

# eSPC, an Online Data Analysis Platform for Molecular Biophysics

## ChiraKit 1.0 User Documentation

February 2026

## **Table of Contents**

### [1. Import data](#)

[1.1. Input file](#)

[1.2. Parameters for molar ellipticity / extinction](#)

[1.3. Processing](#)

### [2. Analysis](#)

[2.1. Creating a dataset](#)

[2.2. Thermal unfolding](#)

[2.3. Chemical unfolding](#)

[2.4. Custom analysis](#)

[2.5. Comparison of spectra](#)

### [3. Spectra decomposition](#)

[3.1. Singular value decomposition \(SVD\)](#)

[3.2. Principal component analysis \(PCA\)](#)

[3.3. Basis spectrum inversion](#)

[3.4. Change of basis](#)

[3.5. Alternative formulation for the explained variance](#)

### [4. Protein secondary structure estimation](#)

[4.1. The Selcon method](#)

[4.2. The SESCA method](#)

### [5. Peptide helicity estimation](#)

[5.1. The ensemble model](#)

[Contact details](#)

## 1. Import data

### 1.1. Input file

ChiraKit can parse many different types of files:

A) A comma-separated-values (**.csv**) file with a header, and two or three columns. In the case of two columns, the first contains the wavelength and the second the CD signal. In the case of three columns, the first contains the wavelength, the second the sample name, and the third the CD signal. In both cases the first column must be called 'wavelength'.

	Standard	Standard	Standard
1	wavelength	time	CD_signal
2	220	1	10
3	220	2	20
4	220	3	30
5	220	4	40

**Figure 1.** Example of a valid CSV format.

B) A csv file (**.csv**) with a header and **more than three columns**: 'wavelength', CD signal of the first sample , ..., CD signal of the n-th sample.The first column must be called 'wavelength' or 'xydata'.

	Standard	Standard	Standard	Standard
1	wavelength	CD_signal_A	CD_signal_B	CD_signal_C
2	220	1	2	3
3	221	1	2	3
4	222	1	2	3
5	223	1	2	3

**Figure 2.** Example of a valid CSV format. Each column represents one CD curve.

C) A csv file (**.csv**) with header lines containing the metadata. The metadata keys and values should be separated by ':'. The CD data should start two lines after a line containing the column heading of 'Wavelength' and should be arranged in columns. The first column has the wavelength data (in nm), and the subsequent columns have the spectral data (e.g., scan repeats). This type of file is exported by the ProData software from AppliedPhotophysics™.

Available Dimensions:		2
Wavelength	Wavelength: 180nm - 290nm	Step Size: 1nm
Repeat	2 repeats in set.	-iter option selected
Available Properties:		1
CircularDichroism		
Data:		
CircularDichroism		
Wavelength	Repeat	
	0	1
290	-0.313281	-0.284654
289	-0.353384	-0.46977
288	-0.488774	-0.488609
287	-0.277936	-0.486426
286	-0.4969	-0.472476

**Figure 3.** Example of a ProData generated CSV.

D) A PCDDB file (**.pcd**, Protein Circular Dichroism Data Bank format) with header lines containing the metadata. The metadata keys and values are organised into two columns, with the second column starting after the 60th character. The CD data starts after the first line containing 'DATA' and 'wavelength', and is arranged in columns. The first column has the wavelength data (in nm), and the subsequent columns have the spectra data (e.g., 1. Wavelength. 2. Final. 3. HT. 4.Smoothed. 5. Avg. Sample. 6. Avg. Baseline.).

Publication Journal: Bioinformatics  
 Publication Title: A reference database for circadian rhythms  
 Publication Volume: 22  
 Publication Pages: 1955-1962  
 Depositor Name: Andrew Miles  
 Department/School name: Crystallography  
 University/Institution/Corporation: Birkbeck  
 Depositor Country: United Kingdom  
 Name of Principal Investigator (if not depositor): B.A. Wallace  
 DATA (1. Wavelength. 2. Final. 3. HT. 4. Smoothed. 5. Avg. Sample. 6. Avg. Baseline.)  
 280.0 8.98482E-02 3.84900E+02 8.75000E-02 1.63333E+00 1.50000E+00  
 279.0 -1.28364E-02 3.84000E+02 -1.25000E-02 1.60000E+00 1.56667E+00

**Figure 4.** Example of a PCDDB file. Original source:

<https://pcddb.cryst.bbk.ac.uk/deposit/CD0000003000&dl=1#>

E) A 'generic' file (.gen, CDTool format) with header lines containing the metadata. The metadata keys and values are organised into two columns, separated by tabs. The CD data starts after the first line with more than three tab divided columns. The first column has the wavelength data (in nm), and the subsequent columns have the spectral data (e.g., 'Final Processed Spectrum', 'HT values (from raw spectrum 1)'). Duplicated or missing data is removed.

```

Smoothing window      5
PDB                  1ed9
Swissprot            P00634
Code                 Lees, J.G., Wien, F., Miles, A.J. & Wallace, B.A., 2006 Bioinformatics A refere
structure space 22 1955-1962
279.0    5.62969E-02    1.53648E+00    5.62969E-02    0.00000E+00    0.00000E+00    0.00000E+00
278.0    2.21733E-01    1.53303E+00    2.21733E-01    0.00000E+00    0.00000E+00    0.00000E+00
277.0    4.74813E-02    1.52912E+00    4.74813E-02    0.00000E+00    0.00000E+00    0.00000E+00

```

**Figure 5.** Example of a ‘generic’ file. Original source:  
<https://pcddb.cryst.bbk.ac.uk/deposit/CD0000002000&dl=1#>

F) A text file (**.dat**) with header lines containing the metadata. The metadata keys and values should be separated by ‘:’. The CD data starts two lines after the line containing ‘MDCDATA’ in it and is arranged in columns. The first column has the wavelength data (in nm), and the subsequent columns have the spectral data. There could be one or more scans separated in blocks. The voltage data is read from the column called ‘CD\_Dynode’.

```
Averaging Time      : 1.000 seconds
Settling Time      : 0.333 seconds
Multi-Scan Wait   : 1.00 seconds

$DATA
$MDCNAM:Scan_#1
$MDCDATA:1:14:2:3:4:9
    X  CD_Signal  CD_Error  CD_Current_(Abs)  CD_Delta_Absorbance  CD_Dynode  Jacket_Temp.
280.000  0.000  0.047  1.013  0.000  242.6  19.99
279.000  -0.006  0.083  1.013  -0.000  242.9  19.98
278.000  0.044  0.148  1.013  0.000  243.2  19.99
```

**Figure 6.** Example of a valid text file. Original source:  
<https://github.com/samirelanduk/CDtool/blob/master/ftests/files/three-aviv-baseline.dat>

