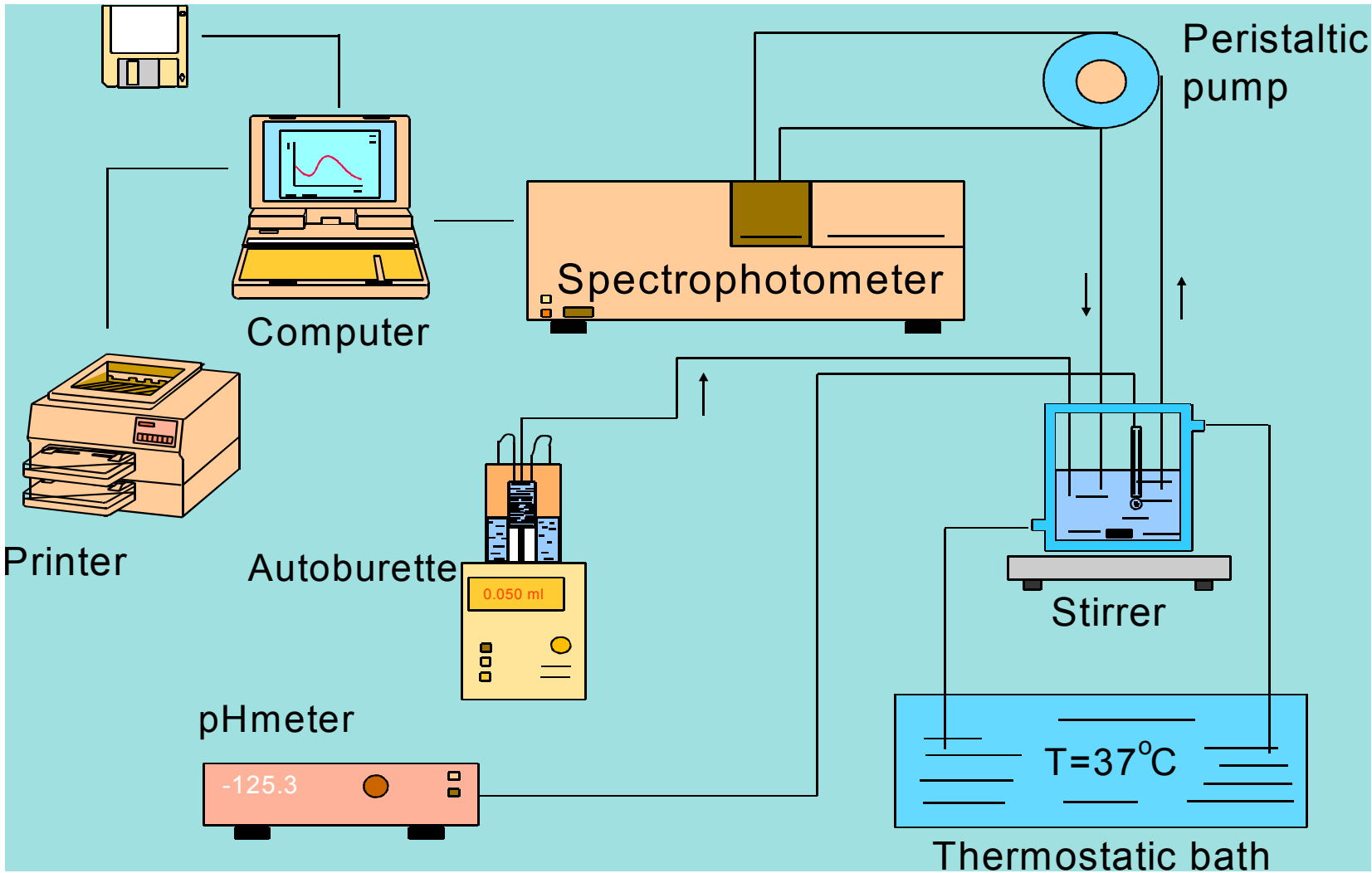
Examples of MCR-ALS applications (from R.Tauler et al.)

- Chromatographic coelution
- Spectrometric titrations of multiequilibria systems
- Process analysis
- continuous flow methods FIA
- melting conformations of polynucleotides
- protein folding
- voltamperometric data (Me-peptide interactions)
- environmental data

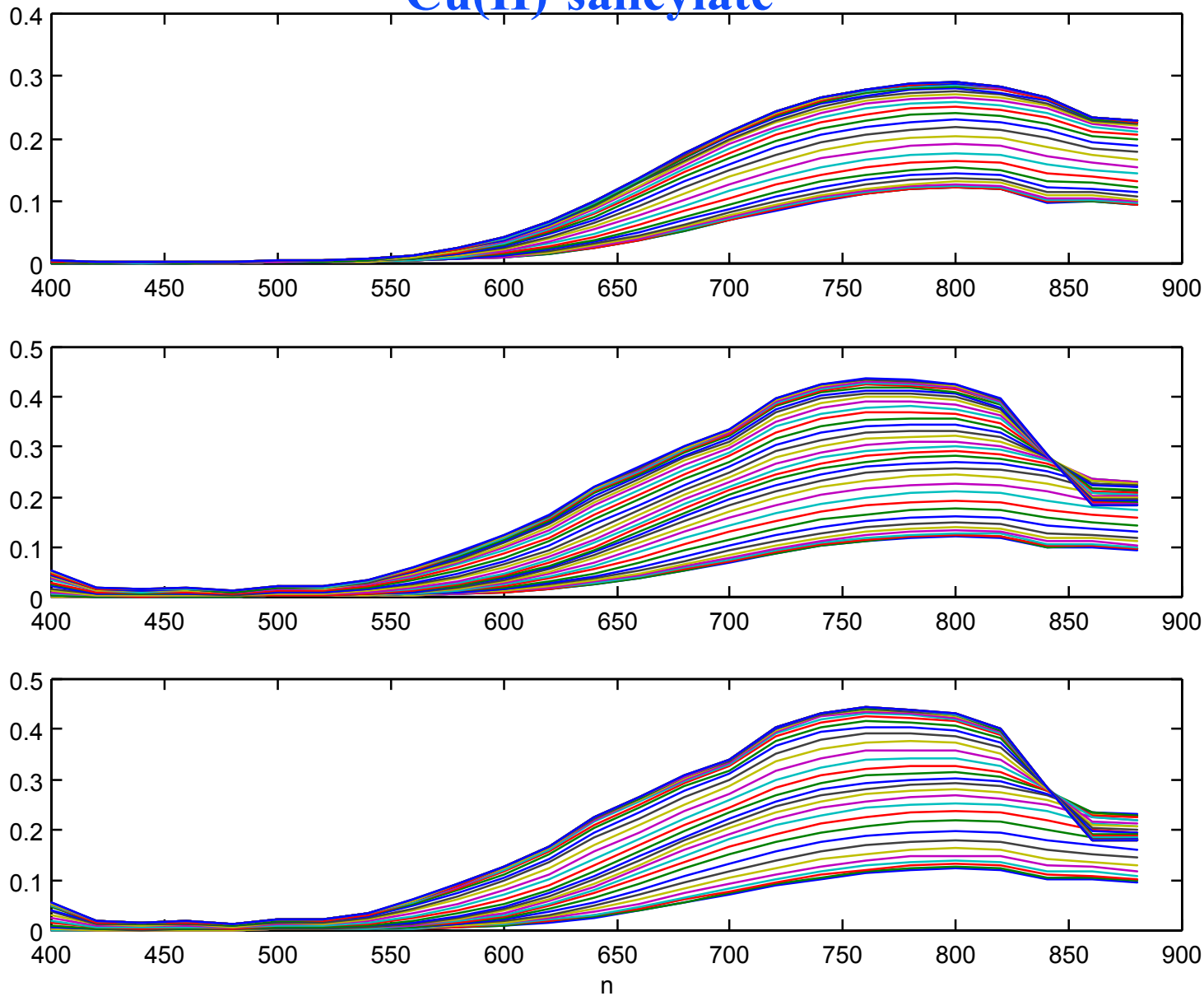
Spectrometric Titrations

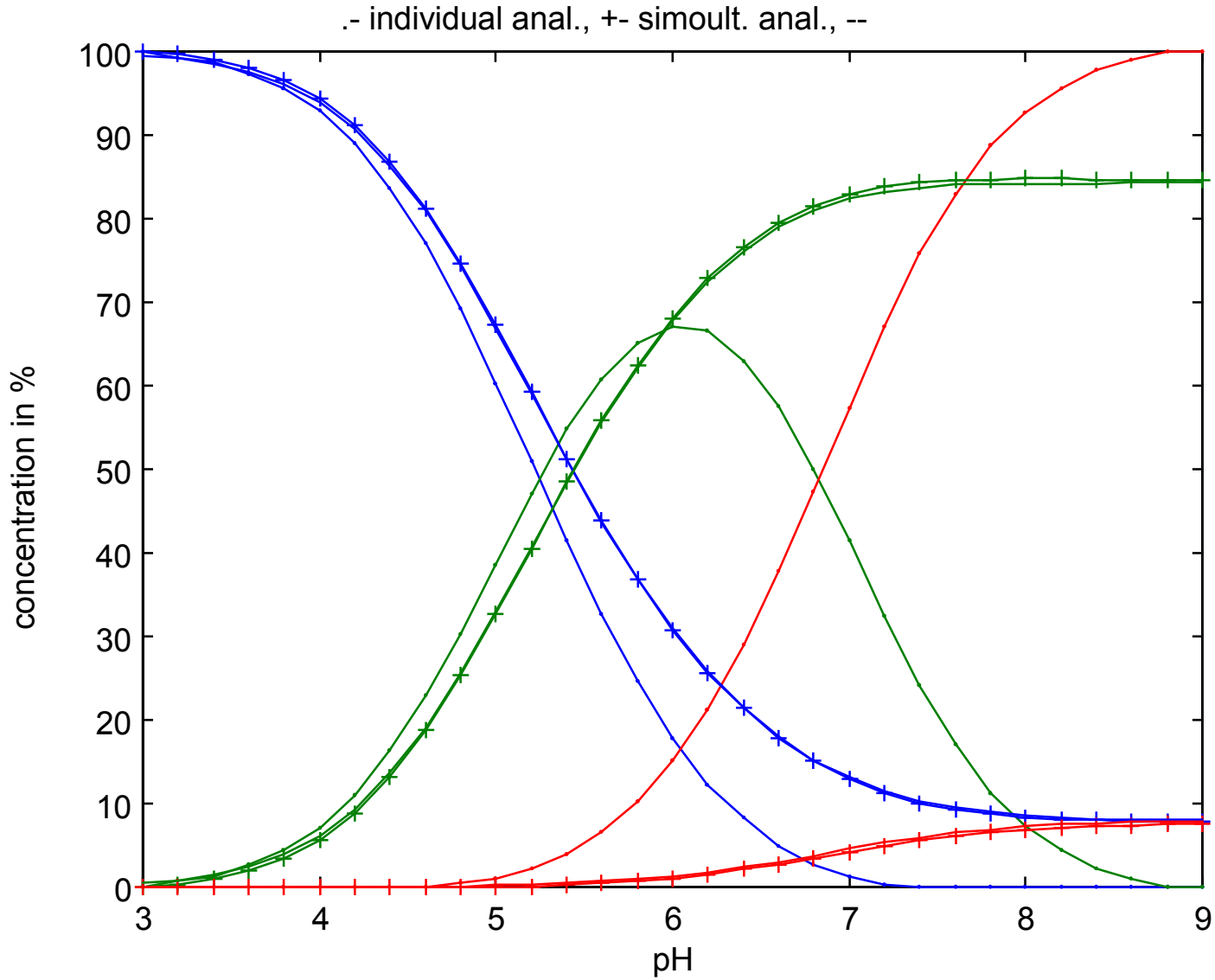
R.Tauler, A.Izquierdo-Ridorsa and E.Casassas
Chemometrics and Intelligent Laboratory Systems, 18 (1993, 293-300

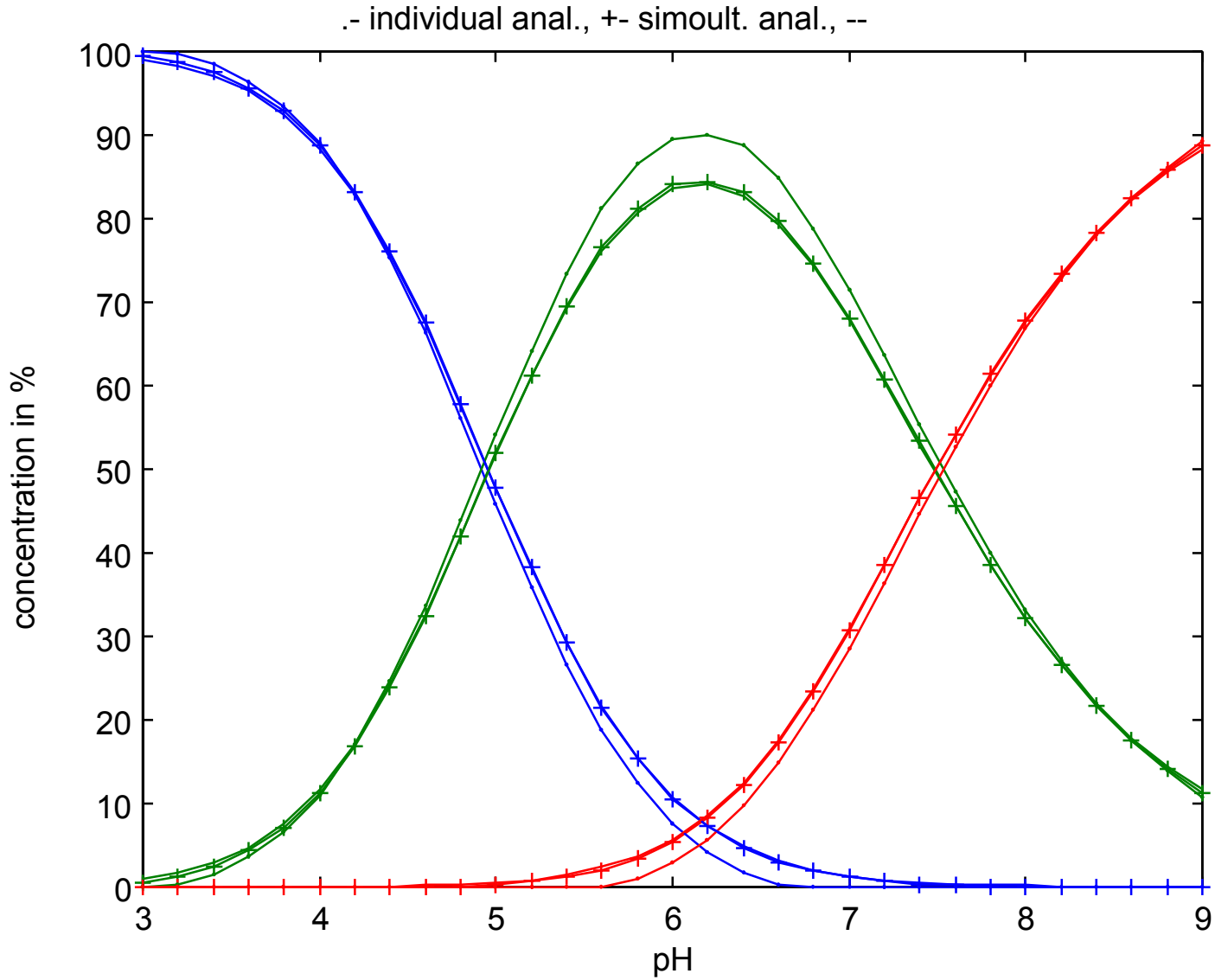
Spectrometric titrations: An easy way for the generation of two- and three-way data in the study of chemical reactions and interactions



Three spectrometric titrations of a multiequilibria system: Cu(II)-salicylate




.- individual anal., +- simoult. anal., --
concentration in %
pH
100
90
80
70
60
50
40
30
20
10
0
3
4
5
6
7
8
9


