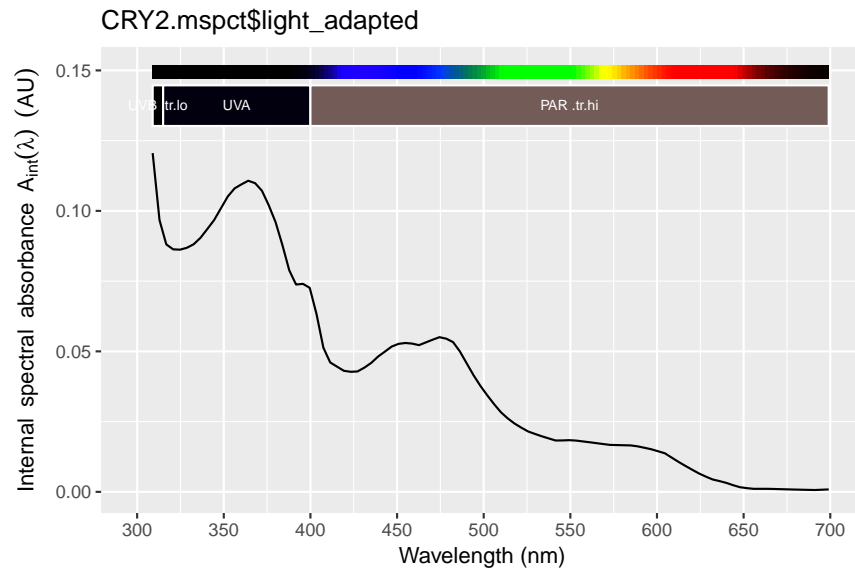
```
ex7.dt <- data.frame(w.length=300:770,
  sigma.r = Phy_Sigma_R(300:770),
  sigma.fr = Phy_Sigma_FR(300:770),
  sigma = Phy_Sigma(300:770))
plot(I(sigma.r/ max(sigma.r)) ~ w.length, data=ex7.dt, type="l", col="red",
  xlab="Wavelength (nm)", ylab=expression(sigma[R]~and~sigma[FR]))