G) Aarhus synchrotron data file (**.dx**, where x means any number) with header lines containing the metadata. The metadata keys and values are separated into two columns where the second column starts after the 32th character (or the character ‘:’). The CD data starts after the first line containing ‘Lambda’ and ‘CD’, and is arranged in columns. The first column has the wavelength data (in nm), the second column has the spectral data (‘CD/mdeg’), the fifth column the voltage data (‘Servo\_Volts’), and the eighth column the temperature data (‘temperature’).

```
;Grating / CD slit          LEG / 08.75
; Comments:
; Sample0: Water
; Cell type: AS 121a123
; 330-170nm 1nm 20av 1sc Slit 8.75mm
;Lambda      CD/mdeg        Y_Comp./mdeg    DC_Bias      Servo_Volts    Z_Motor      Beam_current  temperature
330.000    1.4818         0.0095       6.82440     4.37090      0.3505      180.3981     25.00
329.000    1.0437         0.0095       6.82440     4.36770      0.2660      180.3248     25.00
```

**Figure 7.** Example of a CD data file generated by the AU-SRCD facility at ASTRID2.

H) A csv file (**.csv**) containing a line with the words ‘ORIGIN’ and ‘JASCO’. The CD data is arranged in columns and the column names are defined between the lines ‘XUNITS’ and ‘FIRSTX’. This type of file is exported by Jasco™ circular dichroism instruments.

XUNITS	NANOMETERS
YUNITS	CD [mdeg]
Y2UNITS	HT [V]
Y3UNITS	ABSORBANCE
FIRSTX	260
LASTX	180
NPOINTS	801
FIRSTY	-0, 28448
MAXY	0, 86205
MINY	-8, 74658
XYDATA	
260	-0, 284475 254, 707 0, 758667
259, 9	-0, 279734 254, 753 0, 759227

**Figure 8.** Example of a CD data file exported from a Jasco™ circular dichroism instrument.

I) A csv file (**.csv**) with header lines containing the metadata. The metadata keys and values should be separated by ':'. The CD data starts two lines after the line containing 'Wavelength' and 'Temperature' in it and is ordered in columns. The first column has the wavelength data (in nm), and the subsequent columns have the spectral data (one column per temperature). The associated temperature data is available one line before the CD data starts. This type of file is exported by the ProData software from AppliedPhotophysics™.

## 1.2. Parameters for molar ellipticity / extinction

Each input file can be associated with a certain set of experimental parameters (Box '2. Parameters for molar ellipticity / extinction') . The expected units to input in ChiraKit are:

Molecular weight: Dalton (g/mol)

Number of chromophores: Unitless

Concentration: mg/ml

Path length: millimetre

These parameters are useful to compare different samples. Indeed, the CD signal can be normalised based on the sample concentration (C), cell path length (L), and molecular weight (M) or mean unit molecular weight (M<sub>u</sub>).

A summary of the CD units is presented below.

Name	Formula	Units
Differential absorbance	A <sub>l</sub> - A <sub>r</sub>	Unitless

Differential milliabsorbance	Absorbance / 1000	Unitless
Molar extinction	Absorbance * M / (C*L)	Lts * mol <sup>-1</sup> * cm <sup>-1</sup>
Mean unit molar extinction ( $\Delta\epsilon$ ) <sup>1</sup>	Absorbance * M <sub>u</sub> / (C*L)	Lts * mol <sup>-1</sup> * cm <sup>-1</sup> * chromophores <sup>-1</sup>
Degrees	Absorbance * 32.98	Degrees (°)
Millidegrees	Degrees / 1000	m°
Molar ellipticity	Degrees * M * 100 / (C*L)	°*cm <sup>2</sup> * dmol <sup>-1</sup>
Mean unit molar ellipticity <sup>1</sup>	Degrees * M <sub>u</sub> * 100 / (C*L)	°*cm <sup>2</sup> * dmol <sup>-1</sup> * chromophores <sup>-1</sup>

**Table 1.** Units of CD Measurement.  $A_l$  and  $A_r$  refer respectively to the left- and right-circularly polarised light. ‘chromophores’ refers to the total number of chromophoric units. For measurements of polypeptides in the far-UV region (185 - 240 nm), the number of peptide bonds is used for normalisation, because the amide bond is the main contributor to the CD signal.<sup>1</sup>

### 1.3. Processing

Given a selection of spectra (column ‘Spectrum/a 1’ inside the box ‘3. Processing’), we can:

- 1) Subtract another spectrum (column ‘Spectrum 2’)
- 2) Add another spectrum (column ‘Spectrum 2’)
- 3) Smooth them using a Savitzky-Golay filter (window size of 3, 6, 8 or 10 nm)
- 4) Average them
- 5) Average them in batch mode
- 6) Zero them by subtracting the mean signal within a selected wavelength range interval (3, 5, 10, 20 or 40 nm)

The ‘subtract’, ‘sum’, ‘smooth’ and ‘zero’ operations will produce as many spectra as defined in the column ‘Spectrum/a 1’. The ‘average’ operation will generate one spectrum. The ‘batch average’ operation depends on the selected ‘N’. For instance, if we have six spectra and select ‘N’ equal to 3, we will generate two new spectra.

Regarding the ‘subtract’ and ‘sum’ operations, the data must have been measured with the same wavelength step and wavelength range. If not, a linear interpolation can be activated. In that case, 1) the resulting spectrum will cover the region where

---

<sup>1</sup> Kahn, Peter C. "[16] The interpretation of near-ultraviolet circular dichroism." Methods in enzymology. Vol. 61. Academic Press, 1979. 339-378.

the spectra overlap and 2) a linear interpolation will be performed, implying that the new spectrum will be computed at all the wavelength data points present in both spectra.

The following behaviour is applied for the high tension voltage curves. For the subtract, addition, smooth or zero operations, the generated spectra will have the same high tension voltage curve as the spectra selected in the column ‘Spectrum/a 1’. For the (batch) average operation, the high tension voltage curves will be averaged.

## 2. Analysis

### 2.1. Creating a dataset

When generating a dataset for the thermal /chemical unfolding analysis, custom analysis, or spectra comparison module, the CD signal will be merged based on the wavelength data. In other words, wavelengths present in all spectra will be used. Non-shared wavelengths will be discarded.

### 2.2. Thermal unfolding

#### 2.2.1. Equilibrium two-state model (from monomer to tetramer)<sup>2,3</sup>

We assume that the protein only exists in the native (folded) or unfolded state and that there is an equilibrium between these two states given by the unfolding reaction  $F_n \rightleftharpoons nU$ . The signal is described by the following equation:

$$Signal(T) = f_N(k_N T + b_N) + f_U(k_U T + b_U)n \quad (1)$$

where  $f_N$  and  $f_U$  are the folded and unfolded fractions,  $T$  is the temperature in Kelvin units,  $b_N$  and  $b_U$  are the baseline terms, and  $k_N$  and  $k_U$  are the slopes to take into account the temperature dependence.