.- individual anal., +- simoult. anal., --
concentration in %
pH
100
90
80
70
60
50
40
30
20
10
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3
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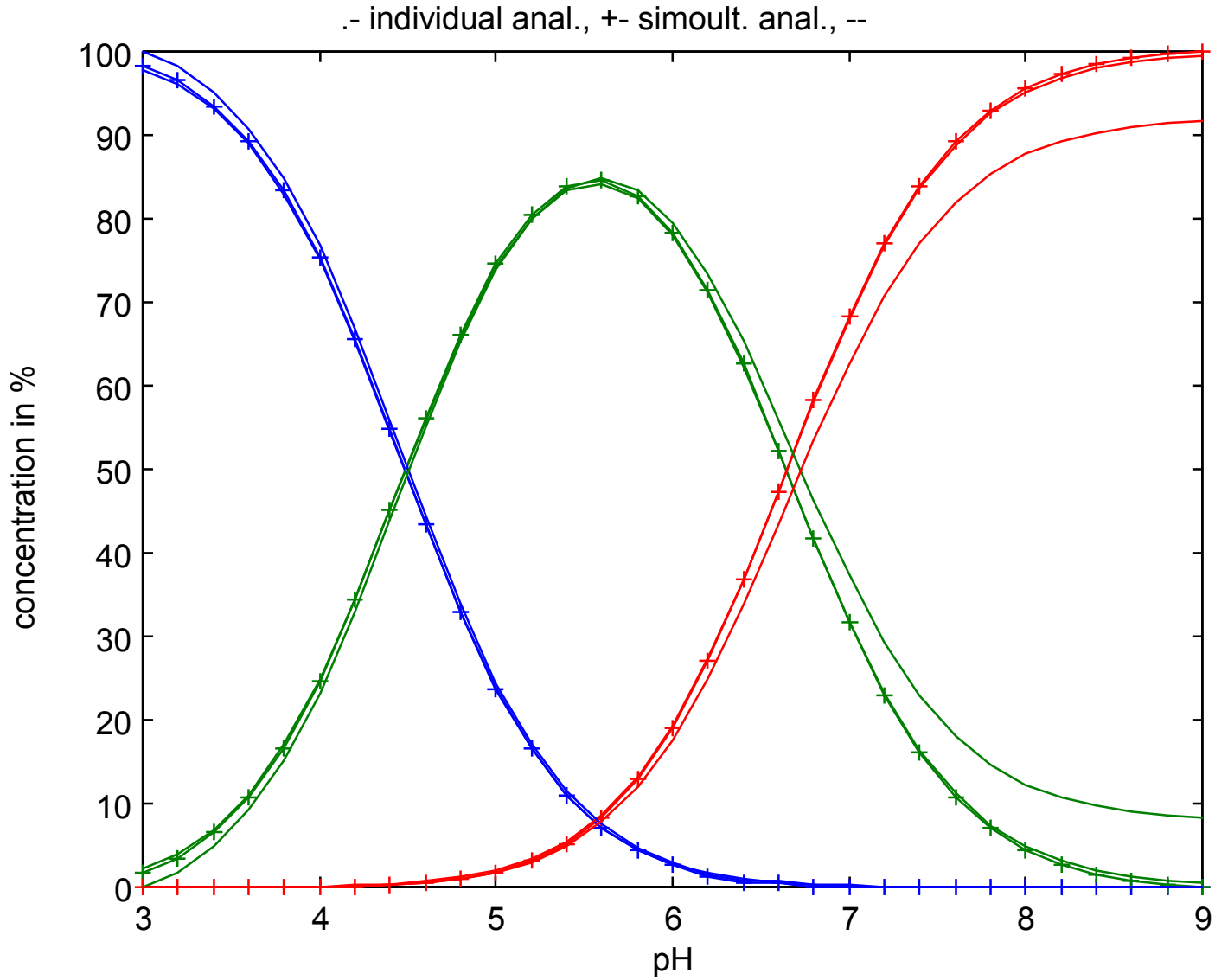
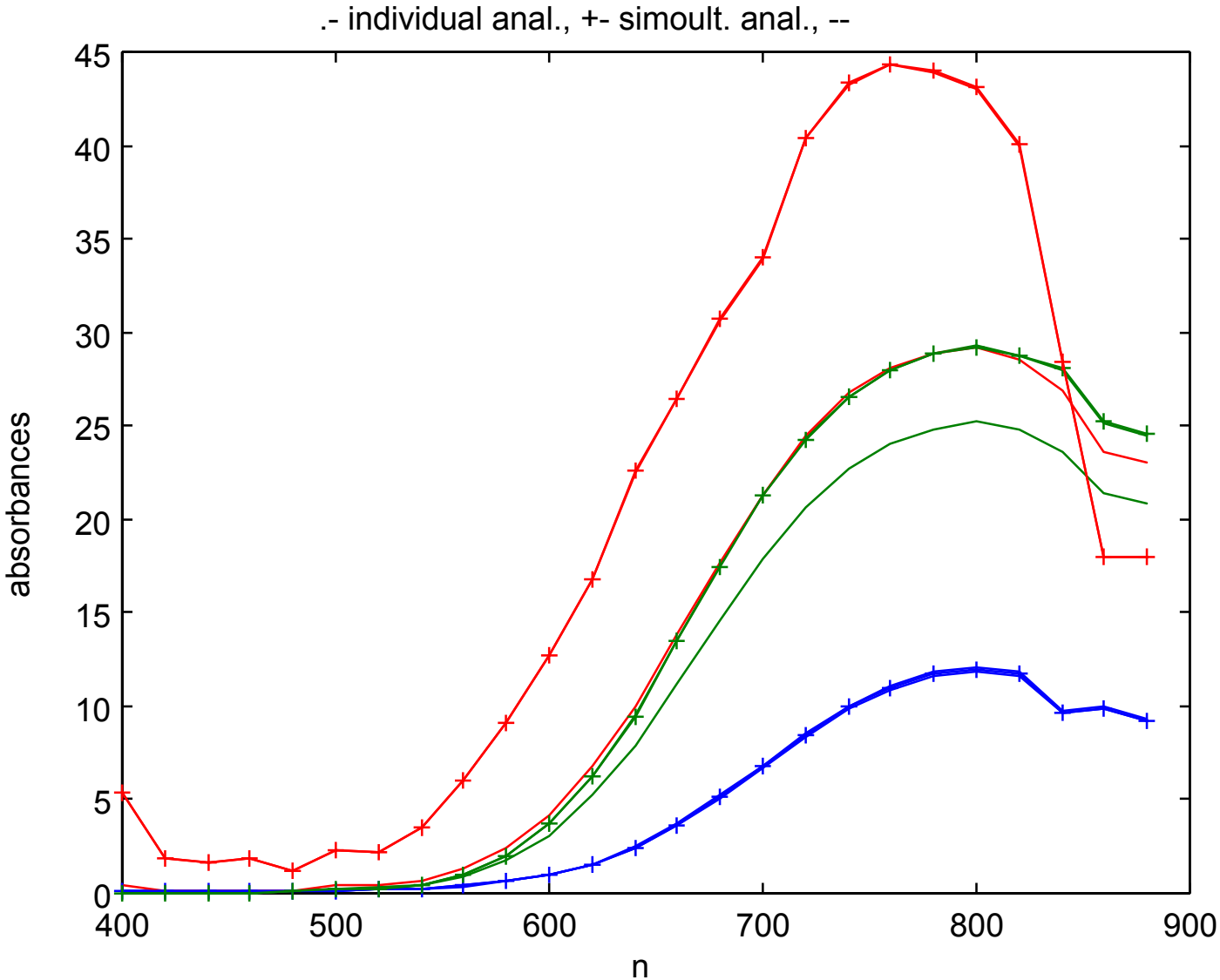
5
6
7
8
9


.- individual anal., +- simoult. anal., --
concentration in %
pH
100
90
80
70
60
50
40
30
20
10
0
3
4
5
6
7
8
9

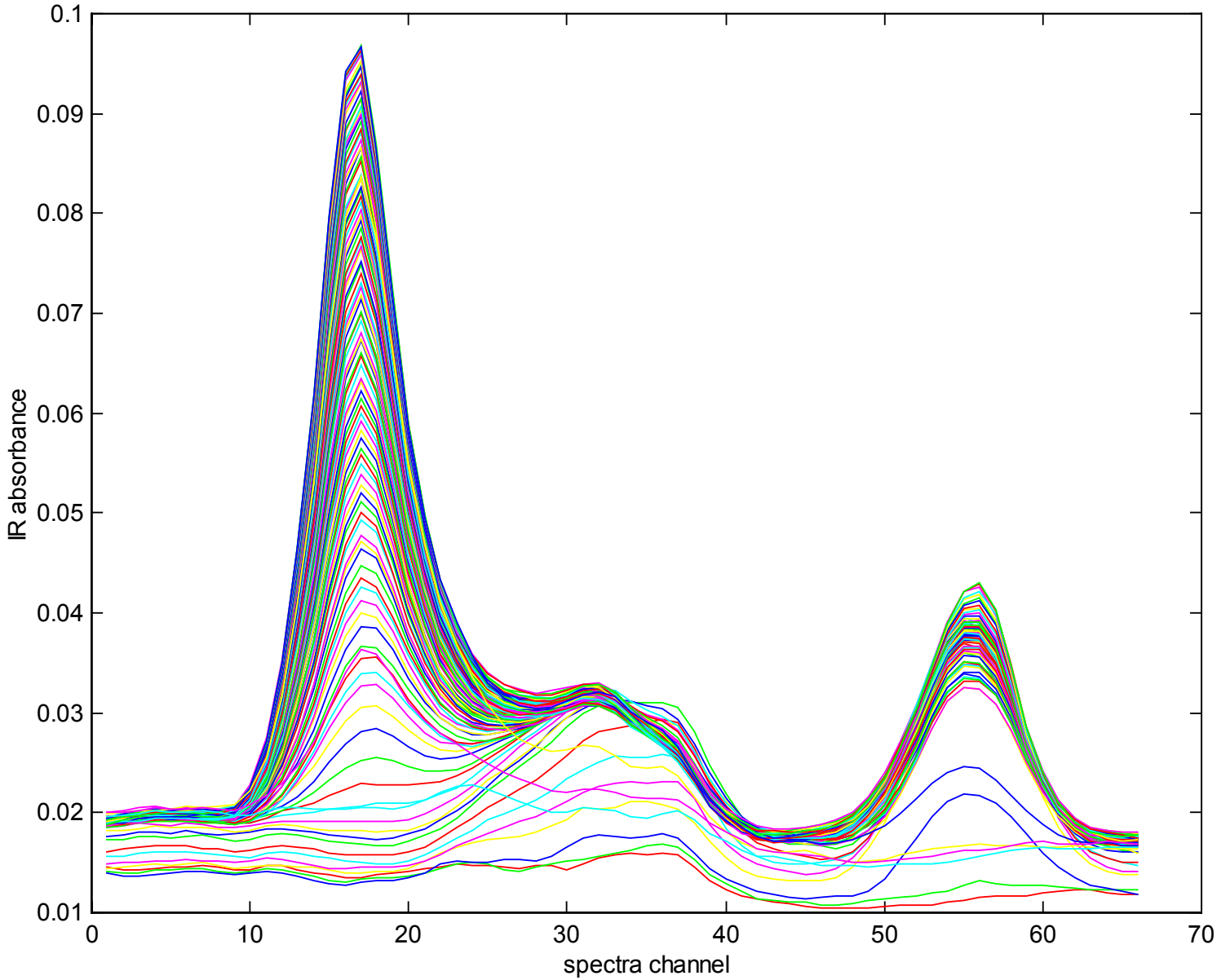

.- individual anal., +- simoult. anal., --
absorbances
n
0
5
10
15
20
25
30
35
40
45
400
500
600
700
800
900

