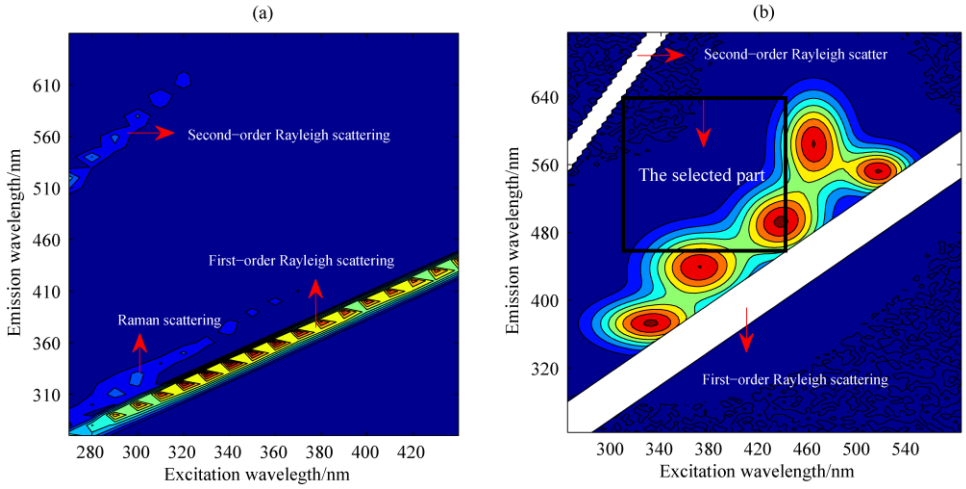

Fig. 1 (a) is the EEM spectra of a water sample, where the light scatterings are signed. (b) is a simulated EEM where Rayleigh scatterings are substituted by missing: the black rectangular scope shows the selected data, suggesting that it is unavoidable to lose massive information by the selecting method.