The concentration of [U] and [F] depend on the equilibrium unfolding constant  $K_u$ :

---

<sup>2</sup> Santoro, M. M., & Bolen, D. W. (1988). Unfolding free energy changes determined by the linear extrapolation method. 1. Unfolding of phenylmethanesulfonyl. alpha.-chymotrypsin using different denaturants. *Biochemistry*, 27(21), 8063-8068.

<sup>3</sup> Bedouelle, H. (2016). Principles and equations for measuring and interpreting protein stability: From monomer to tetramer. *Biochimie*, 121, 29-37.

$$K_u(T) = \frac{[U]^n}{[F_n]} \quad (2)$$

where  $K_u(T)$  is a function of the thermodynamic parameters  $T_m$  (temperature at which  $K_u(T)$  equals one),  $\Delta H$  (enthalpy of unfolding), and  $\Delta Cp$  (heat capacity of unfolding):

$$K_u(T) = e^{-\Delta G / R_{gas} T} \quad (3)$$

$$\Delta G = \Delta H(1 - \frac{1}{T_m}) - \Delta Cp(T_m - T + T \log(\frac{T}{T_m})) \quad (4)$$

where  $R_{gas}$  is the gas constant. For monomers,  $f_N$  and  $f_U$  can be calculated from  $K_u(T)$  only, while for oligomers, the protein concentration is also required.

## 2.2.2. Equilibrium three-state model (with a monomeric intermediate)

We assume that the protein exists in the native (folded), intermediate or unfolded state and that there is an equilibrium between these three states given by the reactions  $F_n \rightleftharpoons nI$  and  $I \rightleftharpoons U$ .<sup>4</sup> The signal is described by the equation:

$$Signal(T) = f_N(k_N T + b_N) + f_U(k_U T + b_U)n + f_I(b_I)n \quad (5)$$

where  $f_N$ ,  $f_I$  and  $f_U$  are the fraction of protein in the folded intermediate and unfolded states,  $T$  is the temperature in Kelvin units,  $b_N$ ,  $b_I$  and  $b_U$  are the baseline terms, and  $k_N$  and  $k_U$  are the slopes to take into account the temperature dependence (of the folded and unfolded states).

The concentration of  $[U]$ ,  $[F]$  and  $[I]$  depend on the unfolding constant  $K_1(T)$  and  $K_2(T)$ :

$$K_1(T) = \frac{[I]^n}{[F_n]} \quad (6)$$

$$K_2(T) = \frac{[U]}{[I]} \quad (7)$$

---

<sup>4</sup> Bedouelle, Hugues. "Principles and equations for measuring and interpreting protein stability: From monomer to tetramer." *Biochimie* 121 (2016): 29-37.

where  $K_x(T)$  ( $x = 1$  or  $2$ ) is a function of the thermodynamic parameters  $T_x$  (temperature at which  $K_x(T)$  equals one),  $\Delta H_x$  (enthalpy of unfolding), and  $\Delta C_{p,x}$  (heat capacity of unfolding):

$$K_x(T) = e^{-\Delta G_x / R_{gas} T} \quad (8)$$

$$\Delta G_x = \Delta H_x(1 - \frac{1}{T_x}) - \Delta C_{p,x}(T_x - T + T \log(\frac{T}{T_x})) \quad (9)$$

where  $R_{gas}$  is the gas constant. For monomers,  $f_N$ ,  $f_I$  and  $f_U$  can be calculated from  $K_1(T)$  and  $K_2(T)$  only, while for oligomers, the protein concentration is also required.

For monomers,  $\Delta C_{p,x}$  are assumed to be zero, or  $\Delta C_{p,1}$  is fitted globally based on the total  $\Delta C_{p,th}$  given by the user ( $\Delta C_{p,th} = \Delta C_{p,1} + \Delta C_{p,2}$ ). For dimers,  $\Delta C_{p,x}$  are assumed to be zero, or  $\Delta C_{p,1}$  is fitted globally based on the total  $\Delta C_{p,th}$  given by the user ( $\Delta C_{p,th} = \Delta C_{p,1} + 2\Delta C_{p,2}$ ). For trimers and tetramers,  $\Delta C_{p,th}$  are assumed to be zero.

### 2.2.3. Equilibrium three-state model (with a n-meric intermediate)

We assume that the protein exists in the native (folded), intermediate or unfolded state and that there is an equilibrium between these three states given by the reactions  $F_n \rightleftharpoons I_n$  and  $I_n \rightleftharpoons nU$ .<sup>5</sup> The signal is described by the equation:

$$Signal(T) = f_N(k_N T + b_N) + f_U(k_U T + b_U)n + f_I(b_I) \quad (10)$$

where  $f_N$ ,  $f_I$  and  $f_U$  are the fraction of protein in the folded intermediate and unfolded states,  $T$  is the temperature in Kelvin units,  $b_N$ ,  $b_I$  and  $b_U$  are the baseline terms, and  $k_N$  and  $k_U$  are the slopes to take into account the temperature dependence (of the folded and unfolded states).

The concentration of  $[U]$ ,  $[F]$  and  $[I]$  depend on the unfolding constant  $K_1(T)$  and  $K_2(T)$ :

$$K_1(T) = \frac{[I_n]}{[F_n]} \quad (11)$$

---

<sup>5</sup> Bedouelle, Hugues. "Principles and equations for measuring and interpreting protein stability: From monomer to tetramer." *Biochimie* 121 (2016): 29-37.

$$K_x(T) = \frac{[U]^n}{[I_n]} \quad (12)$$

where  $K_x(T)$  ( $x = 1$  or  $2$ ) is a function of the thermodynamic parameters  $T_x$  (temperature at which  $K_x(T)$  equals one),  $\Delta H_x$  (enthalpy of unfolding), and  $\Delta C_{p,x}$  (heat capacity of unfolding):

$$K_x(T) = e^{-\Delta G_x / R_{gas} T} \quad (13)$$

$$\Delta G_x = \Delta H_x \left(1 - \frac{1}{T_x}\right) - \Delta C_{p,x} \left(T_x - T + T \log\left(\frac{T}{T_x}\right)\right) \quad (14)$$

where  $R_{gas}$  is the gas constant. For monomers,  $f_N$ ,  $f_I$  and  $f_U$  can be calculated from  $K_1(T)$  and  $K_2(T)$  only, while for oligomers, the protein concentration is also required.

For monomers,  $\Delta C_{p,x}$  are assumed to be zero, or  $\Delta C_{p,1}$  is fitted globally based on the total  $\Delta C_{p,th}$  given by the user ( $\Delta C_{p,th} = \Delta C_{p,1} + \Delta C_{p,2}$ ). For dimers,  $\Delta C_{p,x}$  are assumed to be zero, or  $\Delta C_{p,1}$  is fitted globally based on the total  $\Delta C_{p,th}$  given by the user ( $\Delta C_{p,th} = \Delta C_{p,1} + \Delta C_{p,2}$ ). For trimers,  $\Delta C_{p,th}$  are assumed to be zero.