Process analysis

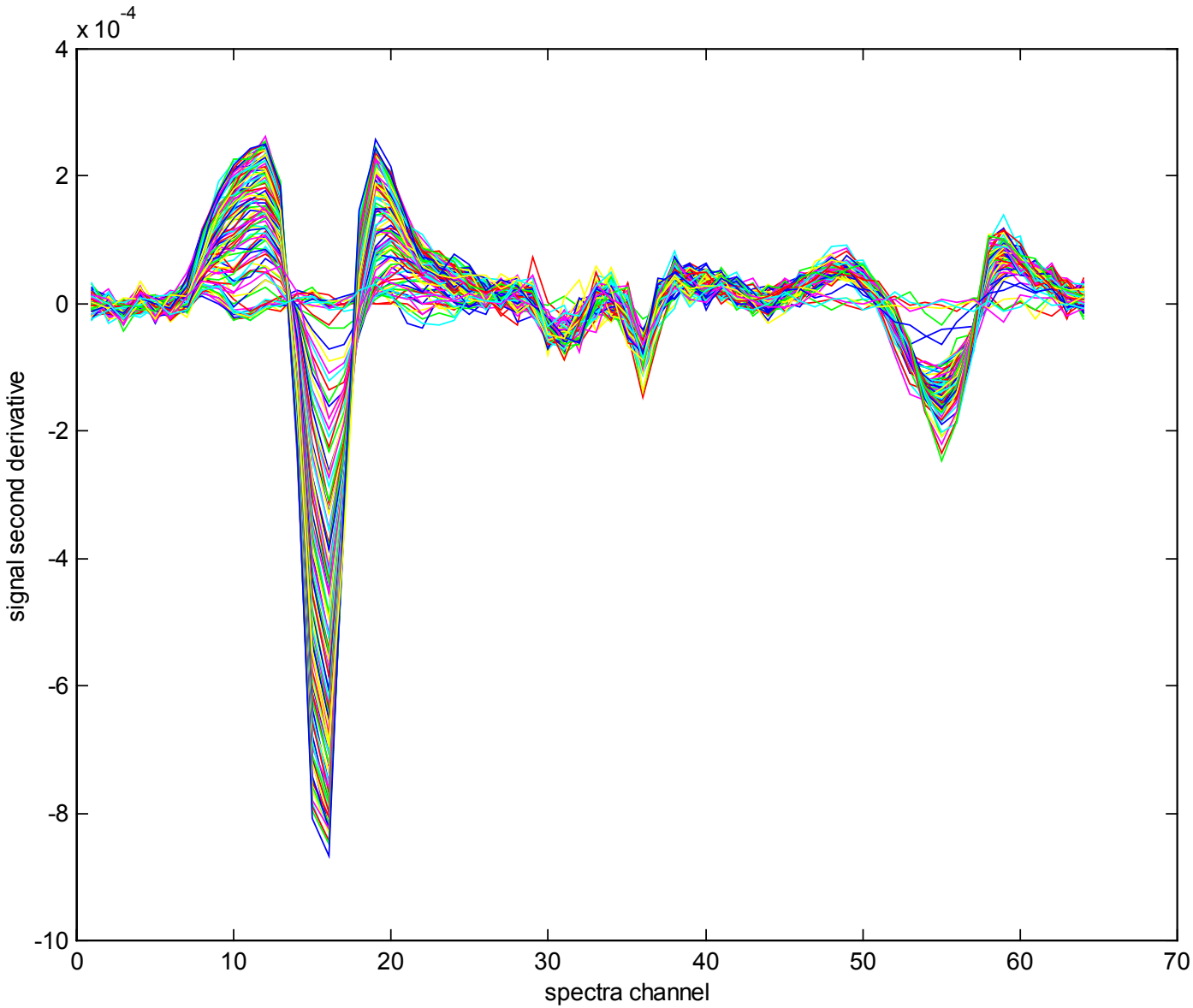
R.Tauler, B.Kowalski and S.Fleming

Anal. Chem., 65 (1993) 2040-47

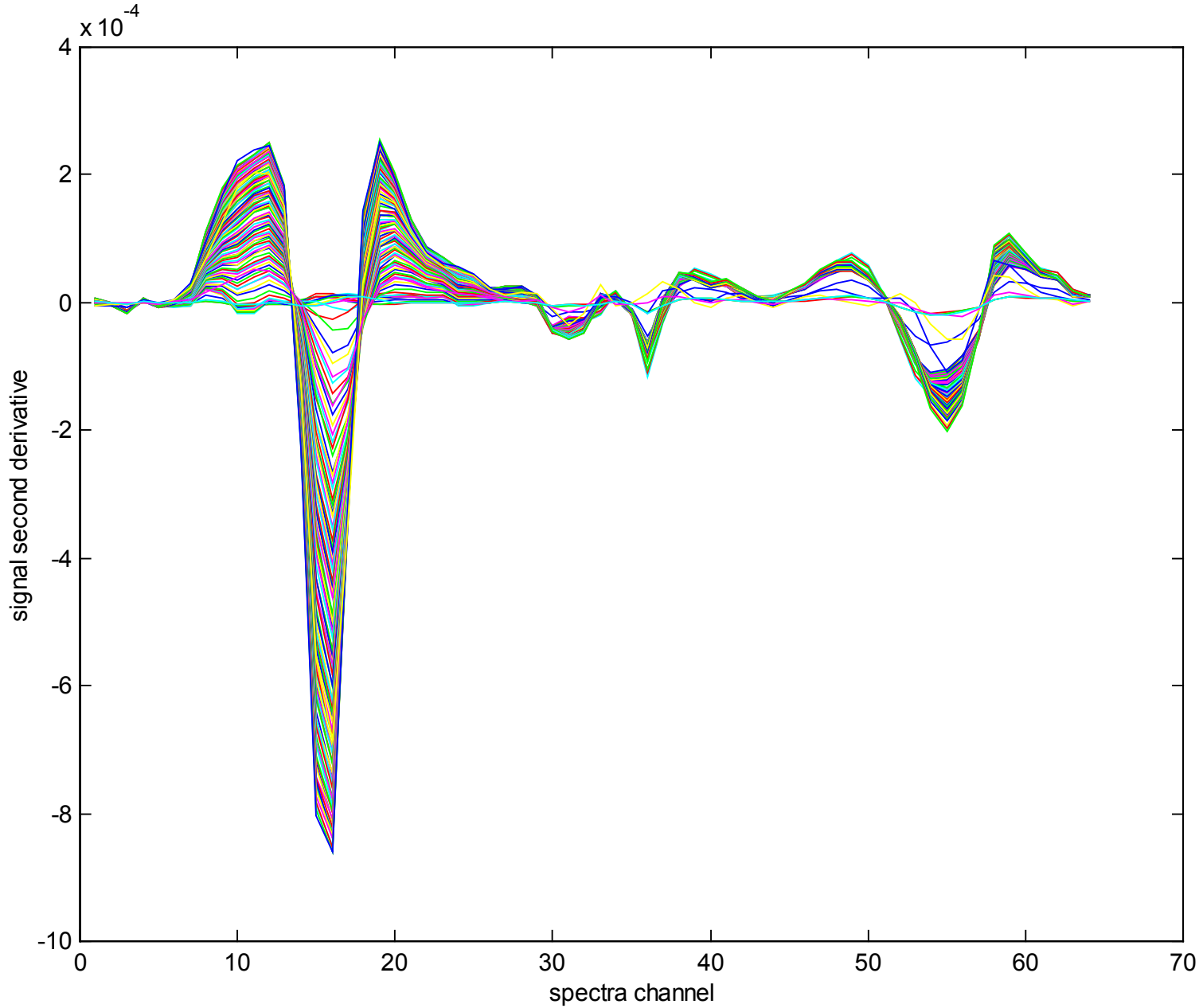
IR raw process data: one run



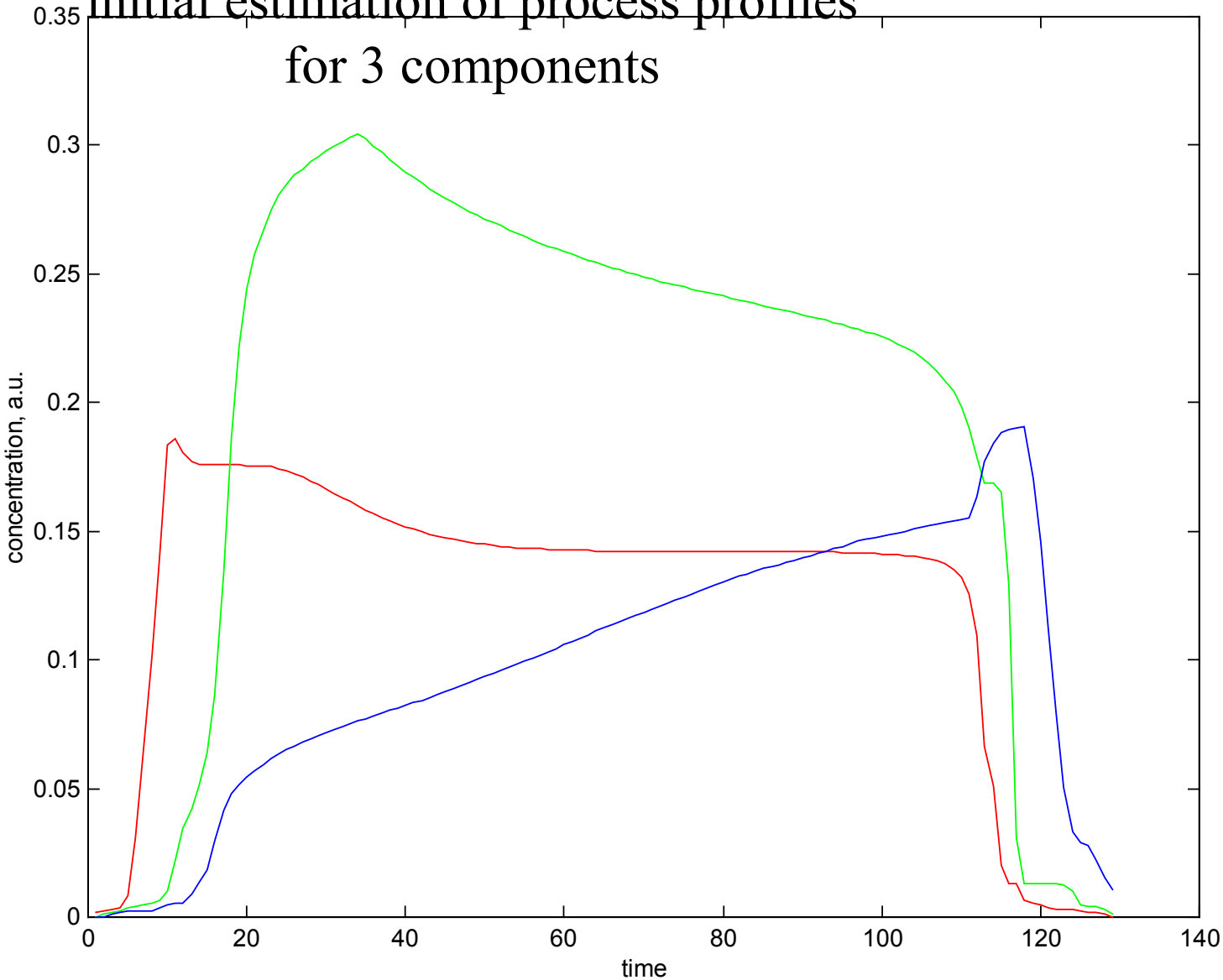
2nd derivative raw process data



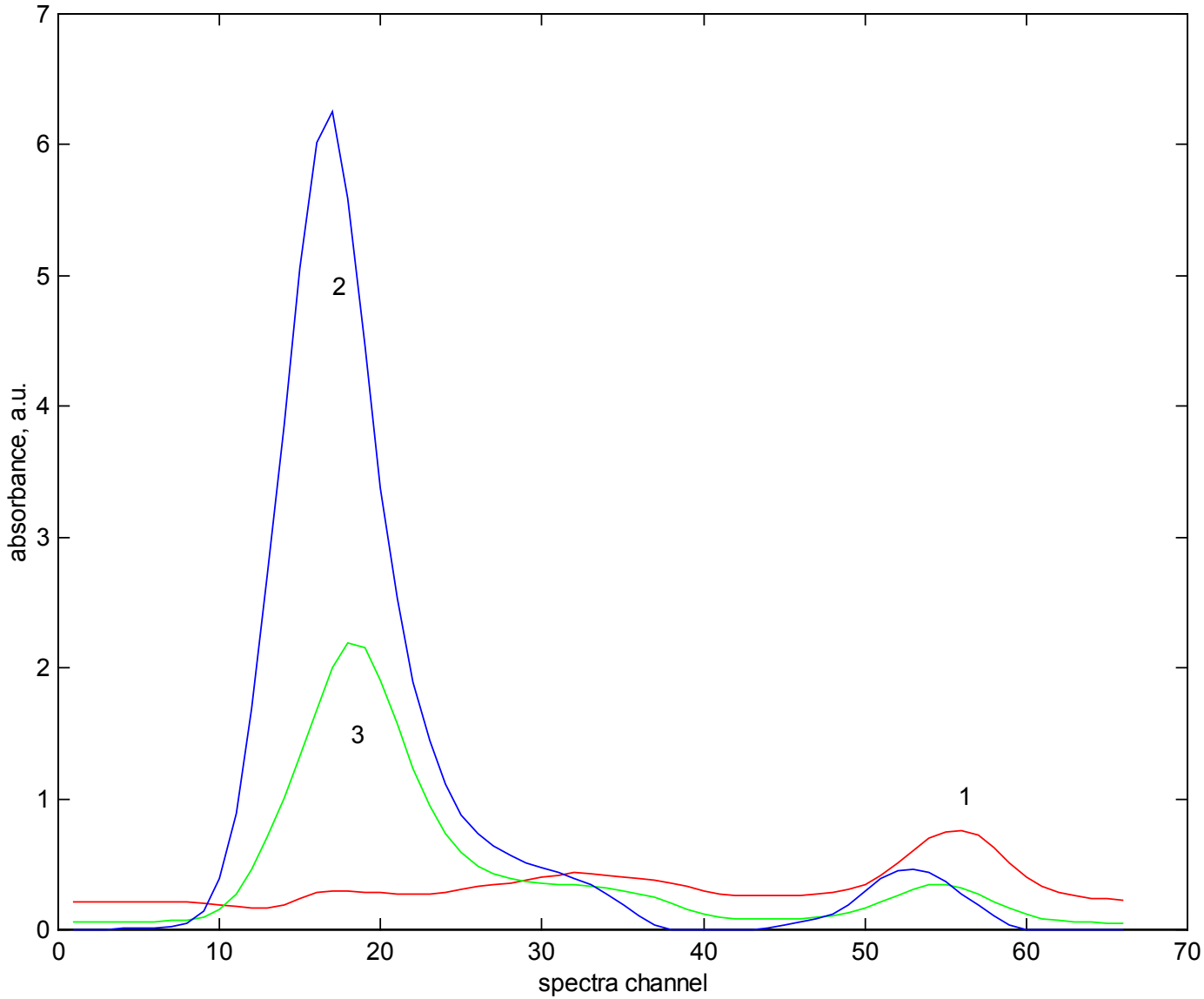
PCA filtered (3 comp.) 2nd derivative raw process data



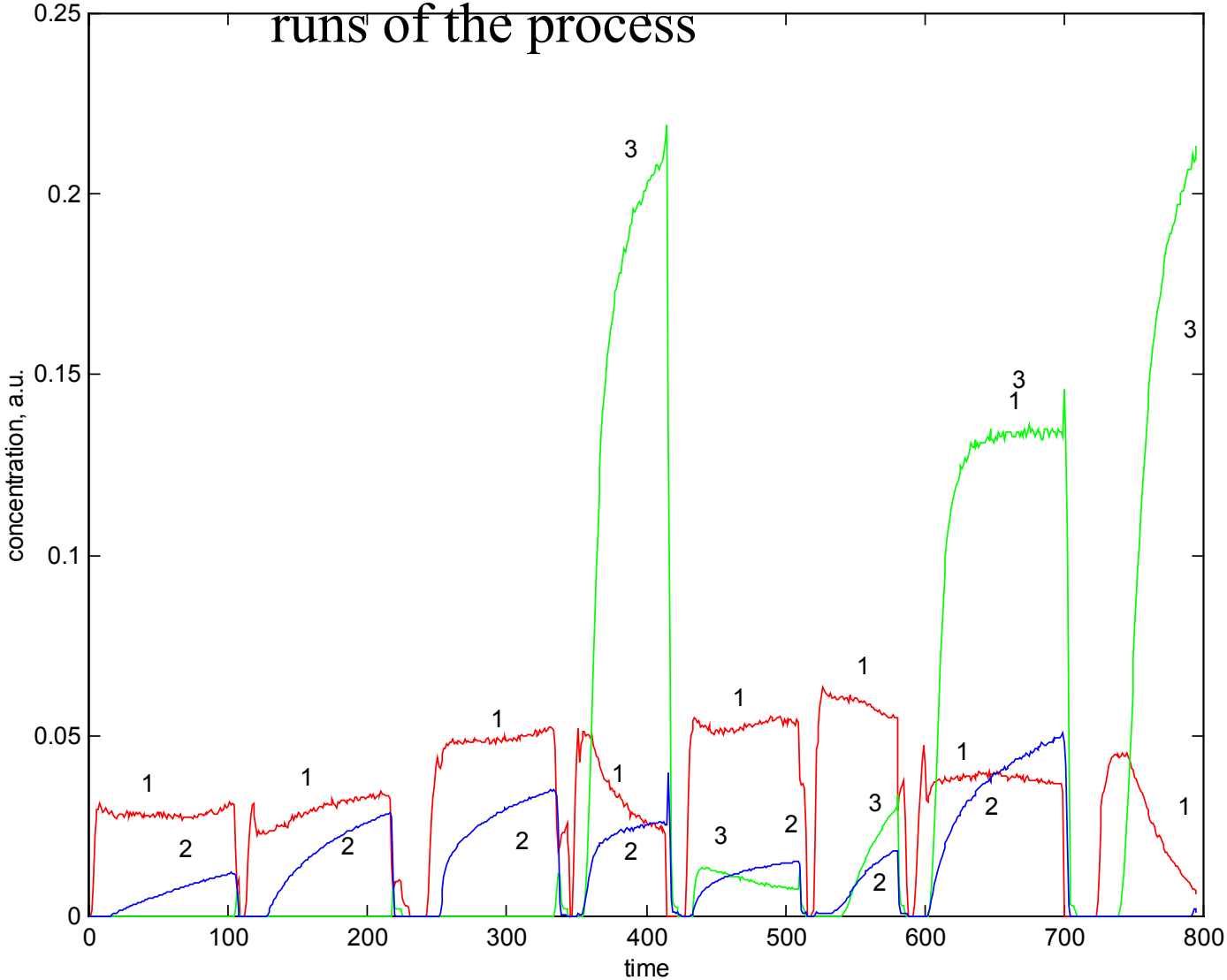
EFA of 2nd derivative data: initial estimation of process profiles for 3 components



ALS resolved pure IR spectra profiles



ALS resolved pure concetration profiles in the simultaneous analysis of eigth runs of the process



Continuous methods of analysis and FIA

J.Saurina, S.Hernandez-Cassou,
R.Tauler, A.Izquierdo-Ridorsa

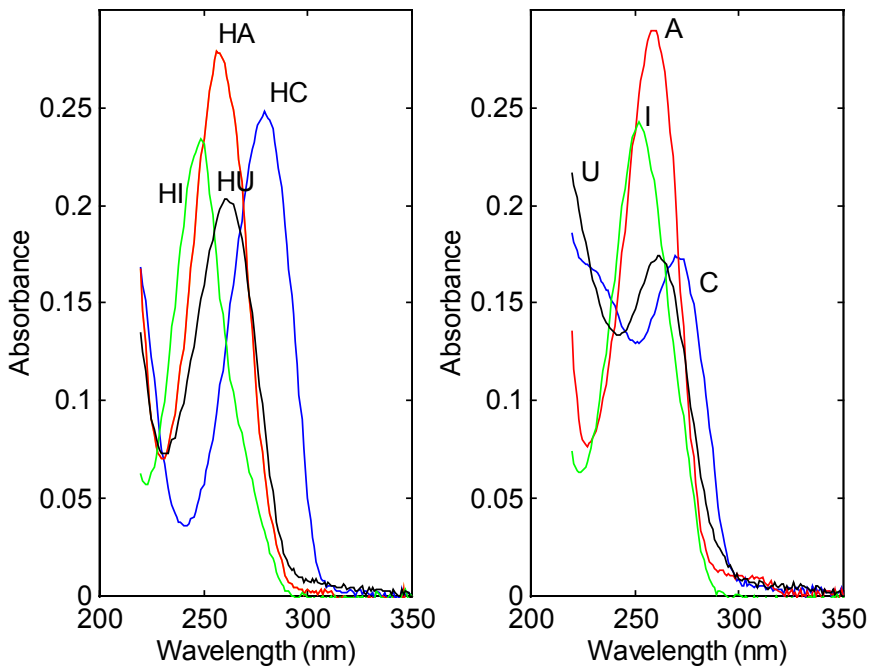
Anal.Chem.,1998

Mixture analysis of nucleic acid constituents by means of continuous flow methods