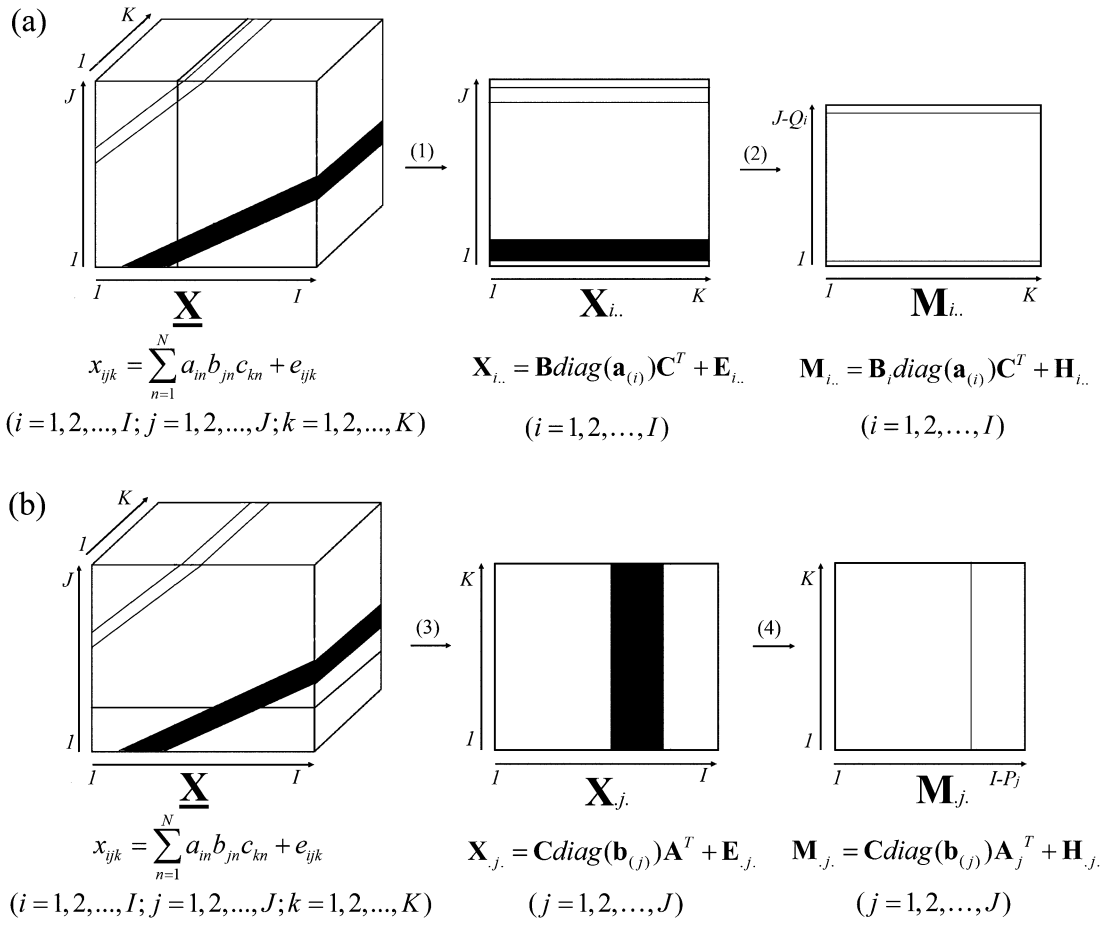

Fig. 2 The graphical representation of procedure of the strategy, two-direction resection for trilinear model: (a) is the process of obtaining the rest matrix $\mathbf{M}_{i..}$ by resecting the Rayleigh scattering region from $\mathbf{X}_{i..}$; similarly, the rest matrix $\mathbf{M}_{.j.}$ could be obtained from (b). The black and gray regions indicate first- and second-order Rayleigh scatterings, respectively. Steps (1), (2), (3) and (4) express the processes of getting $\mathbf{X}_{i..}$, $\mathbf{M}_{i..}$, $\mathbf{X}_{.j.}$ and $\mathbf{M}_{.j.}$ respectively.

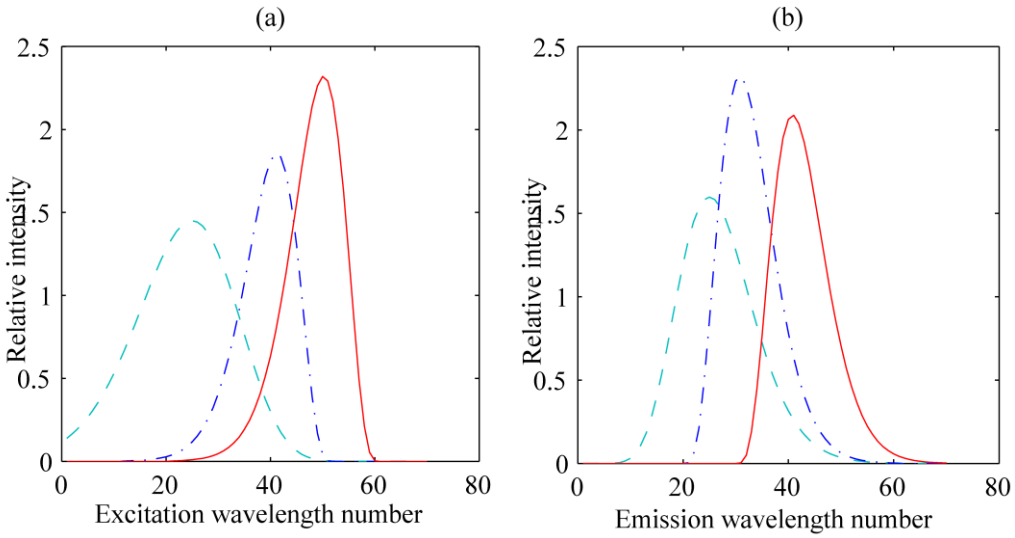

Fig. 3 Normalized profiles of the simulated data: (a) and (b) represent the simulated excitation and emission profiles, respectively. Solid, dot-dashed and dashed lines represent components 1, 2 and 3, respectively.

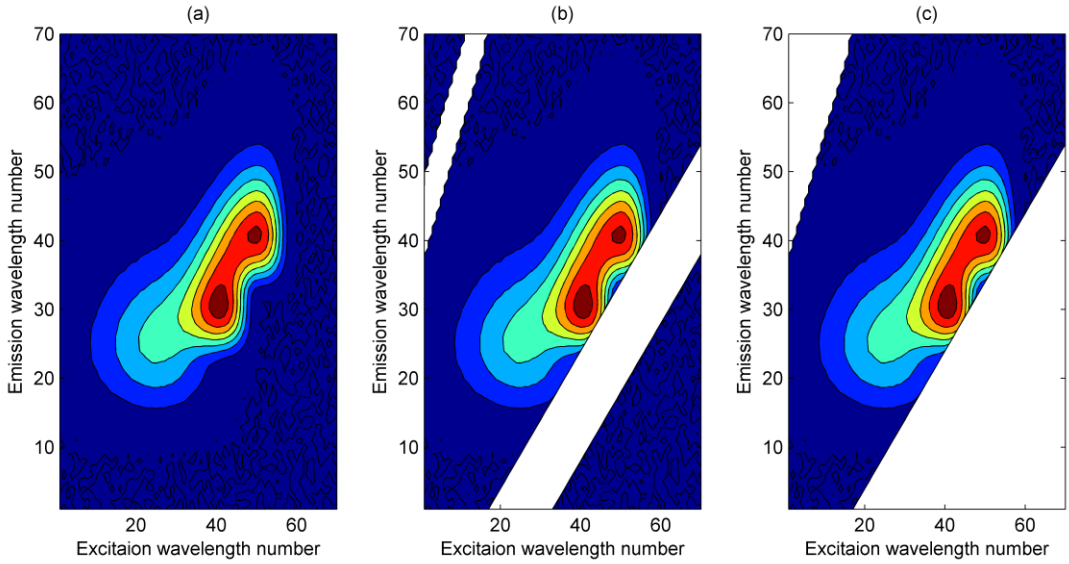

Fig. 4 EEMs of the 10th sample from the simulated data set at the large width of Rayleith scattering: (a) the original data without Rayleigh scattering; (b) Rayleigh scattering added in this EEM is substituted by missing; (c) the EEM treated by IMV-PARAFAC.

