

# Matching sensor overlap

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## The problem

Instruments may measure different spectral ranges using different sensors, resulting in abrupt “jumps” in the reflectance or radiance data. In such cases, the regions between sensors need to be matched, i.e. spliced together.

Unmatched spectra collected with a 3-sensor instrument, such as the SVC HR1024, may look like this:

```
# Path to raw (unmatched) spectra
path_raw = system.file("extdata/svc_raw_and_overlap_matched_serbin/SVC_Files/",
                        package = "spectrolab")

# Read spectra as reflectance and radiance
reflect_raw = read_spectra(path = path_raw,
                          format = "SIG",
                          type = "target_reflectance")
```

```
## Duplicated band values are not allowed!
## Bands updated as follows:
##  band_position original_value updated_value
##           514           975.6      975.6011
##           524          1013.9     1013.9011
```

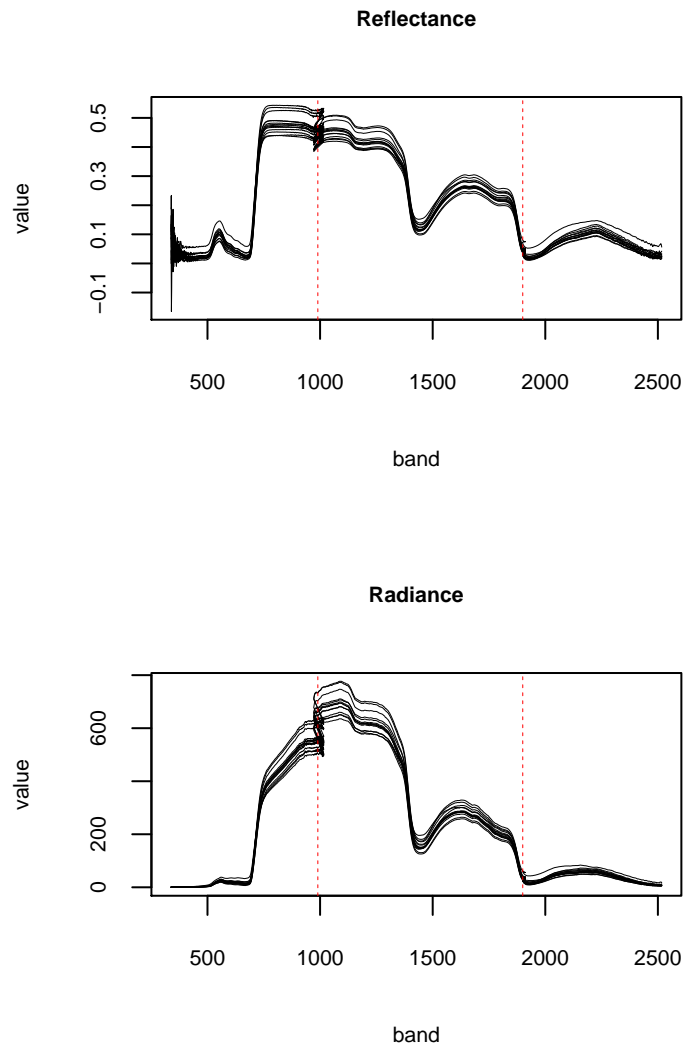
```
radiance_raw = read_spectra(path = path_raw,
                           format = "SIG",
                           type = "target_radiance")
```

```
## Duplicated band values are not allowed!
## Bands updated as follows:
##  band_position original_value updated_value
##           514           975.6      975.6011
##           524          1013.9     1013.9011
```

```
# Sensor overlaps marked with vertical dashed lines
lwd = 0.5
cex = 0.7
par(mfrow = c(2, 1))

plot(reflect_raw, main = "Reflectance",
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)
abline(v = c(990, 1900), col = "red", lty = 2, lwd = lwd)
```

```
plot(radiance_raw, main = "Radiance",
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)
abline(v = c(990, 1900), col = "red", lty = 2, lwd = lwd)
```