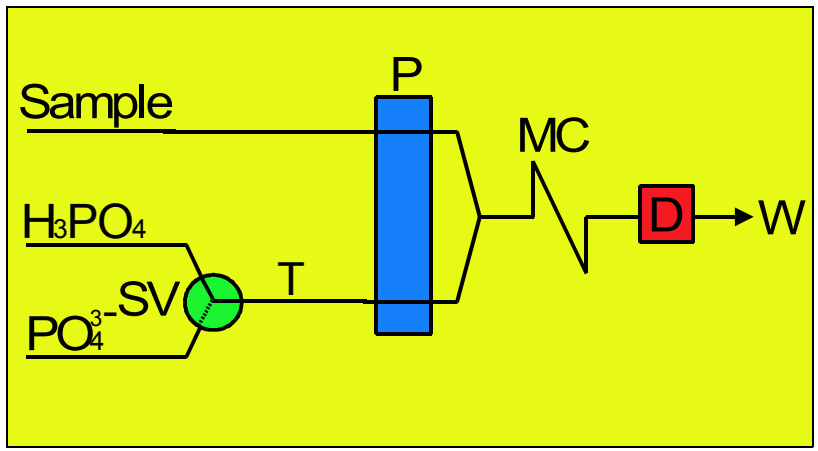
Acid-base properties of the compounds analyzed

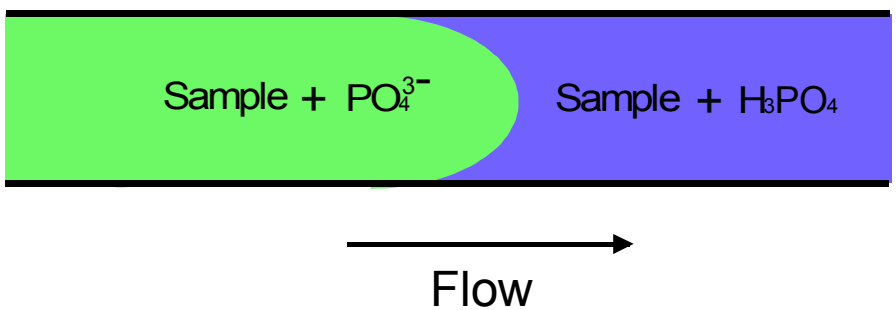
Compound	pK_a	Working conditions
cytosine	4.56 (N(3))	37°C; I=0.15 M
	11.7 (N(1))	25°C; I=0.1 M
cytidine	4.13 (N(3))	37°C; I=0.15 M
adenosine	3.6 (N(1))	25°C; I=0.1 M
uridine	8.855 (N(3))	37°C; I=0.15 M
inosine	8.50 (N(1))	37°C; I=0.15 M
inosine-5'-monophosphate	6.00 (phosphate)	34°C; 0.5 M
	9.27 (N(1))	34°C; 0.5 M

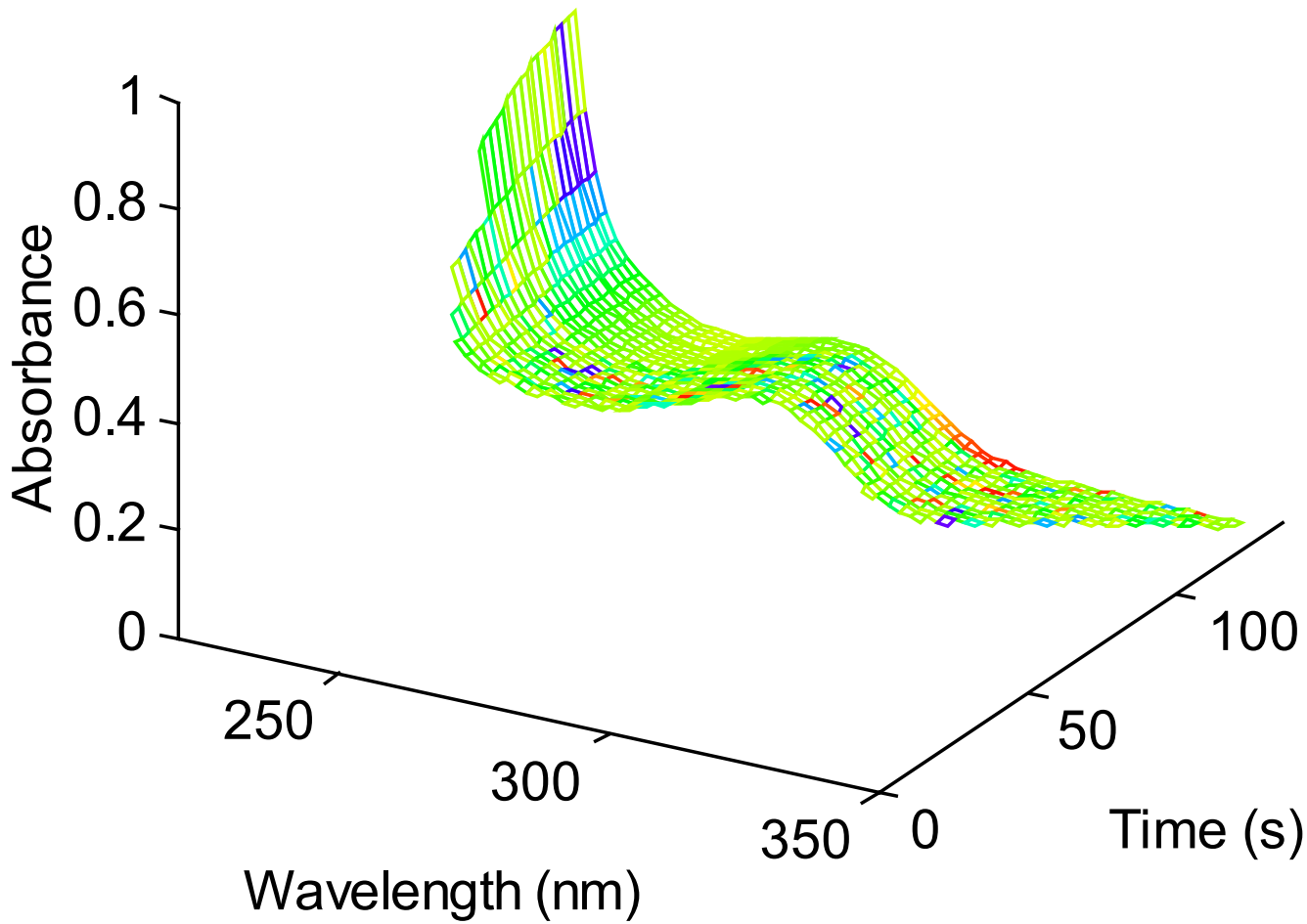
Absorption spectra for the protonated and deprotonated forms of the nucleosides adenosine, cytidine, inosine and uridine



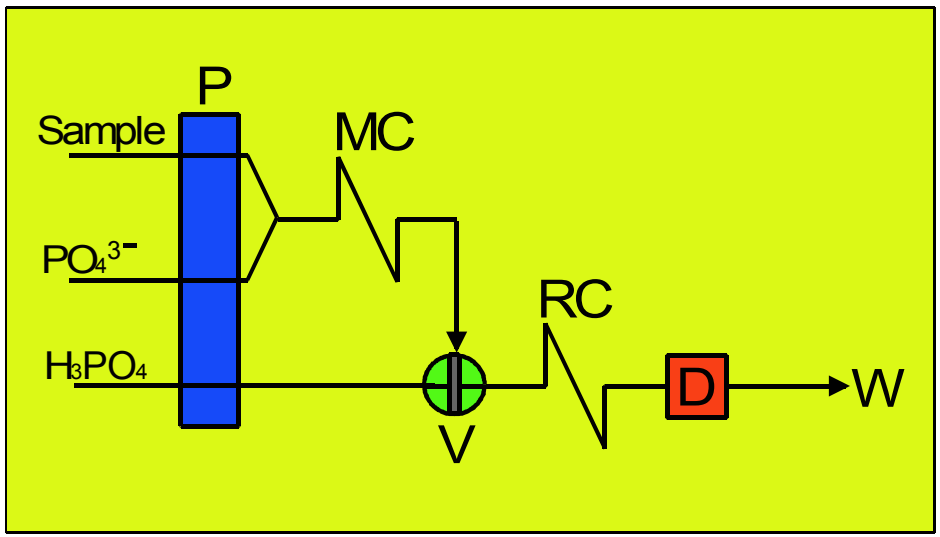
CONTINUOUS-FLOW SYSTEM

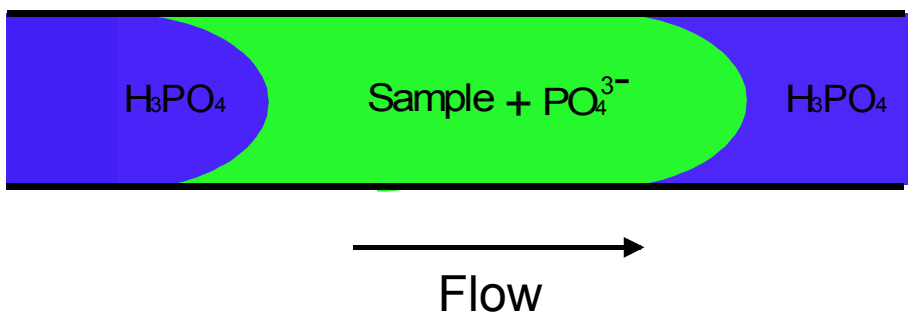


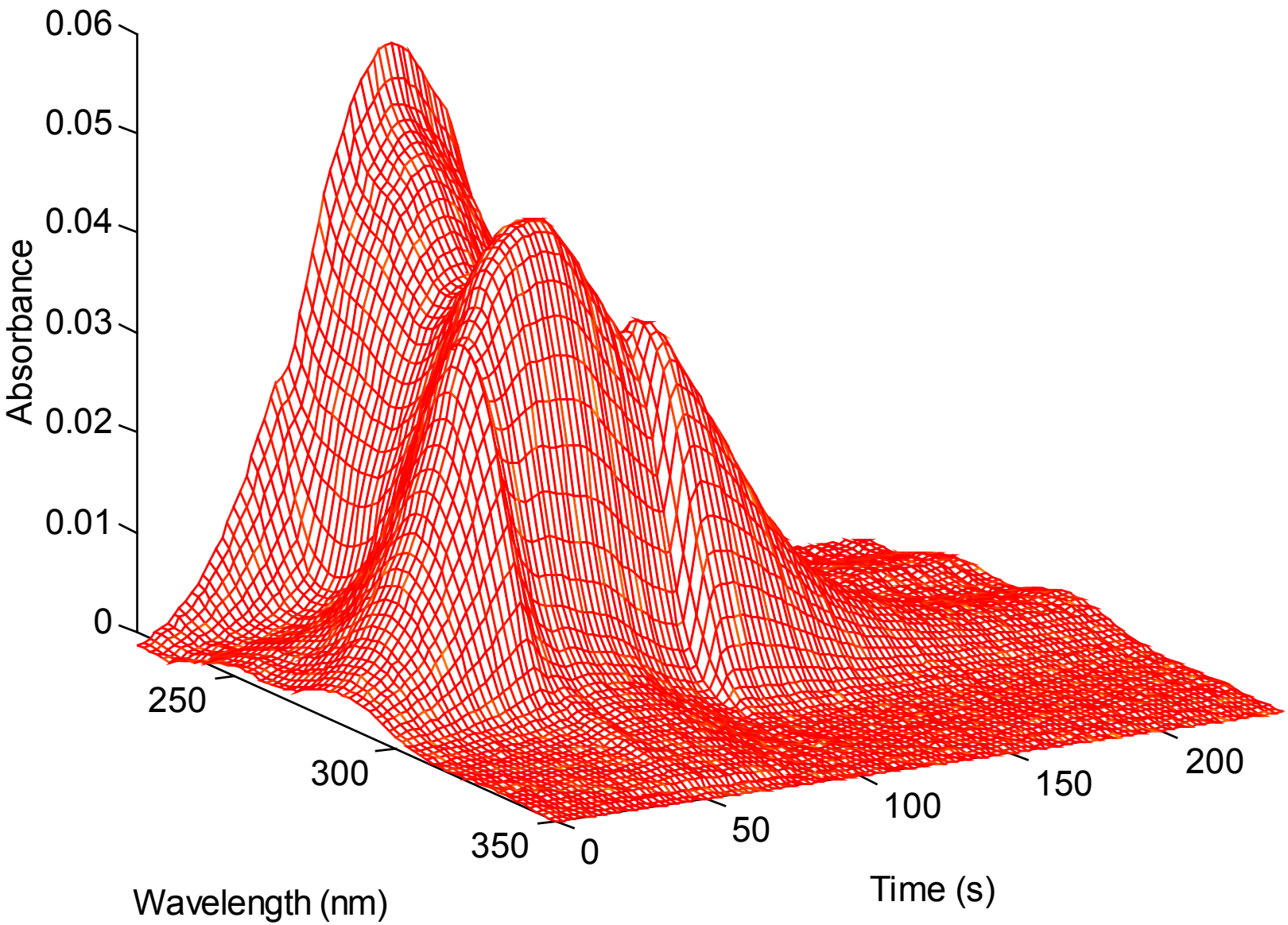



Absorbance
1
0.8
0.6
0.4
0.2
0
250
300
350
Wavelength (nm)
0
50
100
Time (s)

SINGLE INJECTION FLOW-INJECTION SYSTEM



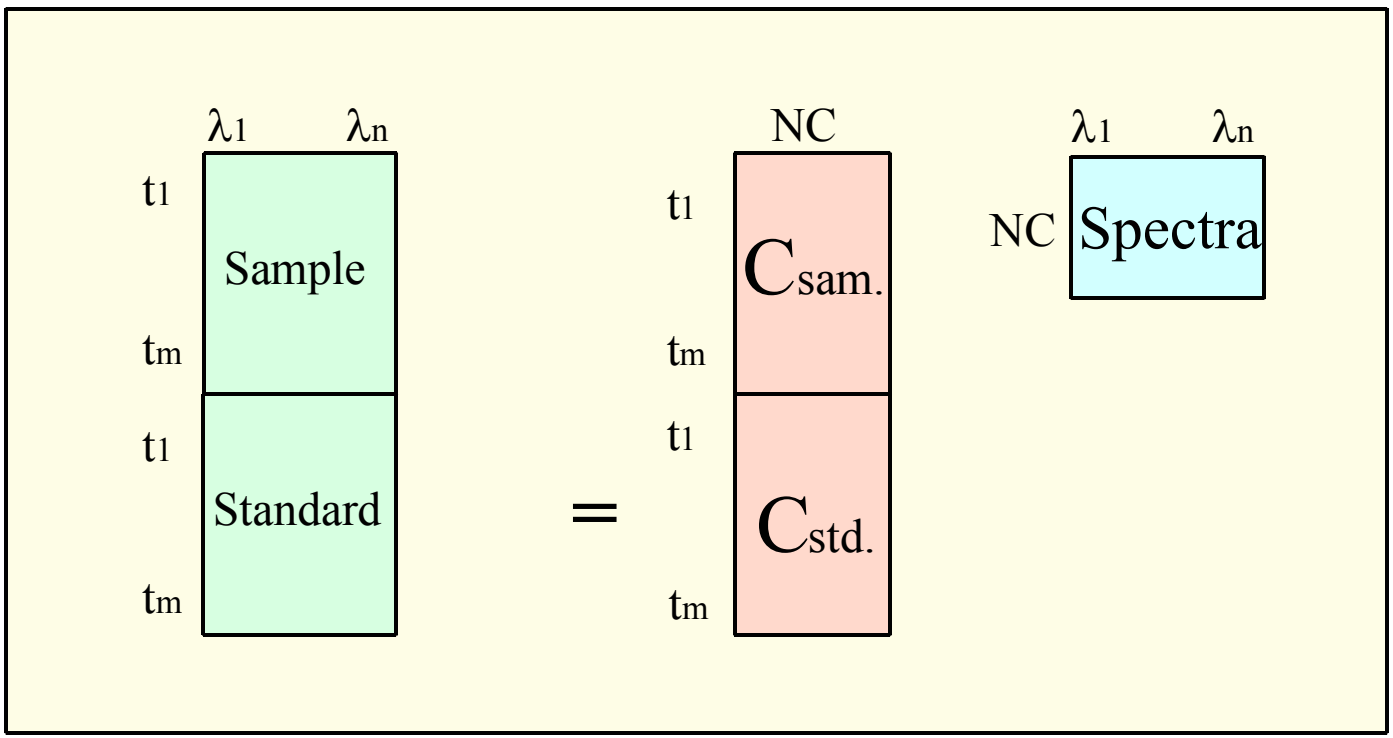



0.06
0.05
0.04
0.03
0.02
0.01
0
Absorbance
250
300
350
Wavelength (nm)
0
50
100
150
200
Time (s)