lines(I(sigma.fr/max(sigma.r)) ~ w.length, data=ex7.dt, col="black")
points(I(Sigma.R/max(Sigma.R)) ~ w.length, data=phytochrome.spct, col="red")
points(I(Sigma.FR/max(Sigma.R)) ~ w.length, data=phytochrome.spct, col="black")
rm(ex7.dt)
```



4 Cryptochromes

```
plot(CRY2.mspct$dark_adapted, plot.qty = "absorbance")
plot(CRY2.mspct$light_adapted, plot.qty = "absorbance")
```

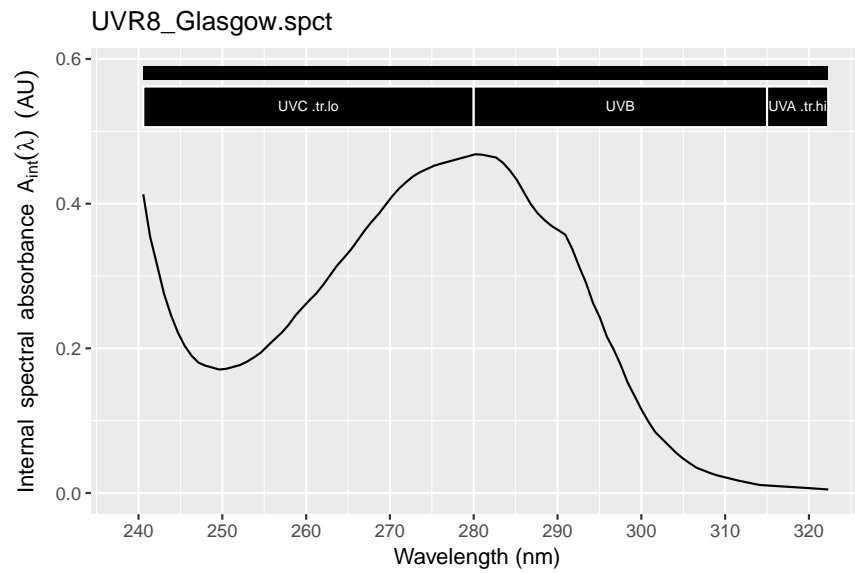
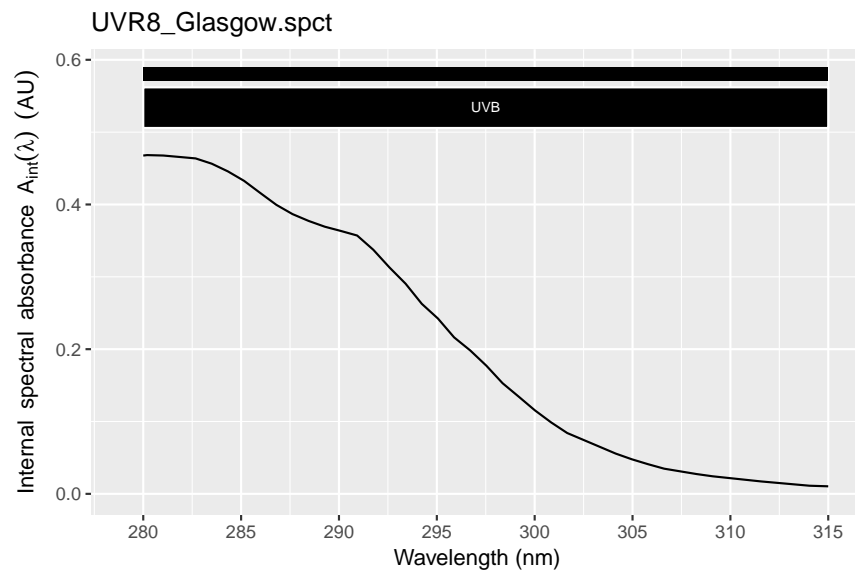




4.1 UVR8 wavebands

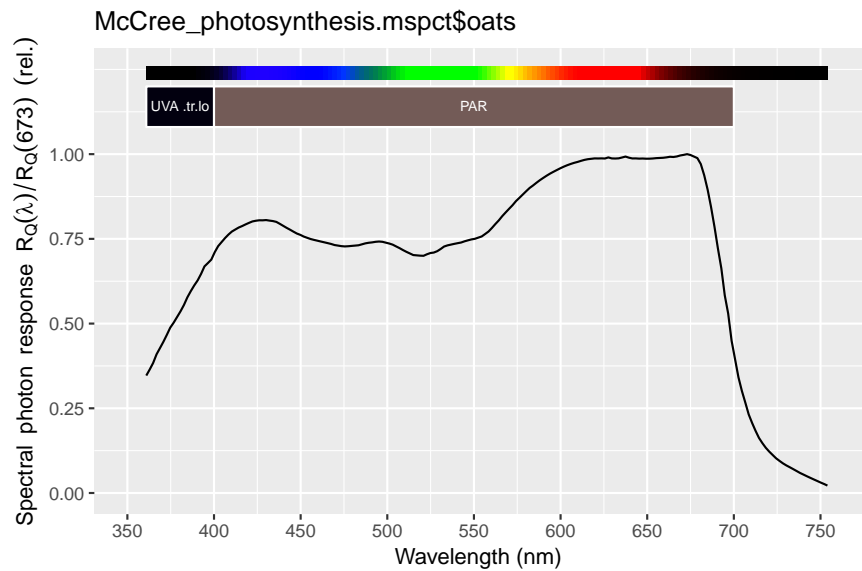
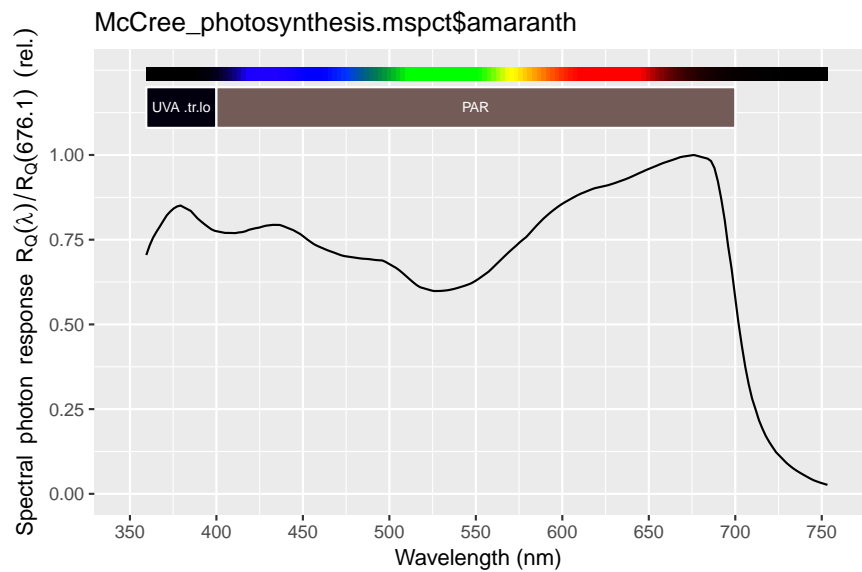
We can limit the plotted wavelengths to a range, even using another waveband object.

```
plot(UVR8_Glasgow.spct, range = UVB(), plot.qty = "absorbance")
