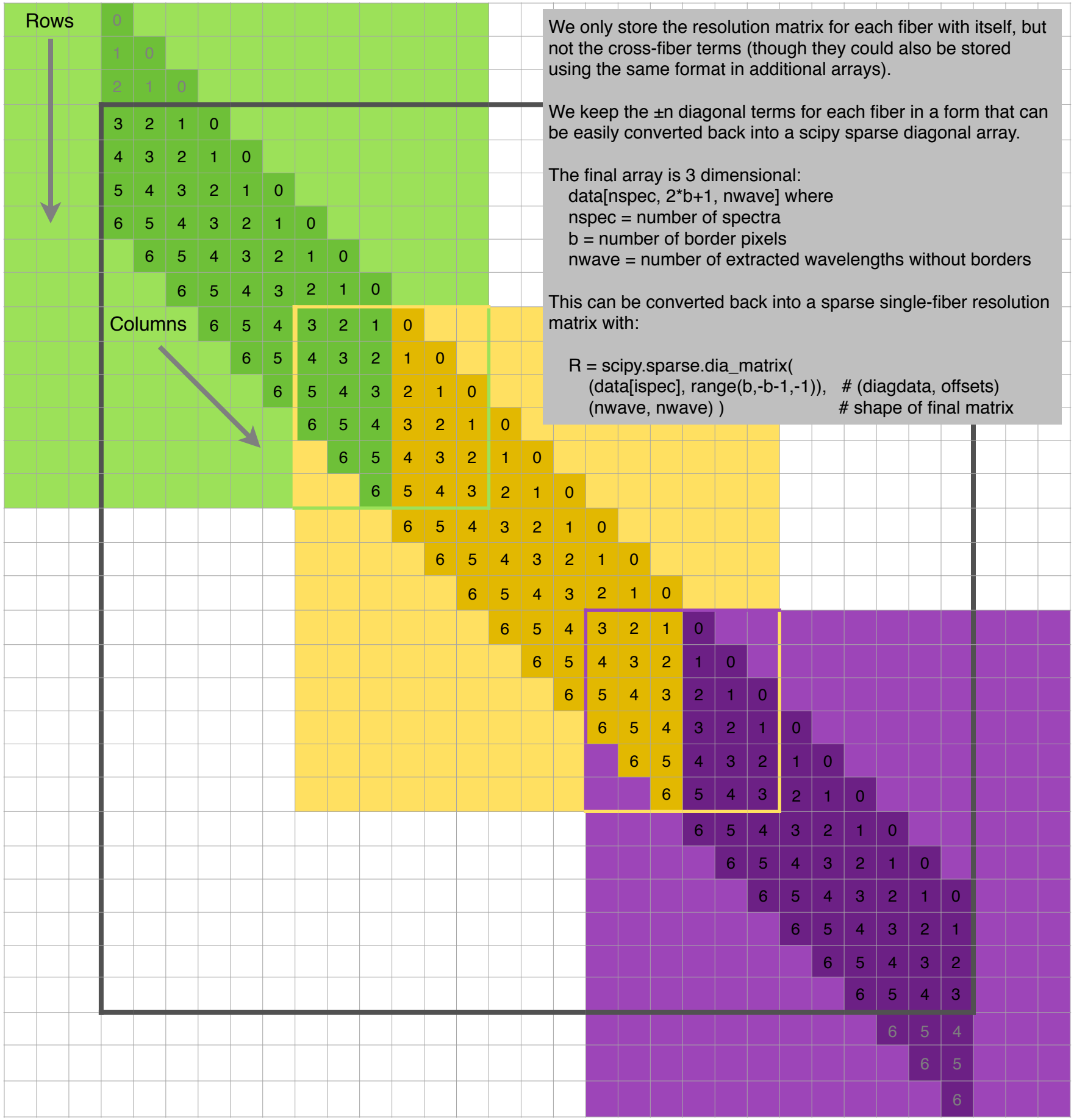
3 extraction subregions; 9 core ± 3 border pixels each



We only store the resolution matrix for each fiber with itself, but not the cross-fiber terms (though they could also be stored using the same format in additional arrays).

We keep the ±n diagonal terms for each fiber in a form that can be easily converted back into a scipy sparse diagonal array.

The final array is 3 dimensional:
data[nspec, 2*b+1, nwave] where
nspec = number of spectra
b = number of border pixels
nwave = number of extracted wavelengths without borders

This can be converted back into a sparse single-fiber resolution matrix with:

```
R = scipy.sparse.dia_matrix(
    (data[ispec], range(b,-b-1,-1)),   # (diagdata, offsets)
    (nwave, nwave) )                   # shape of final matrix
```