RESOLUTION OF THE EXPERIMENTAL DATA WITH THE MCR-ALS METHOD

. Compliance of the linear Beer's law:

$$\mathbf{D_{aug}} = \mathbf{C_{aug}}\,\mathbf{S^T} + \mathbf{E}$$



Species correspondence between matrices

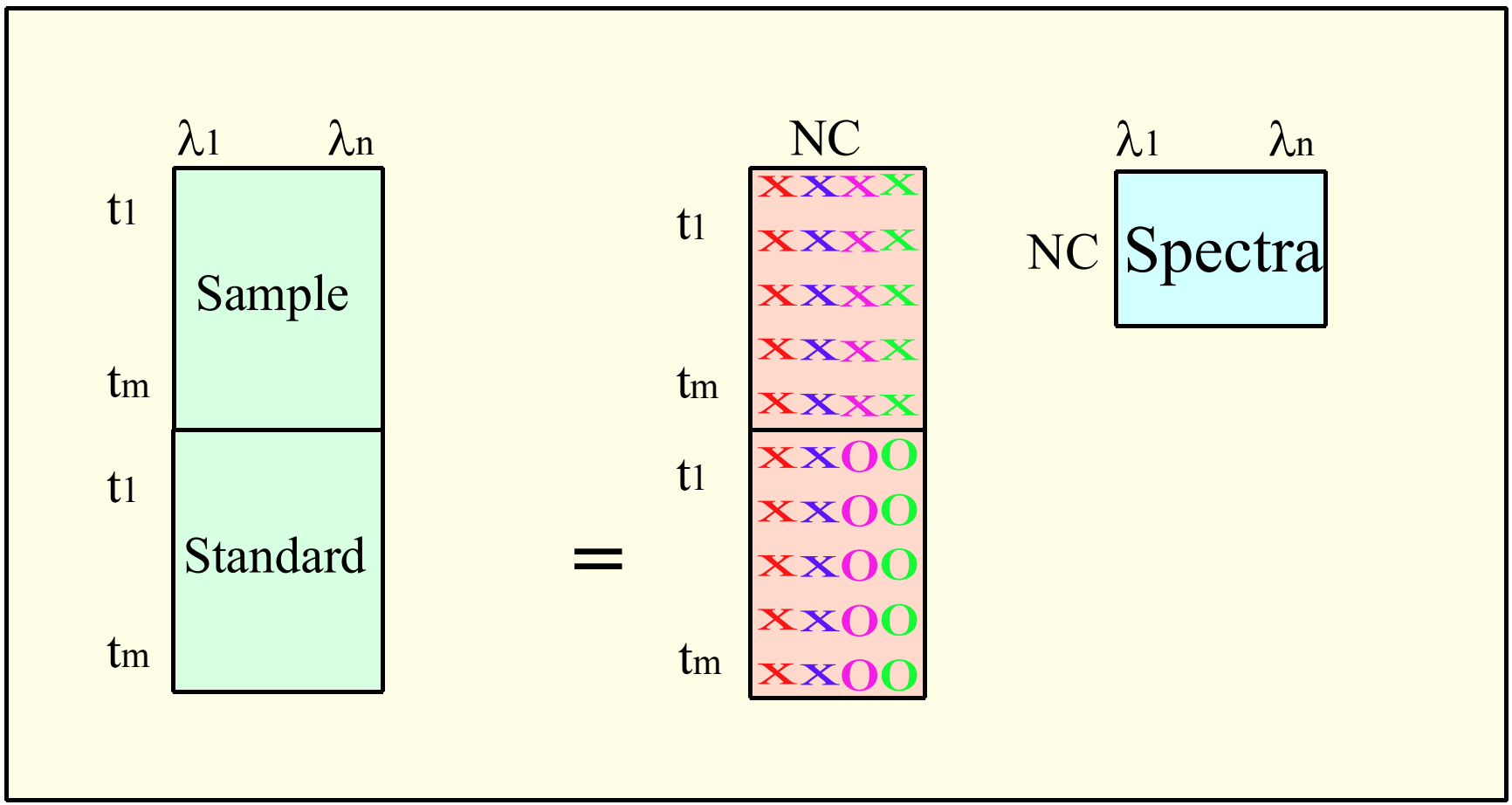
Continuous-flow system

1	1	1	1	1	1	Sample matrix
1	1	1	0	0	0	Standard matrix

Single injection flow-injection system

1	1	1	1	Sample matrix
1	1	0	0	Standard matrix

Initial estimation of the $\mathbf{C_{aug}}$ data matrix



ALS optimization

1st step: $\mathbf{S}^{\mathbf{T}} = (\mathbf{C}_{\mathbf{aug}})^{+}\ \mathbf{D}^{*}_{\mathbf{aug}}$

2nd step: $\mathbf{C}_{\mathbf{aug}} = \mathbf{D}^{*}_{\mathbf{aug}}\ (\mathbf{S}^{\mathbf{T}})^{+}$

These steps are repeated until convergence is achieved.

Constraints applied:

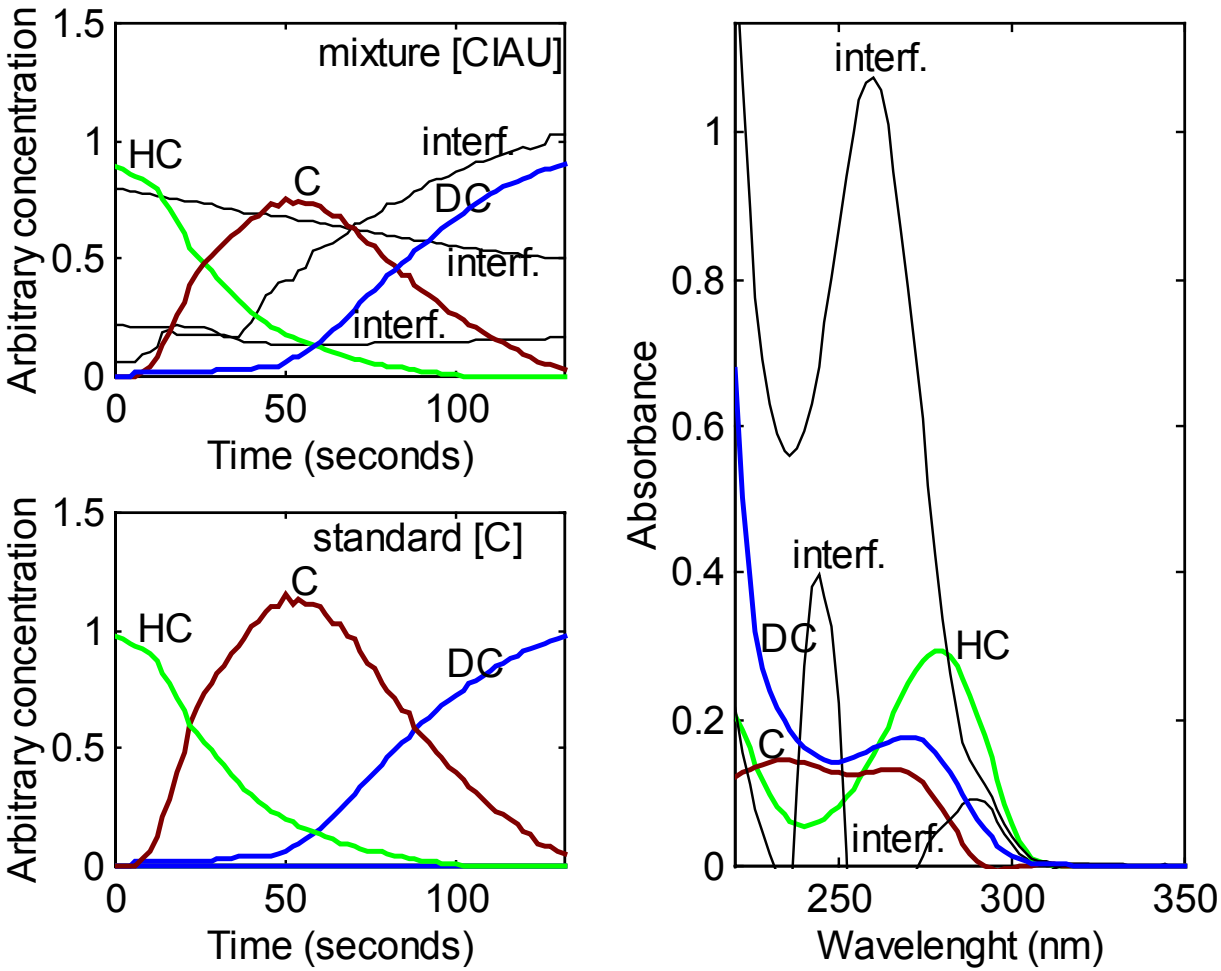
(a) unimodal concentration profiles (not applicable to single injection flow-injection system)

(b) non-negative concentration profiles and pure spectra

(c) the pure spectrum of each species is the same in all runs

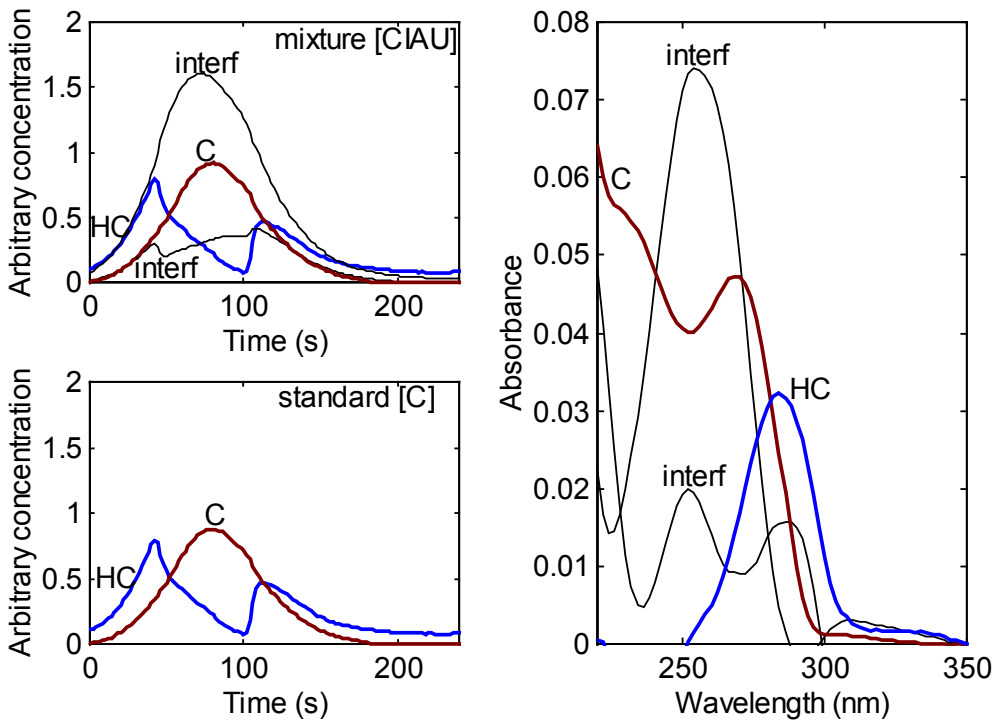
(d) concentration profiles of common species present in different runs have equal shapes.

RESULTS: CONTINUOUS-FLOW SYSTEM



Data matrix	%Prediction error			%fitting error
	Acidic	Basic	Decomposition product	
[CIAU;C]	9.2	51.6	7.8	1.45
[CU;C]	1.9	14.9	1.4	1.07
[CIA;C]	3.6	1.7	0.2	1.31
[drug;S]	2.4	8.6	1.1	1.74

RESULTS: SINGLE INJECTION FLOW-INJECTION



Data matrix	Prediction error		%fitting error
	Acidic	Basic	
[CIAU;C]	1.1	1.3	2.61
[CU;C]	2.8	0.3	6.68
[CIA;C]	17.4	0.5	4.78
[drug;S]	3.4	3.7	5.31

RANK-DEFICIENT MATRICES

A data matrix is rank-deficient when the number of significant contributions to the data variance is lower than the number of chemical components.

In closed reacting systems in which the different concentration profiles are linearly dependent due to the governing equilibrium reactions:

$$\text{Rank}\,(D) \leq \min\,(R+1,\ S)$$

R = number of independent reactions; S = number of species

Acid-base processes:

System	R	S	Rank	
1 analyte	1	2	2	Full-rank
2 analytes	2	4	3	Rank-deficient
3 analytes	3	6	4	Rank-deficient

RANK-AUGMENTATION BY MATRIX-AUGMENTATION

The inclusion of the matrix of the standard in a rank-deficient system increases the rank of the system by one:

Sample	Rank of the matrices		
	Individual	Augmented	
Single analyte	2	2	Full-rank
Binary mixture	3	4	Full-rank
Ternary mixture	4	5	Rank-deficient
Quaternary mixture	5	6	Rank-deficient

For quantitative purposes only partial resolution involving those species to be quantified is required.

This partial resolution is already achieved when the analysis is performed on the augmented matrix which contains the data matrix of the sample and that of the standard.

For quantitative purposes only partial resolution involving those species to be quantified is required.