plot(UVR8_Glasgow.spct, range = UV(), plot.qty = "absorbance")
```



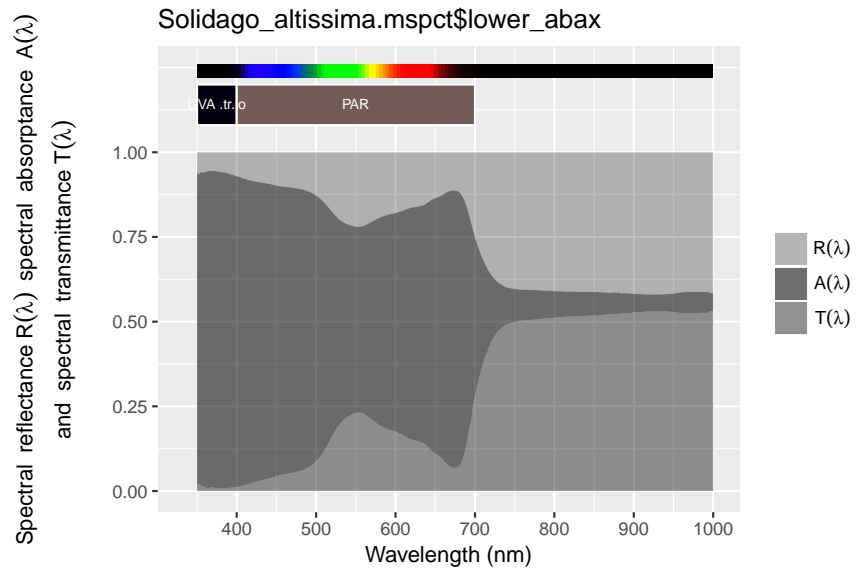
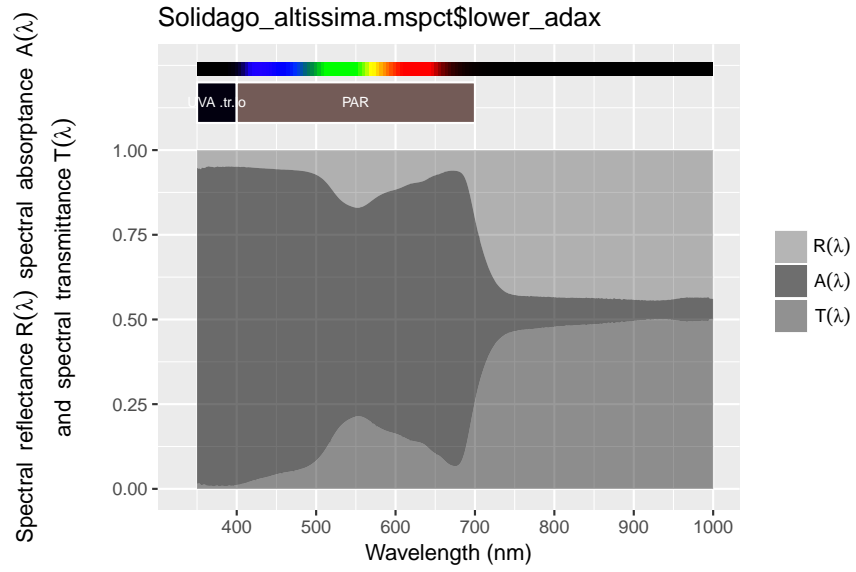
5 Photosynthesis action spectra

```
plot(McCree_photosynthesis.mspct$amaranth)
plot(McCree_photosynthesis.mspct$oats)
```

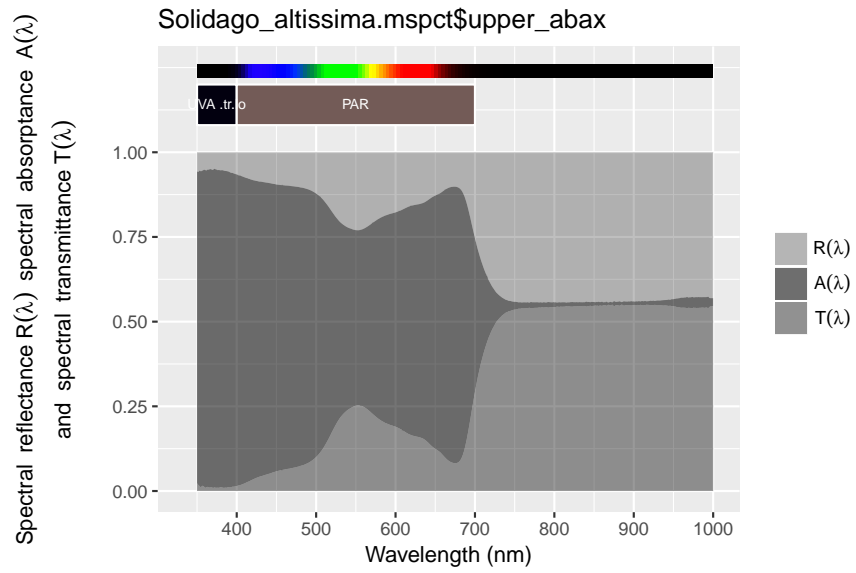
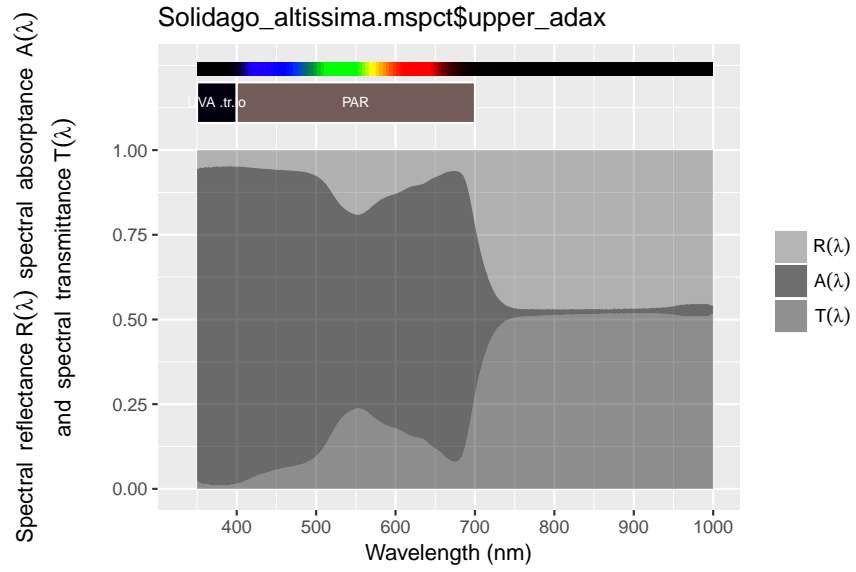