#### 2.2.4. Irreversible two-state model

We assume that the protein only exists in the native (folded) or unfolded state and that the unfolding reaction is irreversible ( $N \rightarrow U$ ).<sup>6</sup> The signal is described by the equation:

$$Signal(T) = f_u(k_u T + b_u) + f_n(k_n T + b_n) \quad (15)$$

where  $T$  is the temperature,  $k_N$ ,  $b_N$  are the slope and intercept of the pre-transition baseline (native), and  $k_u$  and  $b_u$  are the slope and intercept of the post-transition (unfolded) baseline.

The fraction of natively folded molecules  $f_n$  as a function of temperature ( $T$ ) is given by the differential equation:

$$\frac{\partial f_n}{dT} = \frac{-k(T)f_n}{v} \quad (16)$$

---

<sup>6</sup> Mazurenko, Stanislav, et al. "Exploration of protein unfolding by modelling calorimetry data from reheating." *Scientific reports* 7.1 (2017): 16321.

where  $v$  is the scan rate (in degrees per minute), and  $k(T)$  is the rate constant ( $\text{min}^{-1}$ ). The rate constant can be derived from the modified Arrhenius formula:

$$k(T) = e^{(\frac{-Ea}{R}(\frac{1}{T} - \frac{1}{T_f}))} \quad (17)$$

where  $R$  is the gas constant,  $Ea$  is the activation energy, and  $T_f$  is the temperature where  $k(t)$  equals one.  $f_n$  is assumed to be one at the lowest measured temperature.

#### 2.2.5. Irreversible three-state model

We assume that the protein exists in the native (folded), intermediate or unfolded state. The first step is reversible and the second one is irreversible ( $N \rightleftharpoons I \rightarrow U$ ). The signal is described by the equation:

$$\text{Signal}(T) = f_u(k_U T + b_U) + f_n(k_N T + b_N) + f_i(b_I) \quad (18)$$

where  $T$  is the temperature,  $k_N$ ,  $b_N$  are the slope and intercept of the pre-transition baseline (native),  $k_U$  and  $b_U$  are the slope and intercept of the post-transition (unfolded) baseline, and  $b_I$  is the baseline of the intermediate state.  $f_u$ ,  $f_n$  and  $f_i$  are respectively the unfolded, folded and intermediate fractions, which are calculated as:

$$\frac{\partial f_u}{dT} = \frac{-k(T)K(T)(1-f_u)}{v(K(T)+1)} \quad (19)$$

$$f_n = \frac{(1-f_u)}{1+K(T)} \quad (20)$$

$$f_i = 1 - f_n - f_u \quad (21)$$

where  $v$  is the scan rate (in degrees per minute), and  $k(T)$  is the rate constant ( $\text{min}^{-1}$ ). The rate constant can be derived from the modified Arrhenius formula (equation 12).  $K(T)$  is the equilibrium unfolding constant ( $N \rightleftharpoons I$ ) and can be calculated as in equation 3 ( $\Delta Cp$  is assumed to be zero).

#### 2.2.6. Local and global parameters

All curves are simultaneously fitted, constrained to share the same values for the thermodynamic parameters (e.g.,  $\Delta H$ ,  $T_1$ ,  $Ea$ ,  $T_f$ ). The baseline and slopes are allowed to vary, and users also have the option to set the slopes ( $k_u$ ,  $k_n$ ) to zero.

#### 2.2.7. Fitting errors

The standard deviation of all fitted parameters is computed using the square root of diagonal values from the fit parameter covariance matrix reported by `scipy.curve_fit` function. These values are an approximation (**underestimation**) of the real errors. Relative errors are calculated as  $100 * (std(\hat{\theta}) / \hat{\theta})$  where  $\hat{\theta}$  refers to the estimate of the parameter and  $std(\hat{\theta})$  to the standard deviation.

#### 2.2.8. Peptide helix-coil transition

If a peptide adopts only helical or coiled states, the mean unit molar ellipticity at 222 nm ( $[\Theta]_{222}$ ) can be used to obtain thermodynamic parameters.<sup>7</sup>

$$[\Theta]_{222} = \frac{1}{N_{pep}} \sum_{i=1}^M p_i (n_{H,i} [\Theta]_H + n_{C,i} [\Theta]_C) \quad (22)$$

where each i-th conformer has  $n_{H,i}$  helix and  $n_{C,i}$  coil peptide units. These contribute  $[\Theta]_H$  and  $[\Theta]_C$  to the total CD signal.  $p_i$  is the probability of the i-th conformer.  $[\Theta]_H$  and  $[\Theta]_C$  are known parameters.

The  $p_i$  probabilities can be calculated from the partition function  $Q$ , which is defined by two parameters: the nucleation parameter ( $v$ ) and the propagation parameter ( $w$ ).  $v$  is assumed to be constant (equal to 0.07), while  $w$  is temperature-dependent and expressed as:

$$w(T) = e^{(-\frac{1}{R}(\frac{\Delta G_0}{T_0} + \Delta H(\frac{1}{T} - \frac{1}{T_0}) + \Delta C_p(1 - \frac{T_0}{T} - \log(\frac{T}{T_0}))))} \quad (23)$$

where the thermodynamic parameters  $\Delta G_0$ ,  $\Delta H$  and  $\Delta C_p$  are given at the reference temperature  $T_0 = 0^\circ C$  and  $R$  is the gas constant.  $\Delta C_p$  is assumed to be temperature-independent.

---

<sup>7</sup> Zavrtanik, Uroš, Jurij Lah, and San Hadži. "Estimation of Peptide Helicity from Circular Dichroism Using the Ensemble Model." *The Journal of Physical Chemistry B* 128.11 (2024): 2652-2663.

More details can be found in the original publication: [Uroš et al., 2024](#)

## 2.3. Chemical unfolding (and the linear extrapolation model)

### 2.3.1. Equilibrium two-state (from monomer to tetramer)

The equilibrium two-state model assumes a linear dependence of stability on the denaturant concentration.<sup>8,9</sup> The signal is expressed by the following equation:

$$\text{Signal}(D) = f_N(D)(k_N D + b_N) + f_U(D)(k_U D + b_U)n \quad (24)$$

where  $f_N$  and  $f_U$  are the folded and unfolded fractions,  $D$  is the denaturant concentration in molar units,  $b_N$  and  $b_U$  are the baseline terms, and  $k_N$  and  $k_U$  are the slopes to take into account the linear dependence of the signal on  $D$ .