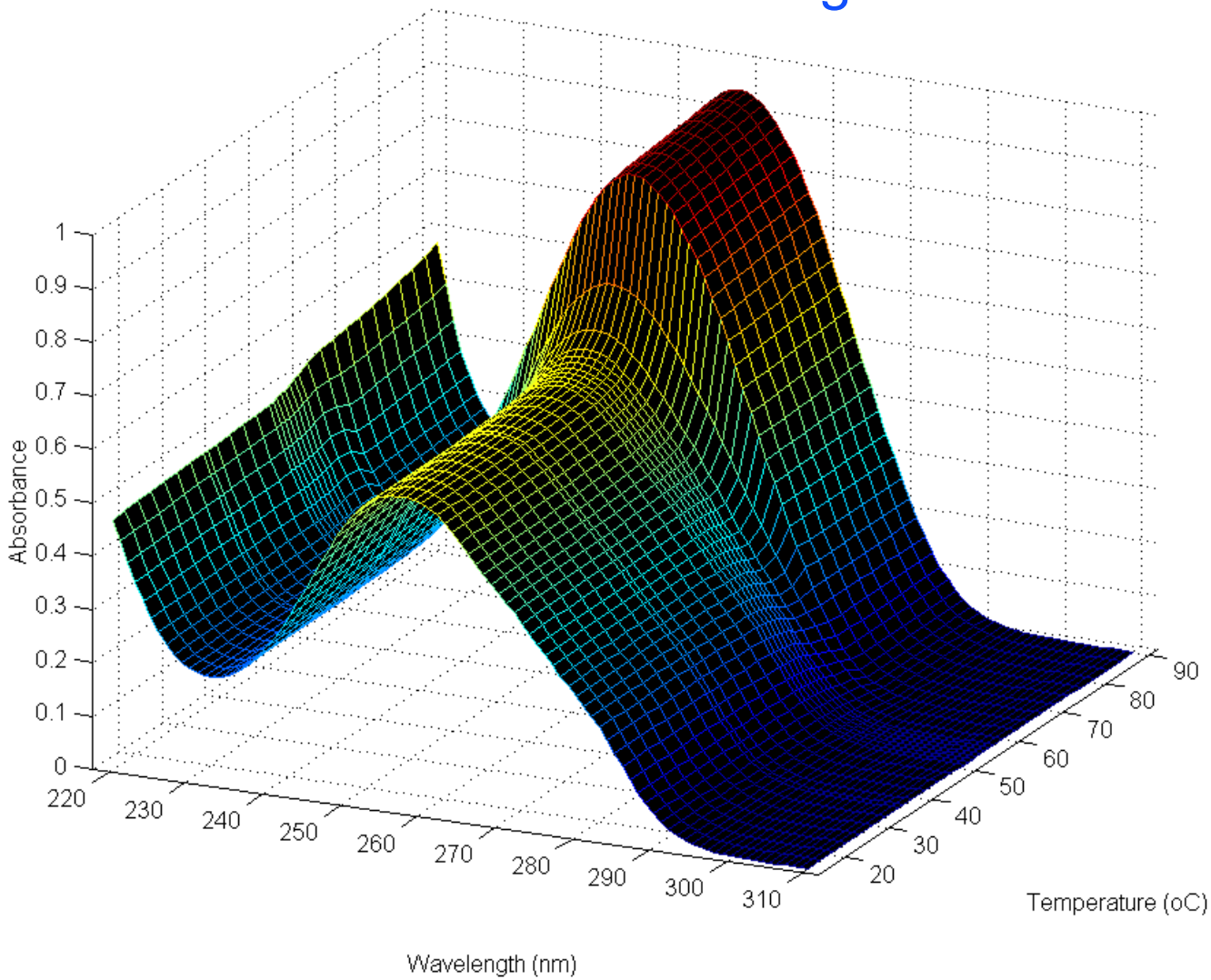
This partial resolution is already achieved when the analysis is performed on the augmented matrix which contains the data matrix of the sample and that of the standard.

Study of conformational equilibria of polynucleotides

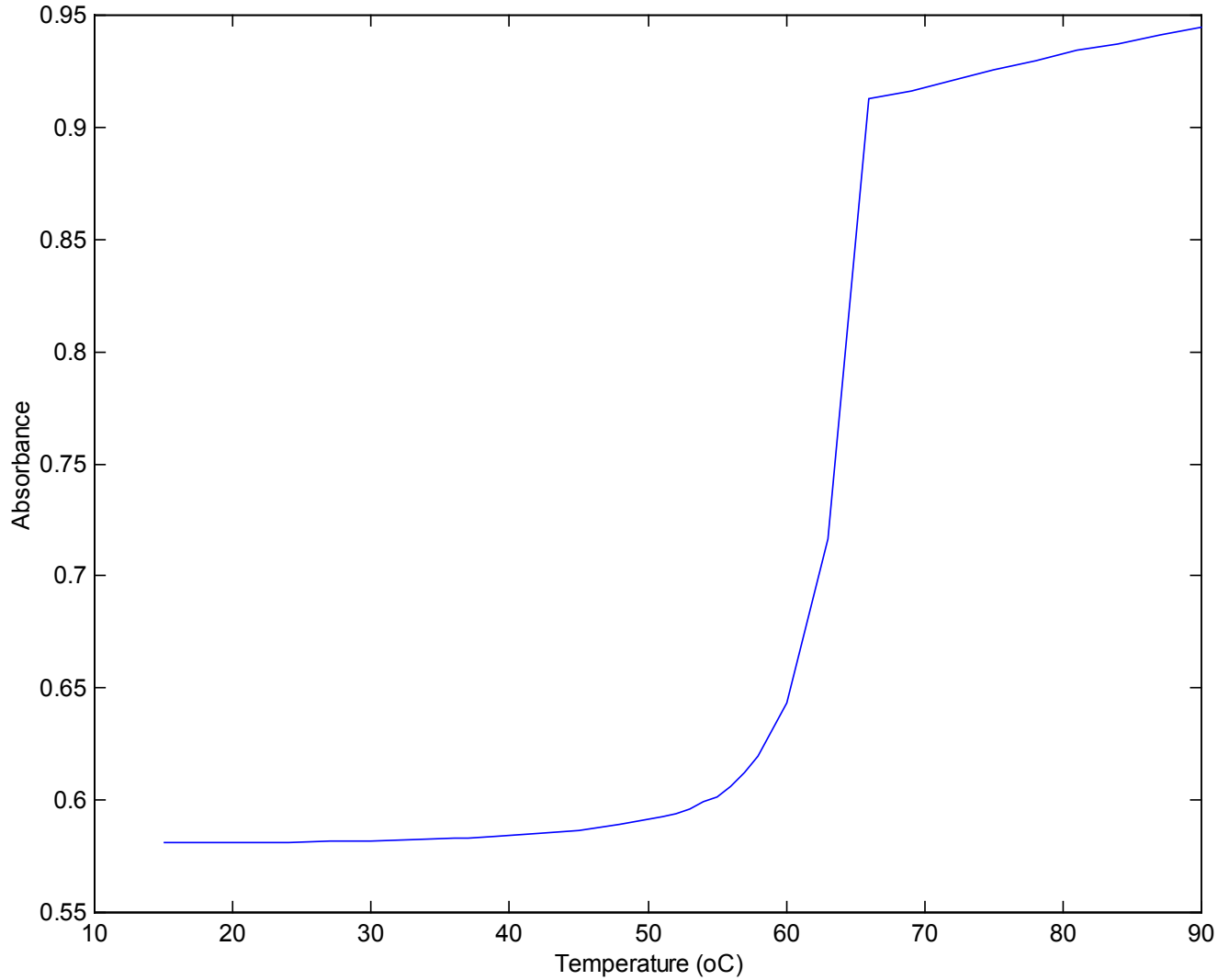
R.Tauler, R.Gargallo, M.Vives and A.Izquierdo-Ridorsa

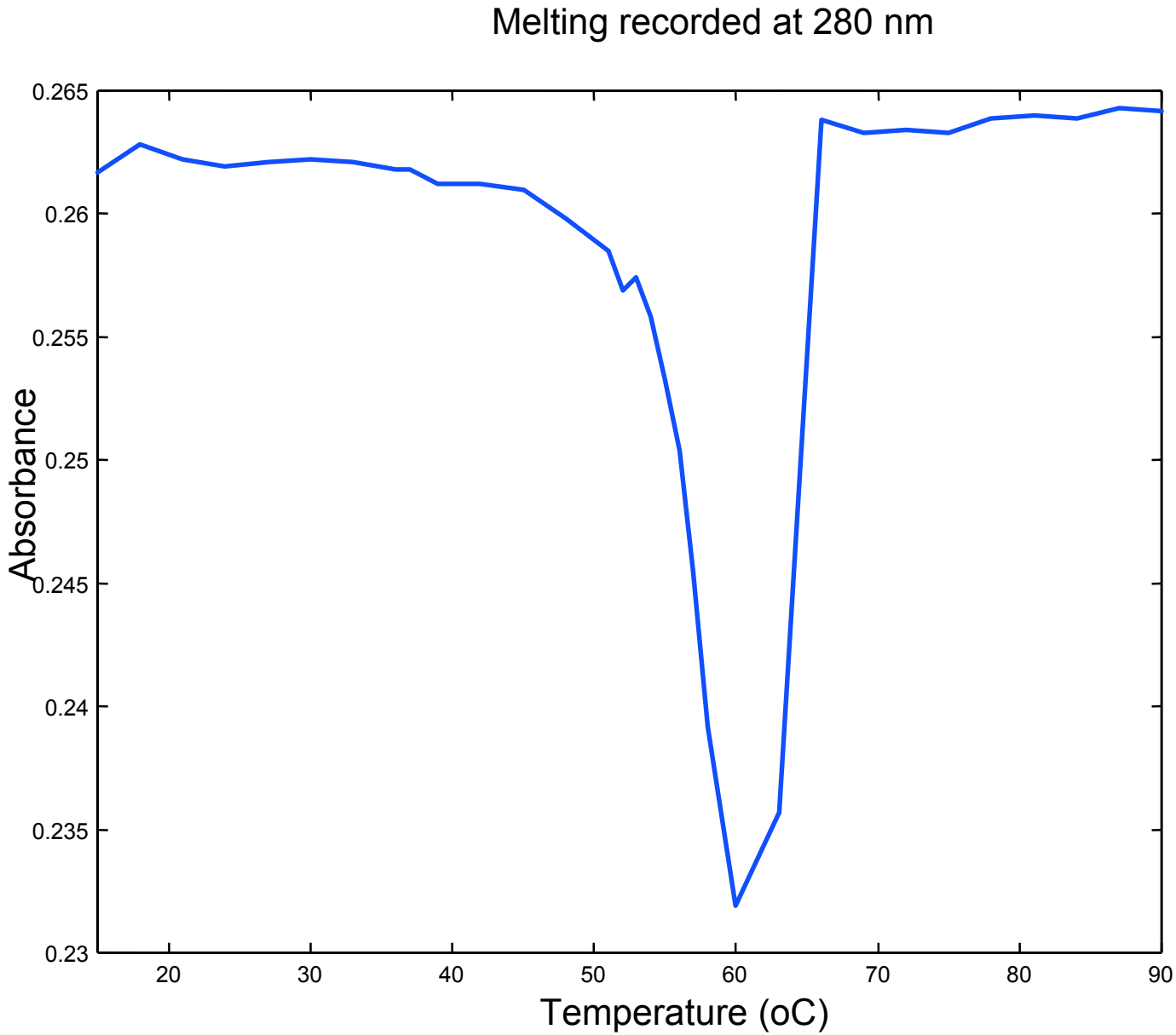
Chemometrics and Intelligent Lab Systems, 1998

poly(adenylic)-poly(uridylic) acid system
Melting data

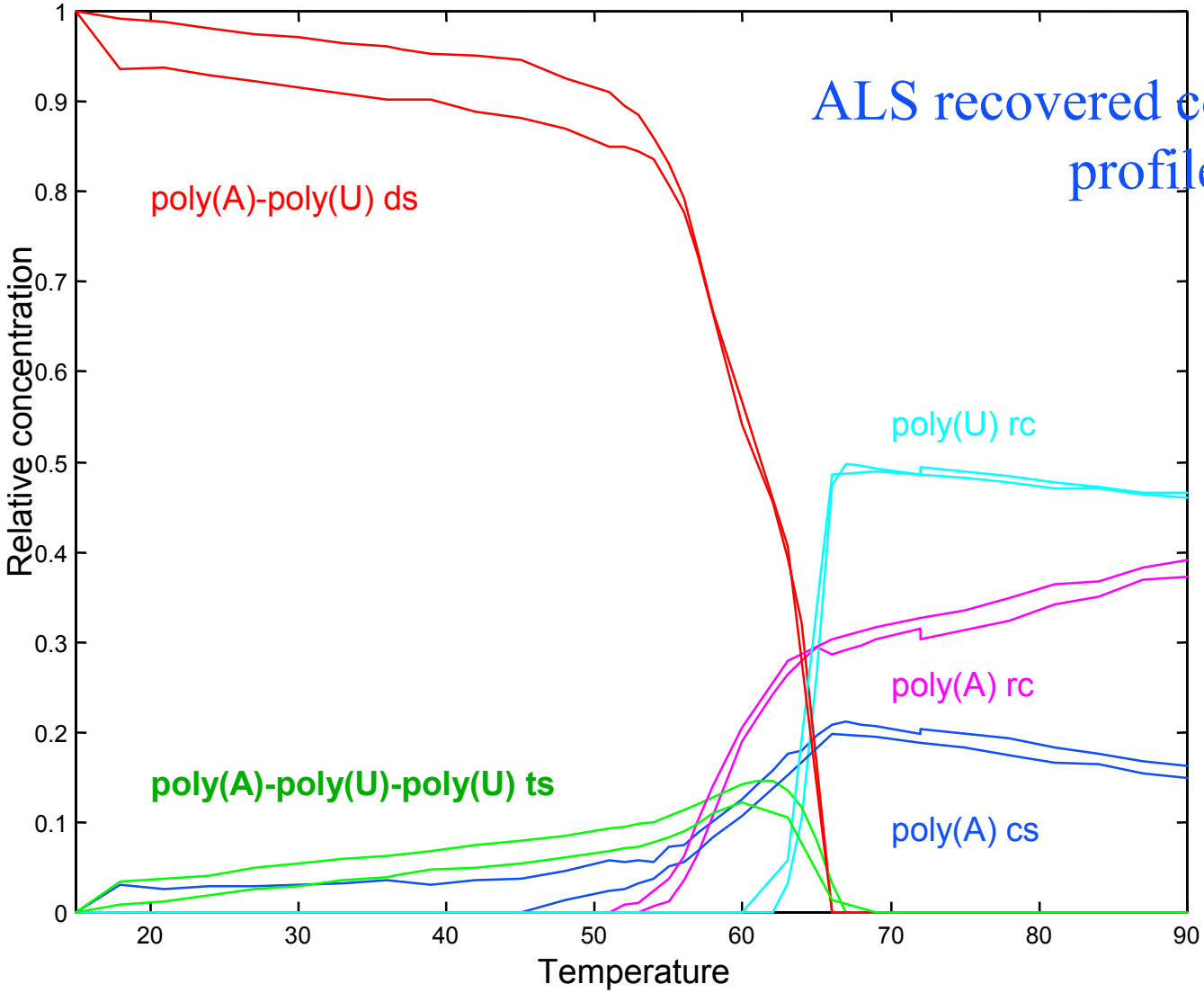


Melting data recorded at 260 nm (univariate data analysis)

