

Resampling spectra

Jose Eduardo Meireles

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`spectrolab` can resample spectra from one resolution to another using the method `resample`. Since version 0.19, `spectrolab` uses a gaussian model that takes the **Full Width at Half Maximum** or **FWHM** to compute the spectrum values at the new wavelengths.

Resampling spectra using inadequate FWHM values can be very problematic. For example, it is common for packages to assume that the FWHM of the

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

s_raw = read_spectra(dir_path)

new_bands = seq(400, 2500, 1)

fwhm_A = make_fwhm(s_raw, new_bands)
fwhm_B = make_fwhm(s_raw, new_bands, return_type = "old")
fwhm_C = 1

AAA = resample_spec_fwhm(s_raw,
                        new_bands = new_bands,
                        fwhm = fwhm_A)
BBB = resample_spec_fwhm(s_raw,
                        new_bands = new_bands,
                        fwhm = fwhm_B)
CCC = resample_spec_fwhm(s_raw,
                        new_bands = new_bands,
                        fwhm = fwhm_C)

plot(s_raw, lwd = 0.2)
plot(AAA, add = TRUE, lwd = 0.1, col = "red")
plot(BBB, add = TRUE, lwd = 0.1, col = "blue")
plot(CCC, add = TRUE, lwd = 0.1, col = "purple")
```