The concentration of [U] and [F] depend on the equilibrium unfolding constant  $K_u$ :

$$K_u(D) = \frac{[U]^n}{[F_n]} \quad (25)$$

$$K_u(T) = e^{-\Delta G(D) / R_{gas} T} \quad (26)$$

where  $T$  is the temperature in Kelvin units and  $R_{gas}$  is the gas constant. Assuming a linear dependence of stability on the denaturant concentration,  $\Delta G(D)$  can be expressed as

$$\Delta G(D) = M(D50 - D) \quad (27)$$

where  $D50$  is the denaturant concentration at which 50% of the molecules are folded and  $M$  the slope  $\frac{\partial \Delta G}{\partial D}$ .

For monomers,  $f_N$  and  $f_U$  can be calculated from  $K_u(D)$  only, while for oligomers, the protein concentration is also required.

<sup>8</sup> Pace,C.N. and Hermans,J. (1975) The stability of globular protein. *CRC Crit. Rev. Biochem.*, **3**, 1–43.

<sup>9</sup> Myers,J.K., Pace,C.N. and Scholtz,J.M. (1995) Denaturant m values and heat capacity changes: relation to changes in accessible surface areas of protein unfolding. *Protein Sci.*, **4**, 2138–2148.

### 2.3.2. Equilibrium three-state (with a monomeric intermediate)

We assume that the protein exists in the native (folded), intermediate or unfolded state and that there is an equilibrium between these three states given by the reactions  $F_n \rightleftharpoons nI$  and  $I \rightleftharpoons U$ .<sup>10</sup> The signal is described by the equation:

$$Signal(D) = f_N(k_N D + b_N) + f_U(k_U D + b_U)n + f_I(b_I)n \quad (28)$$

where  $f_N$ ,  $f_I$  and  $f_U$  are the fraction of protein in the folded intermediate and unfolded states,  $D$  is the denaturant agent concentration in molar units,  $b_N$ ,  $b_I$  and  $b_U$  are the baseline terms, and  $k_N$  and  $k_U$  are the slopes to take into account the linear dependence of the signal on  $D$  (of the folded and unfolded states).

The concentration of  $[U]$ ,  $[F]$  and  $[I]$  depend on the unfolding constant  $K_1(D)$  and  $K_2(D)$ :

$$K_1(D) = \frac{[I]^n}{[F_n]} \quad (29)$$

$$K_2(D) = \frac{[U]}{[I]} \quad (30)$$

where  $K_x(D)$  ( $x = 1$  or  $2$ ) is a function of the “thermodynamic” parameters  $D50_x$  (concentration at which  $K_x(D)$  equals one) and  $M_x$  (equal to  $\frac{\partial \Delta G_x}{\partial D}$ ):

$$K_x(D) = e^{-\Delta G(D)_x / R_{gas} T} \quad (31)$$

where  $T$  is the temperature in Kelvin units and  $R_{gas}$  the gas constant.

For monomers,  $f_N$ ,  $f_I$  and  $f_U$  can be calculated from  $K_1(D)$  and  $K_2(D)$  only, while for oligomers, the protein concentration is also required.

### 2.3.3. Equilibrium three-state (with a n-meric intermediate)

---

<sup>10</sup> Bedouelle, Hugues. "Principles and equations for measuring and interpreting protein stability: From monomer to tetramer." *Biochimie* 121 (2016): 29-37.

We assume that the protein exists in the native (folded), intermediate or unfolded state and that there is an equilibrium between these three states given by the reactions  $F_n \rightleftharpoons I_n$  and  $I_n \rightleftharpoons nU$ .<sup>11</sup> The signal is described by the equation:

$$Signal(D) = f_N(k_N D + b_N) + f_U(k_U D + b_U)n + f_I(b_I) \quad (32)$$

where  $f_N$ ,  $f_I$  and  $f_U$  are the fraction of protein in the folded intermediate and unfolded states,  $D$  is the denaturant agent concentration in molar units,  $b_N$ ,  $b_I$  and  $b_U$  are the baseline terms, and  $k_N$  and  $k_U$  are the slopes to take into account the linear dependence of the signal on  $D$  (of the folded and unfolded states).

The concentration of  $[U]$ ,  $[F]$  and  $[I]$  depend on the unfolding constant  $K_1(D)$  and  $K_2(D)$ :

$$K_1(D) = \frac{[I_n]}{[F_n]} \quad (33)$$

$$K_2(D) = \frac{[U]^n}{[I]} \quad (34)$$

where  $K_x(D)$  ( $x = 1$  or  $2$ ) is a function of the “thermodynamic” parameters  $D50_x$  (concentration at which  $K_x(D)$  equals one) and  $M_x$  (equal to  $\frac{\partial \Delta G_x}{\partial D}$ ):

$$K_x(D) = e^{-\Delta G(D)_x / R_{gas} T} \quad (35)$$

where  $T$  is the temperature in Kelvin units and  $R_{gas}$  the gas constant.

For monomers,  $f_N$ ,  $f_I$  and  $f_U$  can be calculated from  $K_1(D)$  and  $K_2(D)$  only, while for oligomers, the protein concentration is also required.

#### 2.3.4. Local and global parameters

All curves are simultaneously fitted, constrained to share the same values for  $D50$  (or  $D50_{1/2}$ ) and  $M$  (or  $M_{1/2}$ ). The baseline and slopes are allowed to vary, and users also have the option to set the slopes ( $k_u$ ,  $k_n$ ) to zero.

---

<sup>11</sup> Bedouelle, Hugues. "Principles and equations for measuring and interpreting protein stability: From monomer to tetramer." *Biochimie* 121 (2016): 29-37.

### 2.3.5. Fitting errors

See Section '[2.2.7. Fitting errors](#)'.

## 2.4. Custom analysis

### 2.4.1 The fitting function

The CD signal can also be analysed as a function of any experimental parameter. In this case, the fitting function is given by the user. The following rules are required:

- 1) The given experimental parameter should be included in the fitting function string. For example, if the experimental parameter name is 'T', then using 'T\*z' as a fitting function implies that we fit the value of 'z' from the curve of the CD signal against the values of 'T'.
- 2) The function parameters can not contain mathematical characters; e.g., instead of 'dG\_h2o', use 'dG\_water'.
- 3) To use exponential, logarithm or root-square functions, you need to write 'e^(...)', 'log(...)', or 'sqrt(...)'. The parenthesis are obligatory.
- 4) Parameters with the pattern 'Global', e.g., 'TmGlobal' will be shared across all curves.
- 5) Function parameters with the pattern 'Pos' are constrained to be greater than zero. The opposite holds for the parameters with the pattern 'Neg'.

### 2.4.2. Initial parameter estimates

The initial estimates for the function parameters are obtained through a log-spaced grid search. The number of combinations to be tested is fixed, but the limits of the search space can be given by the user. The default behaviour is to explore values between  $10^{-3}$  and  $10^3$ . The combination of initial values resulting in the lowest residual sum of squares is selected.

### 2.4.3. Local and global parameters

When fitting the CD signal against the experimental parameter values, all curves will be simultaneously fitted. The constraint is that they share the same values for parameters with the pattern 'Global'. As for all other parameters, they can vary independently for each curve.