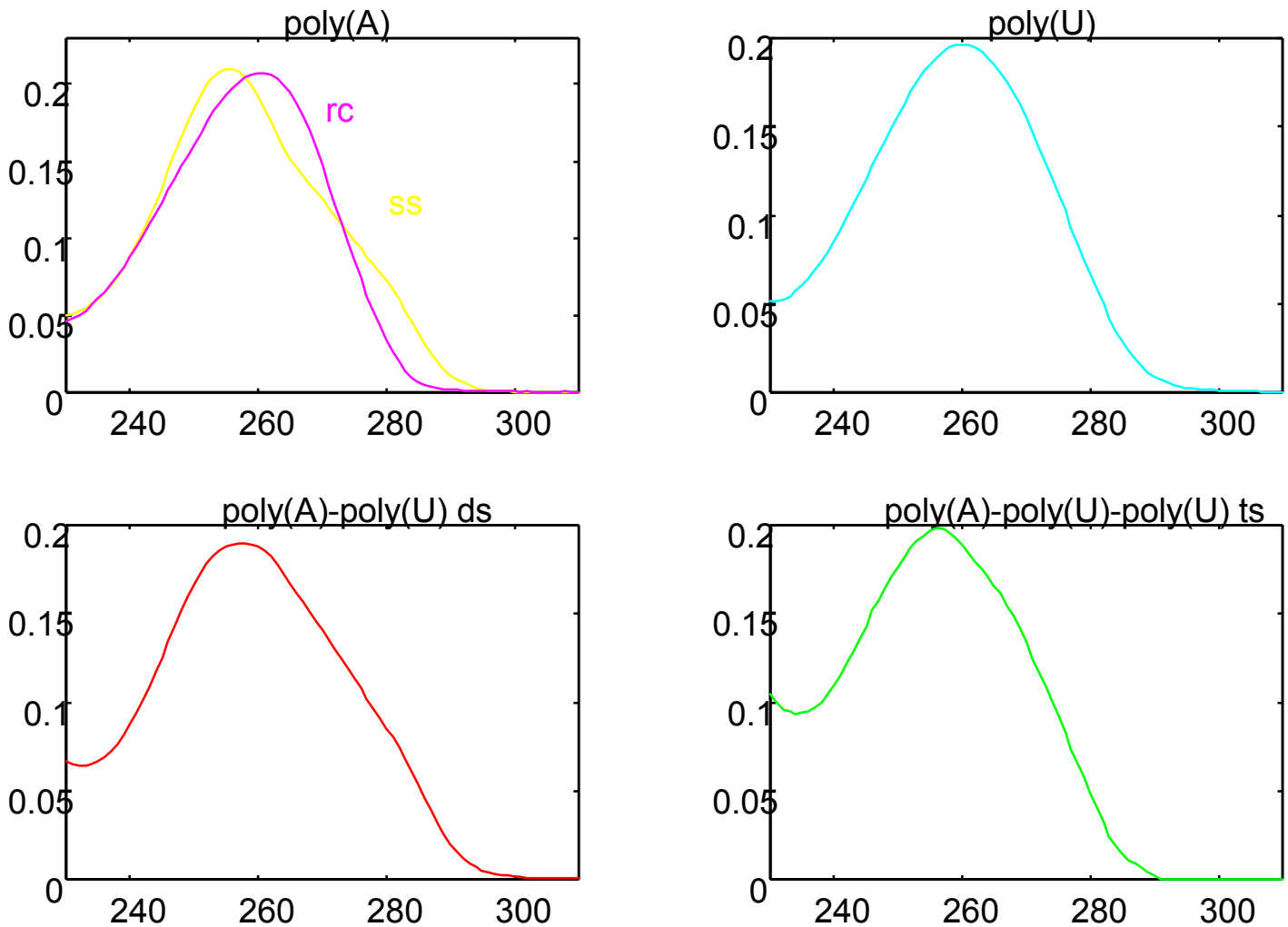



Melting recorded at 280 nm
Absorbance
Temperature (oC)
0.265
0.26
0.255
0.25
0.245
0.24
0.235
0.23
20
30
40
50
60
70
80
90

poly(A)-poly(U) system. Two different melting experiments

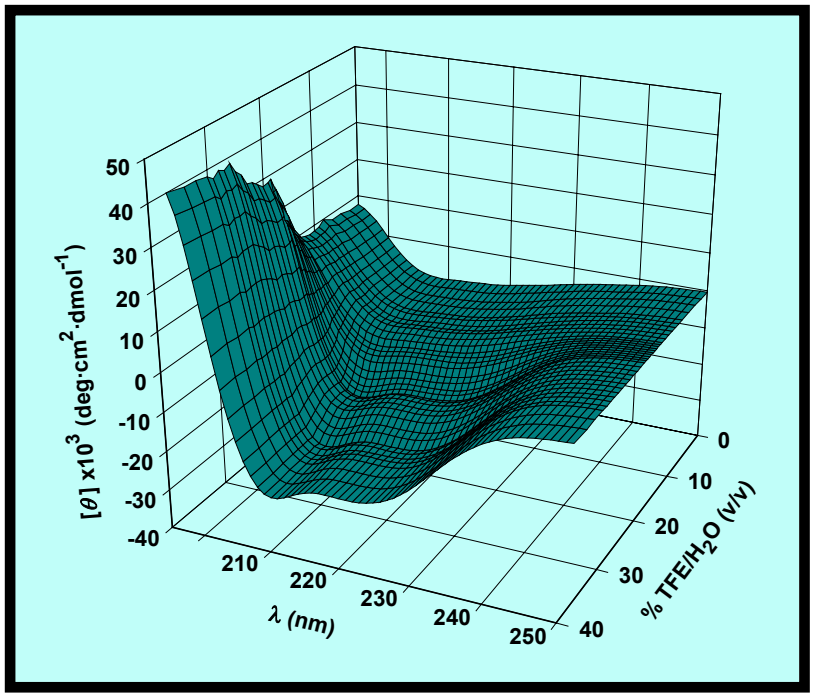


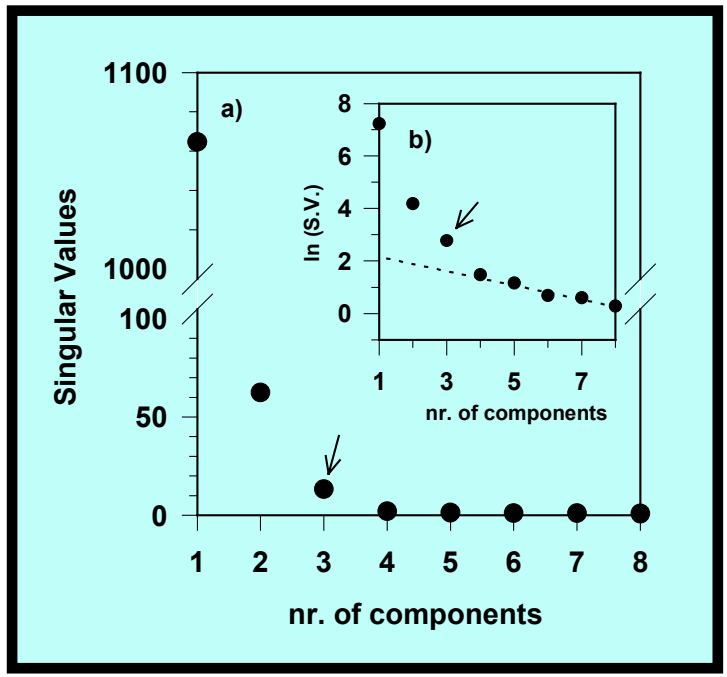
ALS recovered pure spectra



Protein folding

Example: Two-phase induction of the non-native α-helical form of the β-lactoglobulin in the presence of trifluoroethanol (Biophys. J.)





Mendieta J, Folque H. and Tauler R., Biophys. J., *in press*

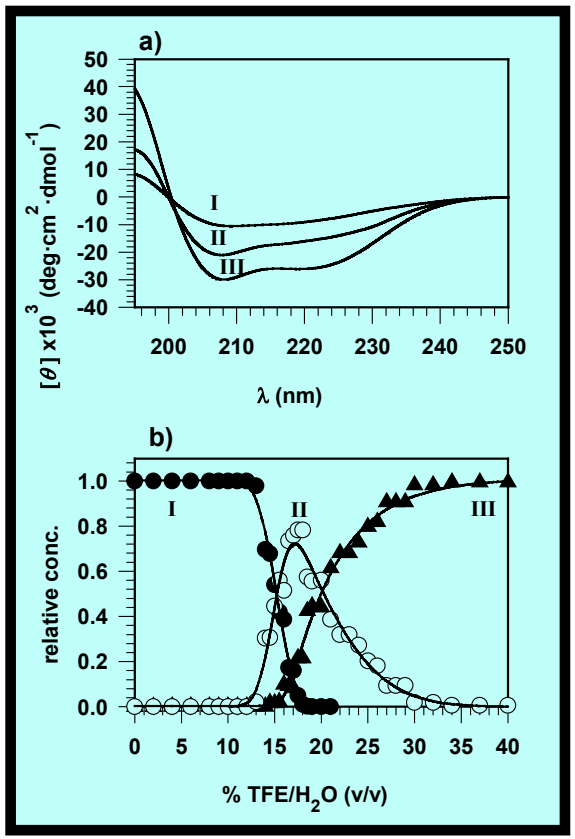
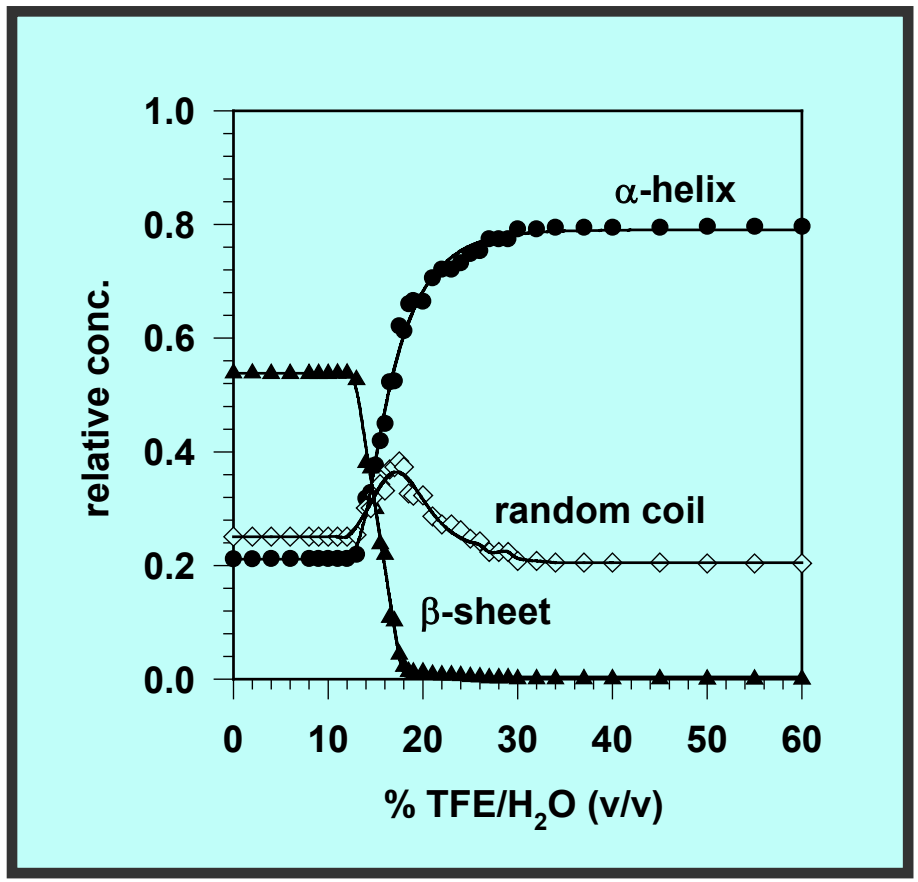


Table 1: Secondary structure of the spectra recovery after ALS optimization

	native like form	Intermediate form	non-native helical form
α-helix	21.14	56.11	79.61
β-sheet	53.81	2.14	0.00
random coil	25.05	41.75	20.39

* The content of secondary structure was evaluated by least squares deconvolution using as basis spectra corresponding to α-helix, β-sheet and random coil, those described by Chen *et al.* (ref *36*)

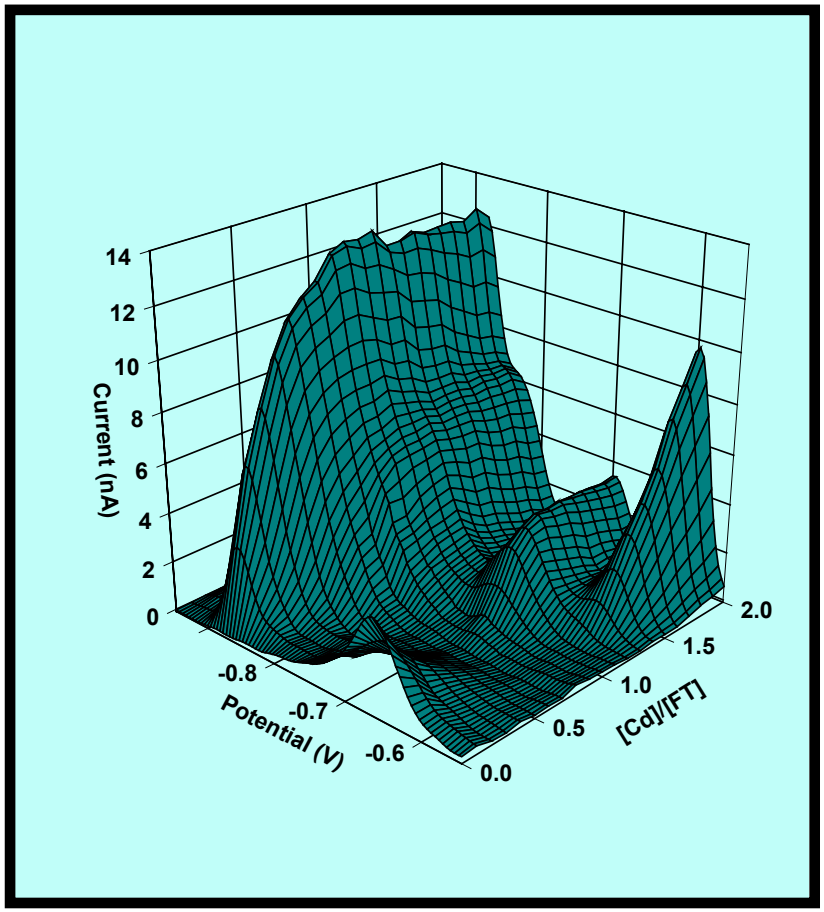
Mendieta J, Folque H. and Tauler R., Biophys. J., *in press*