## The solution

Use the function `match_sensors` to splice the sensor overlap regions as shown below. You must pass the boundary between sensors using the `splice_at` argument. It is **critical** that you get those bands right and every instrument (even from the same vendor) is different. You can use `plot_interactive` zoom into a particular spectral region and decide what the `splice_at` values should be.

```
# Boundaries between sensors
splice_bands = c(990, 1900)
```

```

# Match the reflectance and radiance data
reflect_matched = match_sensors(x          = reflect_raw,
                                splice_at   = splice_bands,
                                interpolate_wvl = c(5, 1))

radiance_matched = match_sensors(x          = radiance_raw,
                                splice_at   = splice_bands,
                                interpolate_wvl = c(5, 1))

lwd = 0.5
cex = 0.7
par(mfrow = c(2, 1))

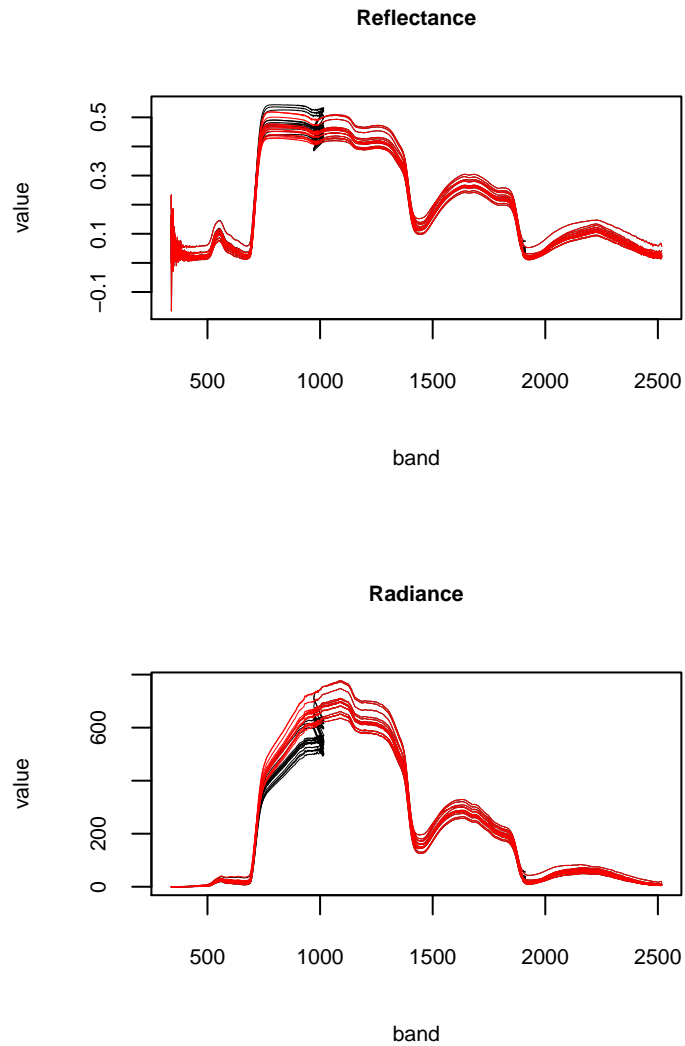
plot(reflect_raw, main = "Reflectance",
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

plot(reflect_matched, col = "red", add = TRUE,
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

plot(radiance_raw, main = "Radiance",
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

plot(radiance_matched, col = "red", add = TRUE,
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

```



And we can check the results from spectrolab's `match_sensors` against SVC's proprietary matching algorithm.

```
path_moc = system.file("extdata/svc_raw_and_overlap_matched_serbin/SVC_Files_moc/",
                        package = "spectrolab")

reflect_moc = read_spectra(path = path_moc,
                           format = "SIG",
                           type = "target_reflectance")

radiance_moc = read_spectra(path = path_moc,
                             format = "SIG",
                             type = "target_radiance")

lwd = 0.5
cex = 0.7
par(mfrow = c(2, 1))
```

```

plot(reflect_moc, main = "Reflectance", col = "black",
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

plot(reflect_matched, col = "red", add = TRUE,
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

plot(radiance_moc, main = "Radiance", col = "black",
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

plot(radiance_matched, col = "red", add = TRUE,
     lwd = lwd, cex.main = cex, cex.lab = cex, cex.axis = cex)

```