#### 2.4.4. Curve fitting and fitting errors

The curve fitting procedure is done by using the non-linear least squares method (`scipy.optimize.curve_fit`<sup>12</sup>). The standard deviation is computed using the square root of diagonal values from the fit parameter covariance matrix. For each parameter, the relative errors (in percentage) are computed as the quotient between the parameter standard deviation and the parameter value multiplied by one hundred.

### 2.5. Comparison of spectra

To comprehend if there are differences between groups of spectra, ChiraKit allows computing averages and the associated standard deviations ('Module 2e. Spectra Comparison', in the app). Moreover, every possible difference spectrum and its associated standard deviation is also computed (through error propagation). ChiraKit provides the euclidean distances between all spectra and a box plot figure with the intra and inter group distributions.

To compare the shapes of spectra and discard the influence of differences in absorbance intensity, the L2 normalisation can be used. This results in the calculation of normalised euclidean distances as defined in the Equation 2 from Oyama, Taiji, et al (2022)<sup>13</sup>.

## 3. Spectra decomposition

To take advantage of all the spectral information, instead of monitoring a single wavelength, the loaded spectra can be decomposed into a set of basis spectra.

The CD values of a given spectrum are decomposed as a linear combination of basis spectra as follows:

$$CD(x) = c_1(x)\phi_1 + c_2(x)\phi_2 + c_3(x)\phi_3 + \dots + c_n(x)\phi_n \quad (36)$$

where each  $\phi_i$  is a basis spectrum and  $c_i$  the associated coefficients. The basis spectra are orthogonal to each other and have unit norm. The variable  $x$  represents the dimension used for the measurement, such as temperature.

---

<sup>12</sup> [https://docs.scipy.org/doc/scipy/reference/generated/scipy.optimize.curve\\_fit.html](https://docs.scipy.org/doc/scipy/reference/generated/scipy.optimize.curve_fit.html)

<sup>13</sup> Oyama, Taiji, et al. "Performance Comparison of Spectral Distance Calculation Methods." Applied Spectroscopy 76.12 (2022): 1482-1493.

To find the set of basis spectra, we can apply singular value decomposition (SVD) directly on the CD data matrix, or SVD on the centred CD data matrix (equivalent to Principal component analysis)<sup>14</sup>.

### 3.1. Singular value decomposition (SVD)

SVD consist of factorizing the data matrix  $M$  of size  $m \times n$  into the matrices  $U$ ,  $\Sigma$  and  $V^T$  such that

$$M = U \Sigma V^T \quad (37)$$

where  $U$  is an  $m \times m$  orthogonal matrix,  $\Sigma$  is an  $m \times n$  non-negative rectangular diagonal matrix, and  $V^T$  is an  $n \times n$  orthogonal matrix.  $U$  contains the left singular vectors (basis spectra),  $V^T$  the right singular vectors and  $\Sigma$  the singular values.

The amount of explained variance associated to each singular value ( $s_i$ ) is given by the following equation:

$$\text{explained variance}(s_i) = s_i^2 / \sum_{j=1}^n s_j^2 \quad (38)$$

The associated coefficients for the i-th basis spectrum and the j-th acquired spectrum is defined as:

$$\phi_{svd,i} \bullet M_j \quad (39)$$

where  $M_j$  is the j-th column (spectrum) of the matrix  $M$ .

### 3.2. Principal component analysis (PCA)

PCA is performed through eigendecomposition of the covariance matrix  $C$ :

$$C = V L V^T \quad (40)$$

---

<sup>14</sup> Kim, Donggun, and Kisung You. "PCA, SVD, and Centering of Data." arXiv preprint arXiv:2307.15213 (2023).

where  $V$  is the matrix containing the eigenvectors (basis spectra) and  $L$  is the diagonal matrix with the eigenvalues (sorted in descending order). The amount of explained variance associated to each eigenvalues ( $\lambda_i$ ) is given by the following equation:

$$\text{explained variance}(\lambda_i) = \lambda_i / \sum_{j=1}^n \lambda_j \quad (41)$$

It is important to remember that here we refer to the variance of the centred matrix. The associated coefficients for the  $i$ -th basis spectrum and the  $j$ -th acquired spectrum is defined as:

$$\phi_{pca,i} \cdot M_{meanned,j} \quad (42)$$

where  $M_{meanned,j}$  is the  $j$ -th column (spectrum) of the centred matrix  $M$ .

### 3.3. Basis spectrum inversion

Any given basis spectrum  $\phi_i$  can be inverted. As a result the explained variance will remain constant, the new spectrum  $\phi'_i$  will be equal to  $(-\phi_i)$  and the weighting function  $c'_i$  will be equal to  $(-c_i)$ .

### 3.4. Change of basis

Given a set of two or three basis spectra, we can rotate them to obtain a new set of basis spectra with the following properties: the first new basis spectrum is similar to the first acquired spectrum (e.g., lowest temperature, lowest denaturant concentration, or lowest 'experimental parameter'), the amount of explained variance remains constant.

#### **Case 1) Two basis spectra**

The new set of basis spectra is calculated as

$$\begin{bmatrix} | & | \\ \phi_1 & , \phi_2 \\ | & | \end{bmatrix} \cdot rotM = \begin{bmatrix} | & | \\ \phi'_1 & , \phi'_2 \\ | & | \end{bmatrix} \quad (43)$$

where  $\phi_1$  and  $\phi_2$  are the original first and second basis spectra,  $\phi'_1$  and  $\phi'_2$  are the new basis spectra, and  $rotM$  is the rotation matrix given by

$$rotM = \begin{bmatrix} \cos(\alpha) & \sin(\alpha) \\ -\sin(\alpha) & \cos(\alpha) \end{bmatrix} \quad (44)$$

where  $\alpha$  is the angle of a right-triangle between a catheti of length  $c_{1,1}$  and the hypotenuse of length  $\sqrt{c_{1,1}^2 + c_{2,1}^2}$ .  $c_{1,1}$  is the associated coefficient for  $\phi_1$  and the first acquired spectrum.  $c_{2,1}$  is the associated coefficient for  $\phi_2$  and the first acquired spectrum.