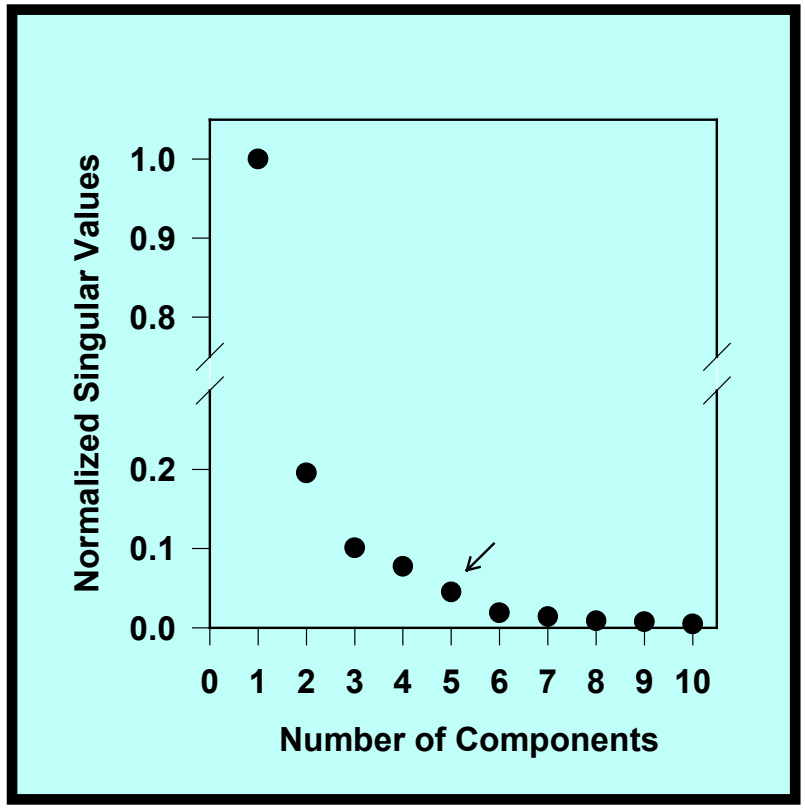


Mendieta J, Folque H. and Tauler R., Biophys. J., *in press*

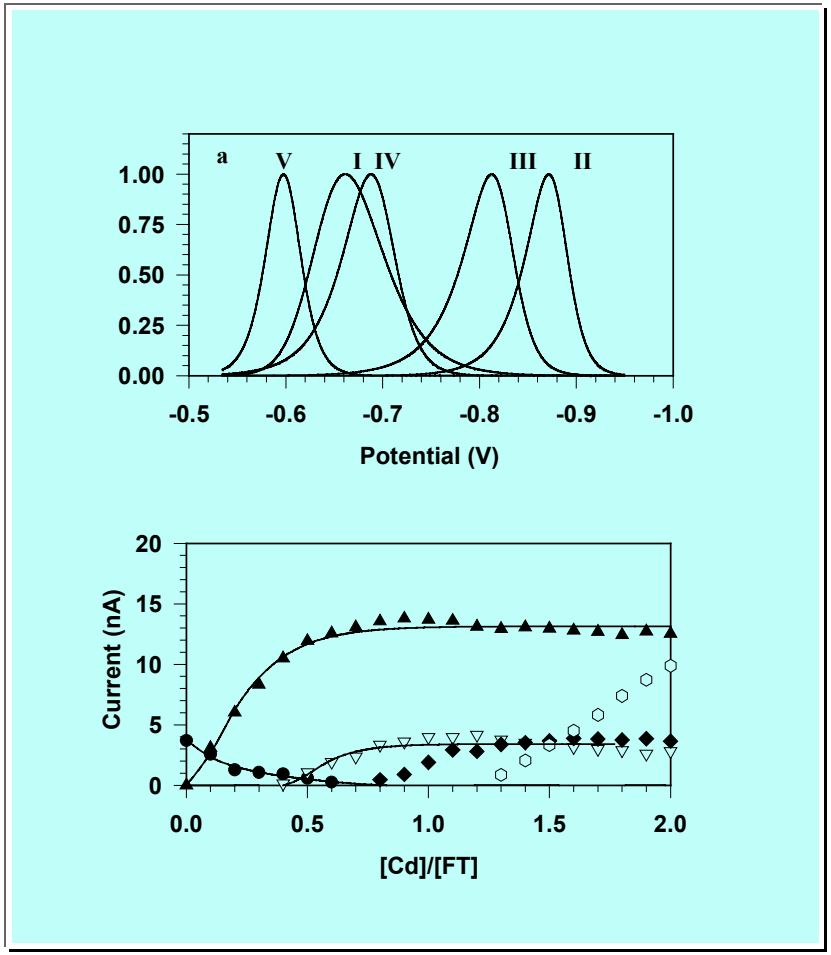
Interactions Me-protein

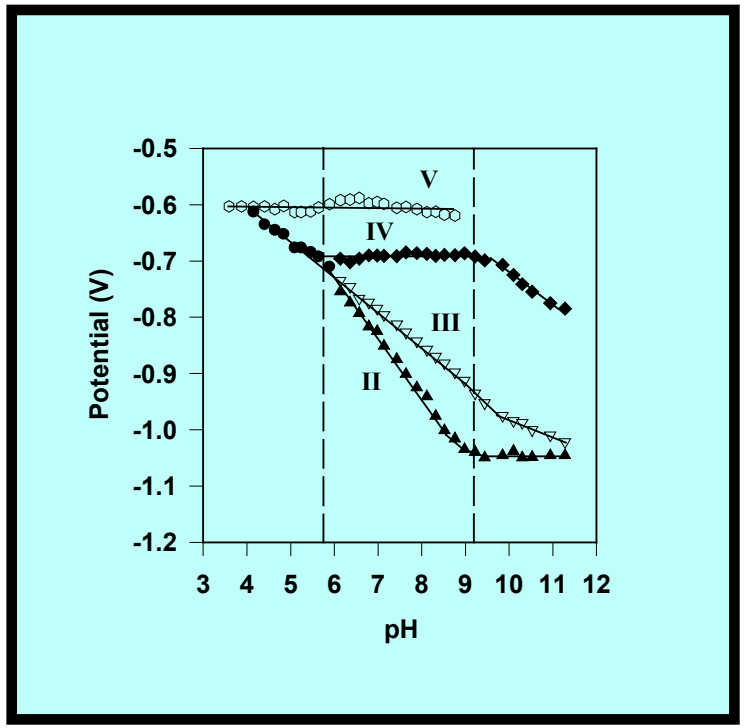
Example: Cadmium binding properties of the C-terminal hexapeptide from mouse methylthionein (submited for publication)



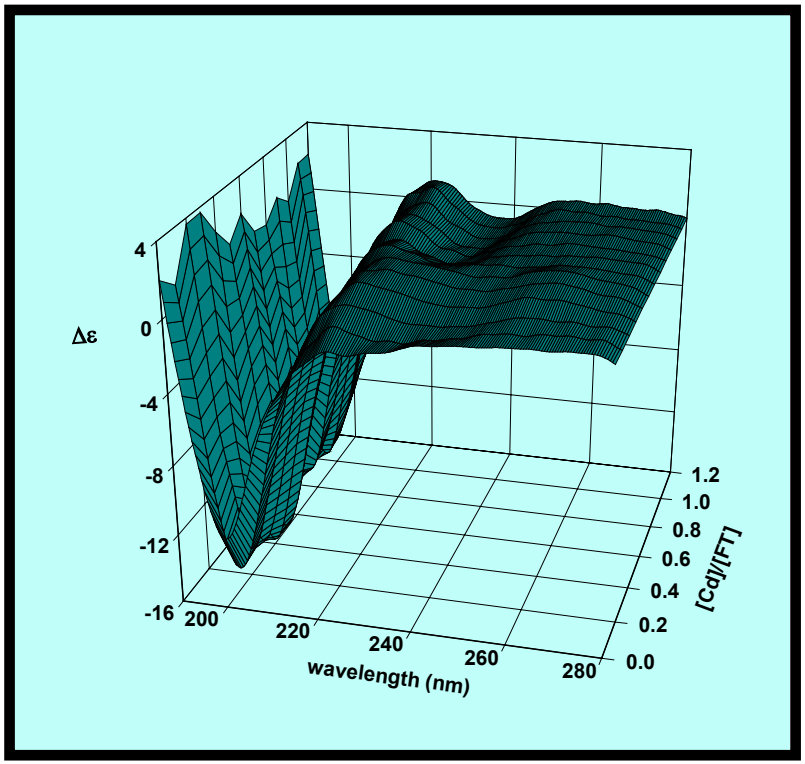


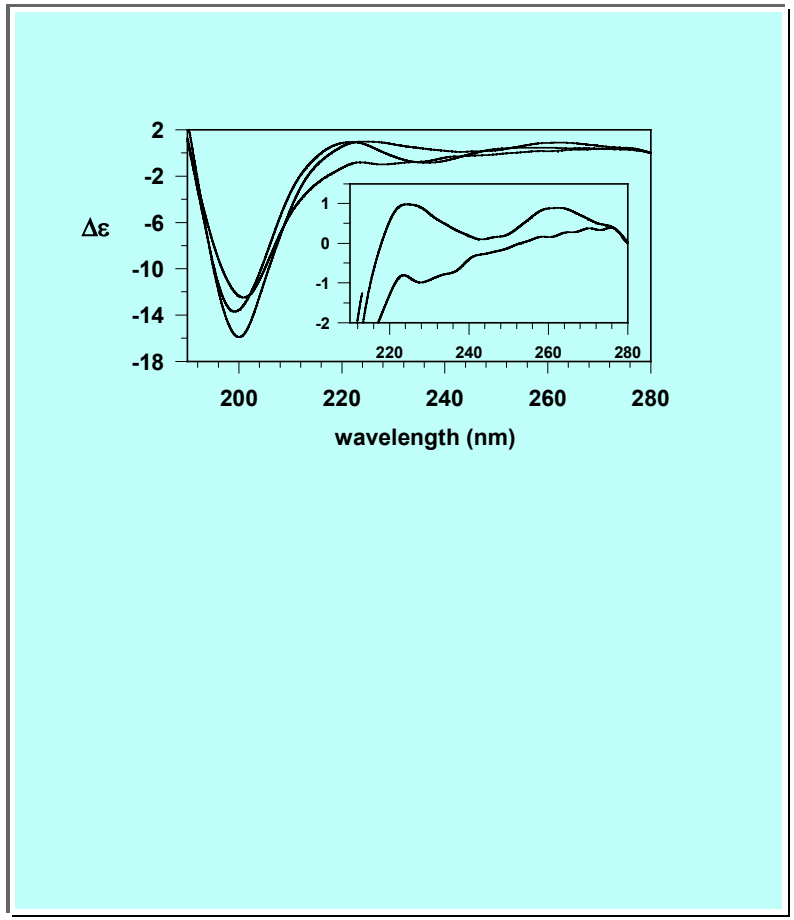
Mendieta J, Diaz-Cruz M.S., Monjonell A., Tauler R., Esteban M., submitted





Mendieta J, Diaz-Cruz M.S., Monjonell A., Tauler R., Esteban M., submitted

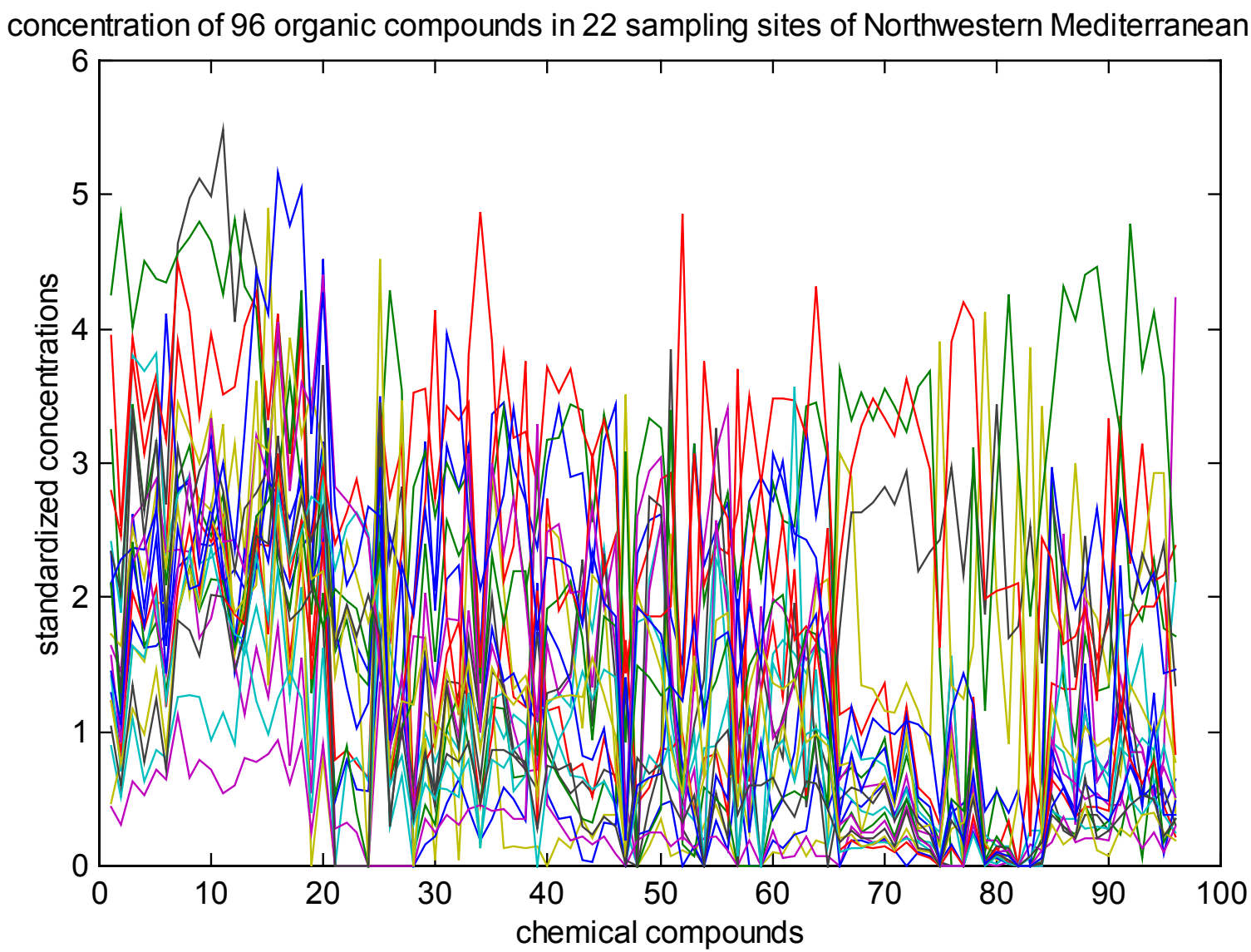


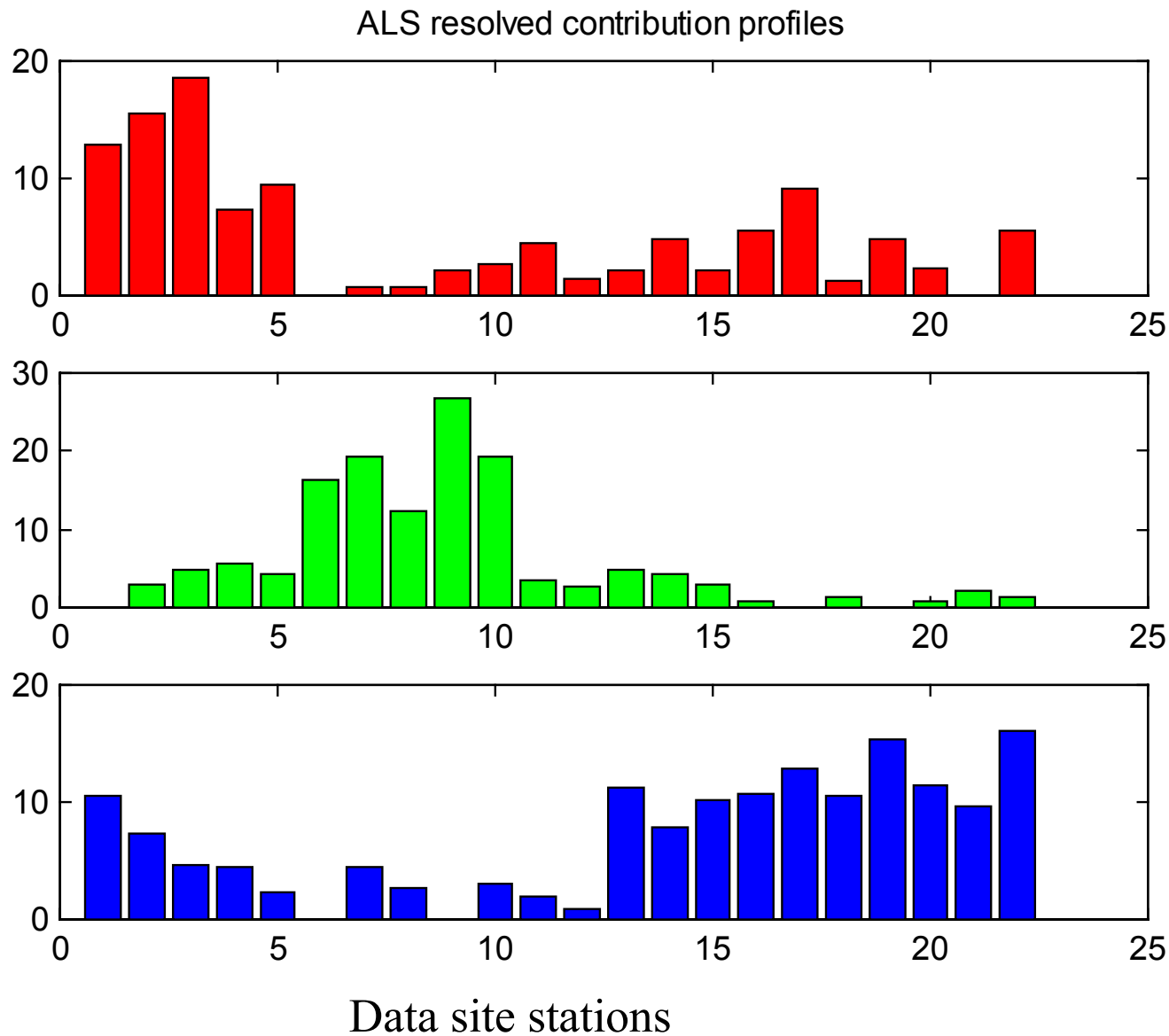


Mendieta J, Diaz-Cruz M.S., Monjonell A., Tauler R., Esteban M., submitted

Environmental data

J.S.Salou, R.Tauler*,J.M.Bayona and I.Tolosa, Environ.Sci.Technol., 31, (1997) 3482-90


concentration of 96 organic compounds in 22 sampling sites of Northwestern Mediterranean Sea
standardized concentrations
chemical compounds
0
1
2
3
4
5
6
0
10
20
30
40
50
60
70
80
90
100


ALS resolved contribution profiles
20
10
0
0
5
10
15
20
25
30
20
10
0
0
5
10
15
20
25
20
10
0
0
5
10
15
20
25
Data site stations