## Appendix 2 -

# Calculation of $\mathbf{R}_{\mathbf{0}}$ from Spectral Overlap with MatLab ${ }^{\circledR}$ 

Courtesy of Joshua Vaughan. Used with permission.

> \% This program will calculate the quantity Ro for FRET between given \% donor and acceptor molecules. The user will need to supply a file \% containing the fluorescence spectrum of the donor (two columns, the \% first with the wavelength range in nm, the second with the intensity $\%$ of the fluorescence) and a file containing the absorption spectrum $\%$ of the acceptor (also two columns, the first with the wavelength in $\%$ nanometers, and the second with the absorption of the acceptor in $\%$ molar decadic extinction coefficients).
\% It is assumed that the user will have already cleaned up these spectra by \% performing any necessary baseline corrections, and by chopping the data, \% and including zeros in place of the chopped data. The user will also need \% to supply the refractive index of the solvent used, the quantum yield of $\%$ the donor, and the parameter $K$ (where $K=k^{\wedge} 2$ ), which is usually $2 / 3$.

NOTE: since the absorbance spectrum is being interpolated at the set of \% fluorescence $x$-values, the absorbance spectrum must contain at least the \% same range of $x$-values that the fluorescence spectrum contains, even if \% it means adding some fake $x$ values for which the corresponding y value \% is zero. One way to do this would be to use absorbance data that ranges \% from 500-800 nm, and fluorescence data that ranges from 532-790 nm.

```
q=.95; % Enter in the quantum yield of the donor
K=2/3; % Enter in the value K (usually 2/3)
n=1.361;
% Before Matlab can load your file, you must change the current directory to
% the directory containing your data (you can use unix commands to do this).
```

```
f=load('dcm_fl.txt'); % Load in the fluorescence spectrum
```

f=load('dcm_fl.txt'); % Load in the fluorescence spectrum
a=load('mg_abs.txt'); % Load in the absorption spectrum

```
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```

\% Interpolate the absorption curve at the set of fluorescence $x$ values.
a1=[f(:,1) interp1(a(:,1),a(:,2),f(:,1))];
f1=[(1e7)*(f(:,1).^-1) f(:,2)]; \% Rewrite the $x$ axis in wavenumbers
a2=[(1e7)*(a1(:,1).^-1) a1(:,2)]; \% Rewrite the $x$ axis in wavenumbers
A=sum(diff(f1(:,1)).*f1(2:end,2)); \% Calculate area of fluorescence curve
f2=[f1(:,1) f1(:,2)/abs(A)]; \% Unit normalize the fluorescence. Note that
\% this means the fluorescence is now in units
\% of reciprocal wavenumbers, or cm.

```
% Calculate the overlap function 0.
0=[f2(:,1) (a2(:,2).*f2(:,2))./(f2(:,1).^4)];
% Calculate the overlap integral J.
J=sum(abs(diff(f2(:,1))).*0(2:end, 2));
% Calculate Ro [cm].
    Ro=((8.8e-25)*(K*q/(n^4))*abs(J))^(1/6)
```