### Case 2) Three basis spectra

The new set of basis spectra is calculated as

$$\begin{bmatrix} | & | & | \\ \phi_1 & \phi_2 & \phi_3 \\ | & | & | \end{bmatrix} \cdot rotZ \cdot rotY = \begin{bmatrix} | & | & | \\ \phi'_1 & \phi'_2 & \phi'_3 \\ | & | & | \end{bmatrix} \quad (45)$$

where  $\phi_1$ ,  $\phi_2$  and  $\phi_3$  are the original first, second and third basis spectra,  $\phi'_1$ ,  $\phi'_2$  and  $\phi'_3$  are the new basis spectra,  $rotZ$  is the rotation matrix given by

$$rotZ = \begin{bmatrix} \cos(\gamma) & \sin(\gamma) & 0 \\ -\sin(\gamma) & \cos(\gamma) & 0 \\ 0 & 0 & 1 \end{bmatrix} \quad (46)$$

where  $\gamma$  is the angle of a right-triangle between a cathetus of length  $c_{1,1}$  and the hypotenuse of length  $\sqrt{c_{1,1}^2 + c_{2,1}^2}$ . Here,  $c_{i,1}$  refers to the associated coefficient for i-th original basis spectrum and the first acquired spectrum. Then,  $rotY$  is the rotation matrix given by

$$rotY = \begin{bmatrix} \cos(\beta) & 0 & \sin(\beta) \\ 0 & 1 & 0 \\ -\sin(\beta) & 0 & \cos(\beta) \end{bmatrix} \quad (47)$$

where  $\beta$  is the angle of a right-triangle between a cathetus of length  $\sqrt{c_{1,1}^2 + c_{2,1}^2}$  and the hypotenuse of length  $\sqrt{c_{1,1}^2 + c_{2,1}^2 + c_{3,1}^2}$ .

### 3.5. Alternative formulation for the explained variance

Given a set of orthogonal vectors (basis spectra) and the associated coefficients, the amount of explained variance for a given vector (basis spectrum) is calculated as:

$$\frac{\|c_i\|^2}{\|\phi_i\|^2} / \|M\|^2 \quad (48)$$

where  $\phi_i$  is the i-th basis spectrum,  $c_i$  the associated coefficients, and  $M$  the data matrix. In the case of PCA,  $M$  is replaced by  $M_{meanned}$ .

## 4. Protein secondary structure estimation

Proteins containing different amounts of secondary structure elements, such as alpha helices, beta sheets, and random coils, produce different CD spectra<sup>15</sup>. Given a certain query spectrum and a reference set, the Selcon or SESCA algorithms can be used to calculate the secondary structure content.<sup>16</sup>

ChiraKit runs an in-house python-based implementation of the Selcon algorithm and the SESCA algorithm v0.97 developed by Gabor Nagy and Helmut Grubmuller (<https://www.mpinat.mpg.de/sesca>).

### 4.1. The Selcon method

The Selcon algorithm can be divided into three versions (1, 2 and 3). ChiraKit will try to run Selcon 3 and if it fails it will run Selcon2.

#### **Selcon version 1**

We start with a set of linear equations that relate the CD spectra with the secondary structure content:

---

<sup>15</sup> Greenfield, Norma J. "Using circular dichroism spectra to estimate protein secondary structure." Nature protocols 1.6 (2006): 2876-2890.

<sup>16</sup> Sreerama, Narasimha, Sergei Yu Venyaminov, and Robert W. Woody. "Estimation of protein secondary structure from circular dichroism spectra: inclusion of denatured proteins with native proteins in the analysis." Analytical biochemistry 287.2 (2000): 243-251.

$$F = XC \quad (49)$$

where  $C$  is the  $m \times n$  matrix containing the CD spectra in delta epsilon units,  $F$  is the  $l \times n$  matrix containing the known secondary structure elements, and  $X$  is the  $l \times m$  matrix that allows the transition between the space of secondary structure elements  $F$  and the space of CD spectra  $C$ . Here,  $n$ ,  $l$  and  $m$  represent, respectively, the number of proteins, secondary structure elements and wavelengths.

Let  $c$  be the query spectrum, an initial guess for the secondary structure components is done based on the most similar spectrum from the reference set, and we build the set of equations

$$F_2 = XC_2 \quad (50)$$

where  $C_2$  now includes  $c$ , has  $(n + 1)$  columns, and is ordered according to the root mean square (RMS) distance to  $c$ .  $F_2$  is also rearranged accordingly. The equation is solved for  $X$  and then the secondary structure  $f$  (of the protein to be analysed) is calculated as

$$f = Xc \quad (51)$$

To solve the equation regarding  $F_2$ ,  $C_2$  is factorized using the SVD algorithm. Indeed, by varying the number of proteins from the reference set (from 2 to  $n$ ) and the number of relevant singular values (from 1 to 7), several solutions are obtained for  $f$ . Those satisfying the following criteria are considered: 1) the sum of the secondary structure elements' fractions lies between 95% and 105%, and 2) each secondary structure element fraction is greater than - 2.5 %. If no acceptable solutions are found during this step, the rules are relaxed by adding a tolerance of 1 % to the total sum of fractions, and of 0.5 % to the individual fractions.

For each set of valid solutions that share a certain number of proteins from the reference set but vary in the number of relevant singular values, only the solution whose sum of secondary structure element fractions is closest to 100% is kept. Let  $N_p$  be the number of valid solutions, we will have at most  $2 \leq N_p \leq n$  solutions.

The  $N_p$  solutions are averaged to obtain  $f_1$ , which replaces the initial guess in the matrix  $F_2$  as the second approximation. Finally, the same process is repeated until the RMS difference between two successive solutions is less than 0.0025 delta epsilon units.

## Selcon version 2

The Selcon Version 2 method starts with the same algorithm as Selcon Version 1. After self-consistency is achieved, the final  $N_p$  set of valid solutions are filtered by removing those where the RMS between the reconstructed spectrum and the query spectrum  $c$  is larger than 0.25 delta epsilon units. If the filter does not leave any solution, the tolerance is relaxed using 0.01 delta epsilon units steps until at least one solution is found. Finally, the mean solution of the filtered solutions is reported.

### Selcon version 3

The Selcon Version 3 method follows the same procedure as Selcon Version 2 with the difference that one more rule is applied. The  $N_p$  set of valid solutions is further filtered based on the amount of alpha helix.

Let  $h_i$  be the alpha-helix content fraction of the  $i$ -th solution,  $h_q$  the predicted alpha-helix content fraction for the query spectrum (after the Selcon 2 method); and  $h_{min}$ ,  $h_{ave}$  and  $h_{max}$  the minimum, average, and maximum fraction of alpha-helix content, respectively, considering all the reference proteins required to obtain the  $N_p$  solutions. Then, for the  $i$ -th solution to be valid, it needs to satisfy any of these criteria:

$$\text{Case 1)} \quad h_q > 0.65 \& h_i > 0.65 \quad (52)$$

$$\text{Case 2)} \quad 0.25 \leq h_q \leq 0.65 \& \frac{h_q + h_{max}}{2} - 0.03 \leq h_i \leq \frac{h_q + h_{max}}{2} + 0.03 \quad (53)$$

$$\text{Case 3)} \quad 0.15 \leq h_q \leq 0.25 \& \frac{h_q + h_{ave}}{2} - 0.03 \leq h_i \leq \frac{h_q + h_{ave}}{2} + 0.03 \quad (54)$$

$$\text{Case 4)} \quad h_q < 0.15 \& \frac{h_q + h_{min}}{2} - 0.03 \leq h_i \leq \frac{h_q + h_{min}}{2} + 0.03 \quad (55)$$

### Reference sets

By default, two reference sets are provided: AU\_SP175 and 2) AU\_SM180. These sets contain CD spectra from the same group of proteins as the original SP175<sup>17</sup> and SMP180<sup>18</sup> sets. AU\_SP175 contains the CD spectra of 71 soluble proteins measured down to 175 nm. AU\_SM180 contains the AU\_SP175 set and 57 additional CD

<sup>17</sup> Lees, Jonathan G., et al. "A reference database for circular dichroism spectroscopy covering fold and secondary structure space." Bioinformatics 22.16 (2006): 1955-1962.

