

```
Sys.info()
```

```
##      sysname      release      version      nodename      machine
##      "Windows"    "10 x64"  "build 10586"  "MUSTI"      "x86-64"
##      login        user effective_user
##      "aphalo"     "aphalo"  "aphalo"
```

```
sessionInfo()
```

```
## R version 3.3.1 (2016-06-21)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 10586)
##
## locale:
## [1] LC_COLLATE=English_United Kingdom.1252
## [2] LC_CTYPE=English_United Kingdom.1252
## [3] LC_MONETARY=English_United Kingdom.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United Kingdom.1252
##
## attached base packages:
## [1] tools      stats      graphics  grDevices  utils      datasets  base
##
## other attached packages:
## [1] stringr_1.0.0 knitr_1.13
##
## loaded via a namespace (and not attached):
## [1] magrittr_1.5  formatR_1.4   stringi_1.1.1 highr_0.6      methods_3.3.1
## [6] evaluate_0.9
```

```
library(tibble)
```

```
tibble(a = 1:20, b = 20:1)
```

```
## # A tibble: 20 x 2
##       a     b
##   <int> <int>
## 1     1    20
## 2     2    19
## 3     3    18
## 4     4    17
## 5     5    16
## 6     6    15
```

```
## 7      7      14
## 8      8      13
## 9      9      12
## 10     10     11
## 11     11     10
## 12     12      9
## 13     13      8
## 14     14      7
## 15     15      6
## 16     16      5
## 17     17      4
## 18     18      3
## 19     19      2
## 20     20      1
```

```
library(photobiology)
```

```
source_spct(w.length = 300:500, s.e.irrad = 1)
```

```
## Object: source_spct [201 x 2]
```

```
## Wavelength range 300 to 500 nm, step 1 nm
```

```
## Error in .setupMethodsTables(fdef, initialize = TRUE): trying to
## get slot "group" from an object of a basic class ("NULL") with no slots
```

```
sessionInfo()
```

```
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## Running under: Windows 10 x64 (build 10586)
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```
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```

```
## attached base packages:
```

```
## [1] tools      stats      graphics  grDevices  utils      datasets  base
```

```
##
```

```
## other attached packages:
```

```
## [1] photobiology_0.9.8 tibble_1.1      stringr_1.0.0
```

```
## [4] knitr_1.13
##
## loaded via a namespace (and not attached):
## [1] R6_2.1.2          lazyeval_0.2.0    assertthat_0.1    magrittr_1.5
## [5] formatR_1.4       DBI_0.4-1         dplyr_0.5.0       Rcpp_0.12.6
## [9] lubridate_1.5.6   stringi_1.1.1     highr_0.6         methods_3.3.1
## [13] evaluate_0.9
```