6 Optical properties of leaves

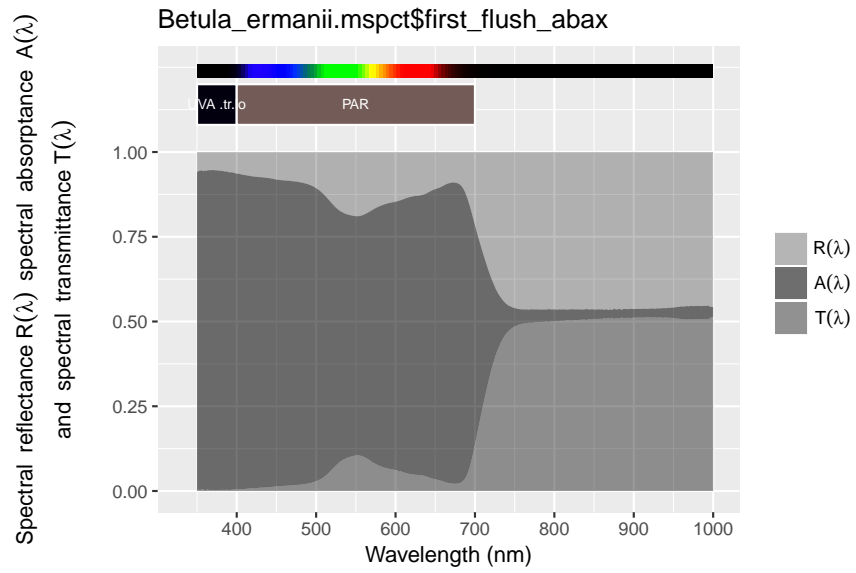
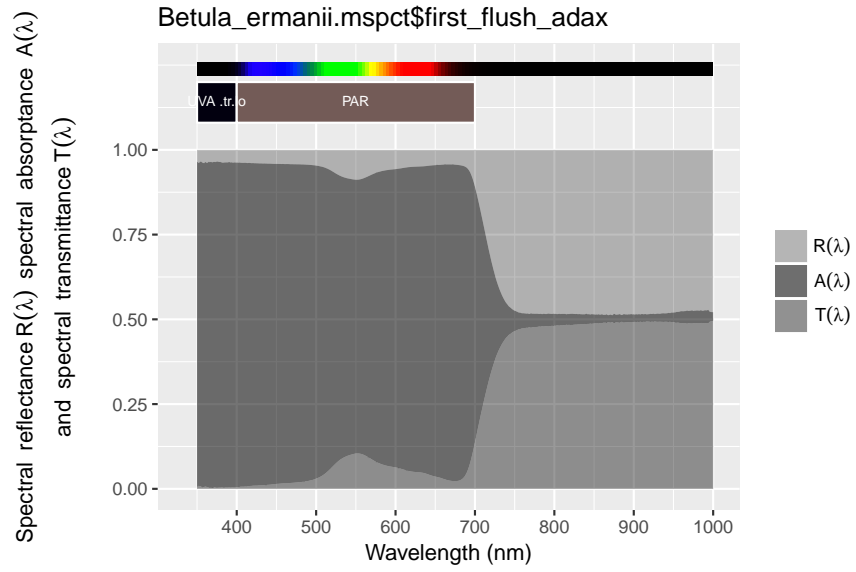
```
plot(Solidago_altissima.mspct$lower_adax)
plot(Solidago_altissima.mspct$lower_abax)
```



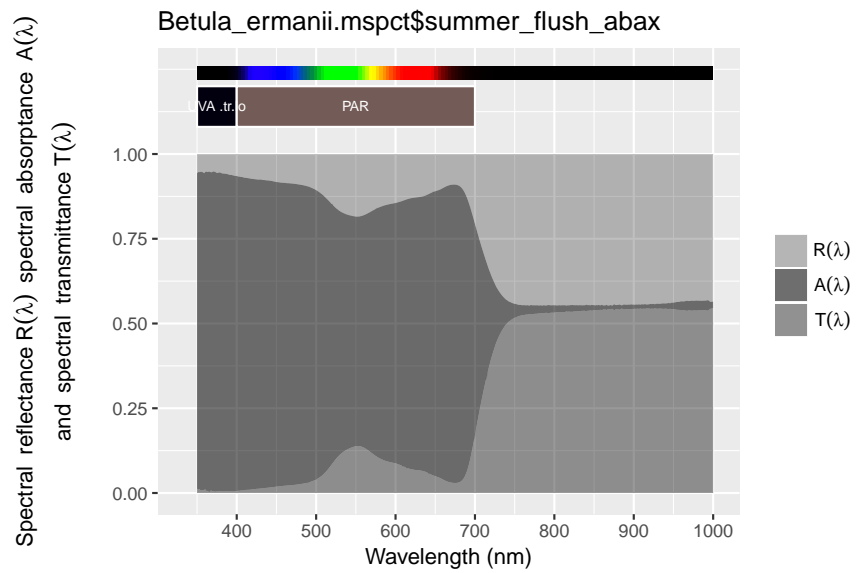
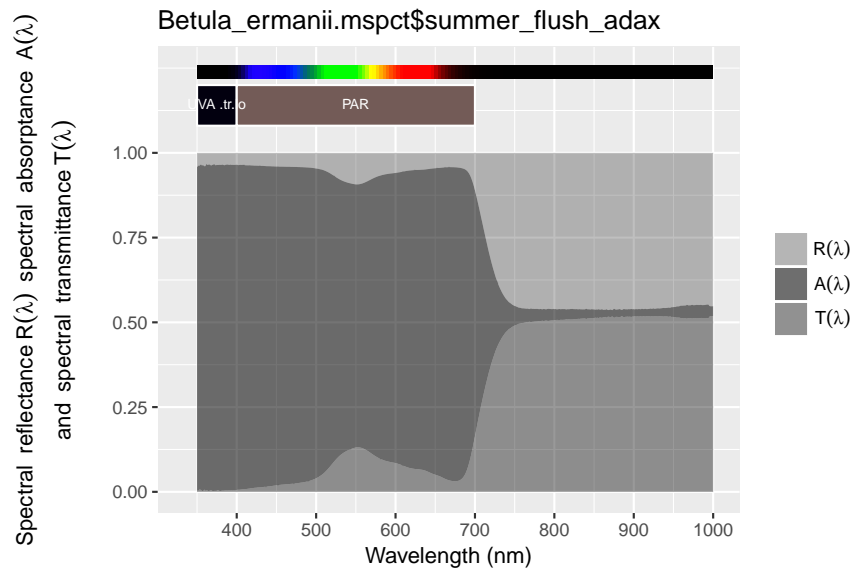
```
plot(Solidago_altissima.mspct$upper_adax)
plot(Solidago_altissima.mspct$upper_abax)
```



```
plot(Betula_ermanii.mspct$first_flush_adax)
plot(Betula_ermanii.mspct$first_flush_abax)
```



```
plot(Betula_ermanii.mspect$summer_flush_adax)
plot(Betula_ermanii.mspect$summer_flush_abax)
```

```
plot(Betula_ermanii.mspect$senesced_adax)
plot(Betula_ermanii.mspect$senesced_abax)
```