<sup>18</sup> Abdul-Gader, Ali, Andrew John Miles, and Bonnie A. Wallace. "A reference dataset for the analyses of membrane protein secondary structures and transmembrane residues using circular dichroism spectroscopy." Bioinformatics 27.12 (2011): 1630-1636.

spectra, including membrane proteins. The lower limit of the AU\_SM180 set is 180 nm. In both cases, the data sets have 1 nm steps and start at 240 nm.

The number of secondary structure elements to be detected depends on the reference set (or the lower wavelength limit). Six secondary structure elements for values lower than 180 nm (AU\_SP175), and four secondary structure elements for values between 180 and 190 nm (AU\_SM180). **No calculation is possible if the query spectrum does not go to at least 190 nm.**

To select the reference data, the CD spectra were downloaded from the Protein Circular Dichroism Data Bank (PCDDB)<sup>19</sup>. In case that many versions were available, the latest one was chosen (September 2023). In two cases we did not use the PCDDB data directly: The Human Serum Albumin CD spectrum was replaced with an in-house measured spectrum. The Lysozyme spectrum CD0000045100 was zeroed again and averaged with the spectrum CD0000045000.

Custom reference sets can be imported too. The requisite is to import the corresponding matrices F (secondary structure elements) and C (reference spectra). C is arranged column-wise (one spectrum per column) and the CD data goes from the highest wavelength to the lowest wavelength. F should have the same columns as C, and as many rows as different secondary structure elements.

## Secondary structure elements

All secondary structures elements come from the DSSP routine<sup>20</sup>. Following the method of Sreerama, Narasimha et al., 1999, the secondary structure elements are further categorised as regular or distorted alpha-helix, regular or distorted beta-sheet, turns and 'other'. Alpha helix are the sum of fractions H and G. Beta sheets are the fraction E. Turns are fraction T. All other fractions (I, B, S, C) are assigned to 'other'. The alpha helix fraction is divided into two groups: Alpha\_D (distorted) which are the two first and two last residues in a helix and the rest are Alpha\_R (regular). If the helix is less than 4 residues all go into the Alpha\_D fraction. The same division is made for beta sheets, with the difference that only the first and the last residue of a beta strand goes into the distorted fraction Beta\_D. The rest goes into the regular fraction Beta\_R.

For a given spectrum with an unknown associated secondary structure, if the lower wavelength range value is below 180 nm, the six secondary structure elements can be detected. If the lower limit is between 180 and 190 nm (inclusive), four different

---

<sup>19</sup> <https://pcddb.cryst.bbk.ac.uk/>

<sup>20</sup> Kabsch, Wolfgang, and Christian Sander. "Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features." Biopolymers: Original Research on Biomolecules 22.12 (1983): 2577-2637.

fractions will be estimated: Alpha, Beta, Turns and Other (Alpha = Alpha\_R + Alpha\_D, Beta = Beta\_R + Beta\_D).

## 4.2. The SESCA method (SESCA\_bayes)<sup>21</sup>

The SESCA algorithm is based on spectrum predictions from empirical basis spectrum sets and joint probability distribution maps for scaling factors and non-secondary structure distributions. SESCA\_bayes provides estimates of each SS element (e.g., alpha-helix) with an associated error. It's important to consider that besides the error provided by SESCA\_bayes, there's another source of (unreported) error that originates from the way that basis spectra sets are created.

### Bayesian secondary structure (SS) probabilities

Given a certain experimental spectrum (CD), the probabilities of SS compositions can be inferred according to:

$$P(SS_j | CD) \propto P(CD | SS_j)P(SS_j) \quad (56)$$

where  $P(CD | SS_j)$  is the probability of observing the measured spectrum for a protein with a given SS composition  $j$  and  $P(SS_j)$  is the prior probability of the given SS composition.

The likelihood  $P(CD | SS_j)$  is computed in five steps. Firstly, the signal is predicted from the  $SS_j$  composition of interest and the selected basis spectra set. Then, depending on the basis spectra set, side chain corrections are included. Thirdly, the measured CD spectrum is rescaled to minimise the root-mean-square deviation ( $RMSD_j$ ). This way, we obtain a scaling factor  $a_j$  which is used together with the  $RMSD_j$  to determine the likelihood (from the joint probability distribution).

### Joint probability distributions

The joint probability distribution functions of CD deviations were constructed as the sum of 70 two-dimensional Gaussian functions, each representing the estimated scaling factors and non-SS contributions of a reference spectrum from the SP175 set.

---

<sup>21</sup> Nagy, Gabor, and Helmut Grubmuller. "Implementation of a Bayesian secondary structure estimation method for the SESCA circular dichroism analysis package." *Computer Physics Communications* 266 (2021): 108022.

## 5. Peptide helicity estimation

Certain peptides adopt only helix or coil conformations. The helix conformation has two minima at 208 and 222 nm, while the coil conformation has a negative peak at 200 nm. If the peptide can only populate these two states, an isodichroic point around 203 nm should be observed for the transition<sup>22</sup>. The minima at 222 nm can be used to estimate the peptide helicity.<sup>23</sup>

### 5.1. The ensemble model

The ensemble model assumes that there exists different helical conformers of varying lengths, and that each of them produces different signals. The peptide can have one or two helical segments. Triple or higher helical segments are not considered because of their low probability. The model is explained in [Uroš Zavrtanik et. al. 2024](#) and implemented in <https://github.com/sanhadzi/Dichroic-CD-model>.

## Contact details

For further assistance, please contact us:

 spc@embl-hamburg.de

 EMBL (c/o DESY), Notkestrasse 85, Build. 25a, 22607 Hamburg, Germany

---

<sup>22</sup> Toniolo, Claudio, Fernando Formaggio, and Robert W. Woody. "Electronic circular dichroism of peptides." Comprehensive chiroptical spectroscopy: applications in stereochemical analysis of synthetic compounds, natural products, and biomolecules 2 (2012): 499-544.

<sup>23</sup> Zavrtanik, Uroš, Jurij Lah, and San Hadži. "Estimation of Peptide Helicity from Circular Dichroism Using the Ensemble Model." The Journal of Physical Chemistry B 128.11 (2024): 2652-2663.