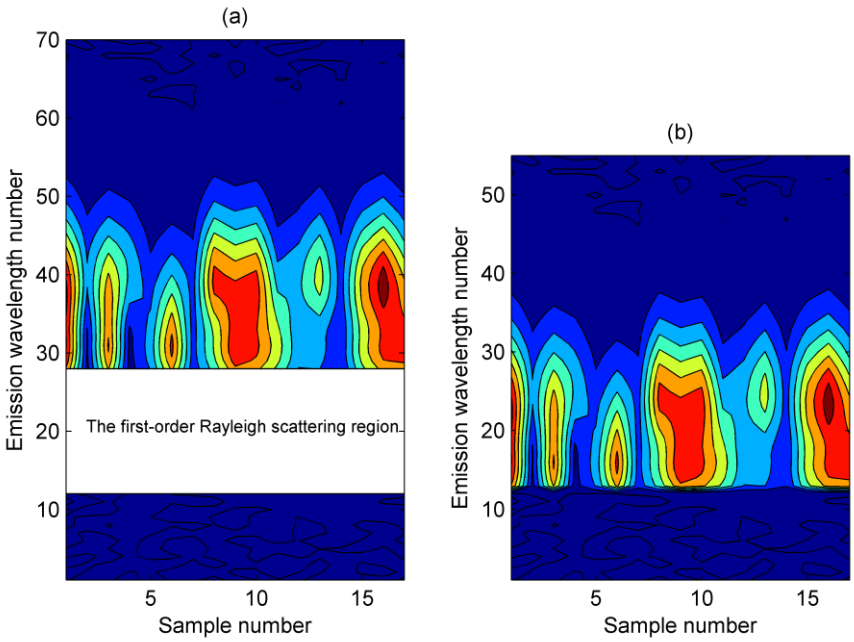

Fig. 5 The process of handling the matrix $\mathbf{X}_{i,.}$ (i=45) by TDR-PARAFAC: (a) the original EEM; (b) its scattering region is removed.

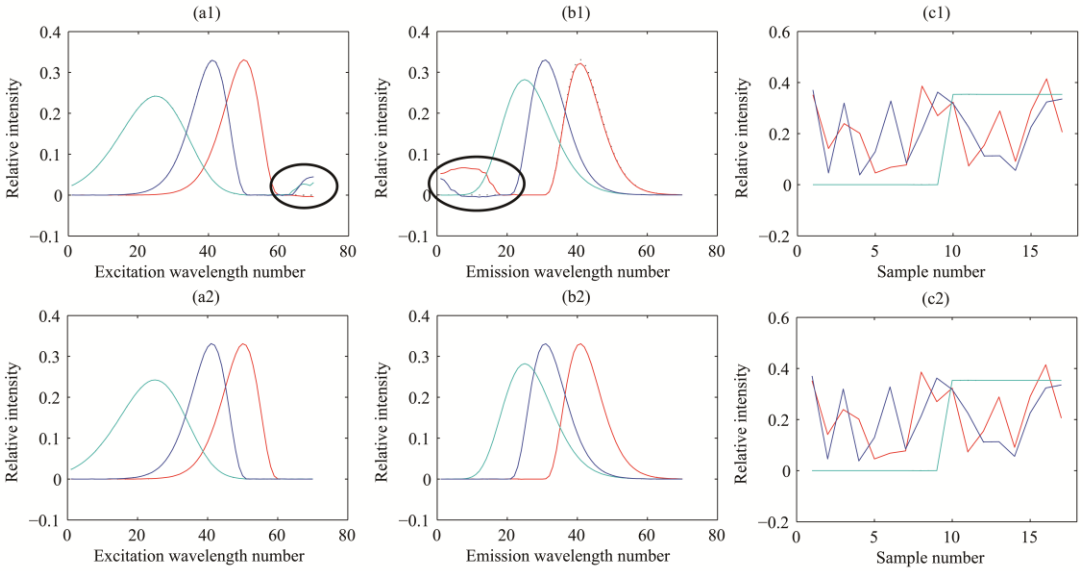

Fig. 6 Normalized resolved (solid line) and actual (dotted line) profiles of the simulated data with the small bandwidth of Rayleigh scattering: (a1)-(b1)-(c1) for IMV-PARAFAC; (a2)-(b2)-(c2) for TDR-PARAFAC.

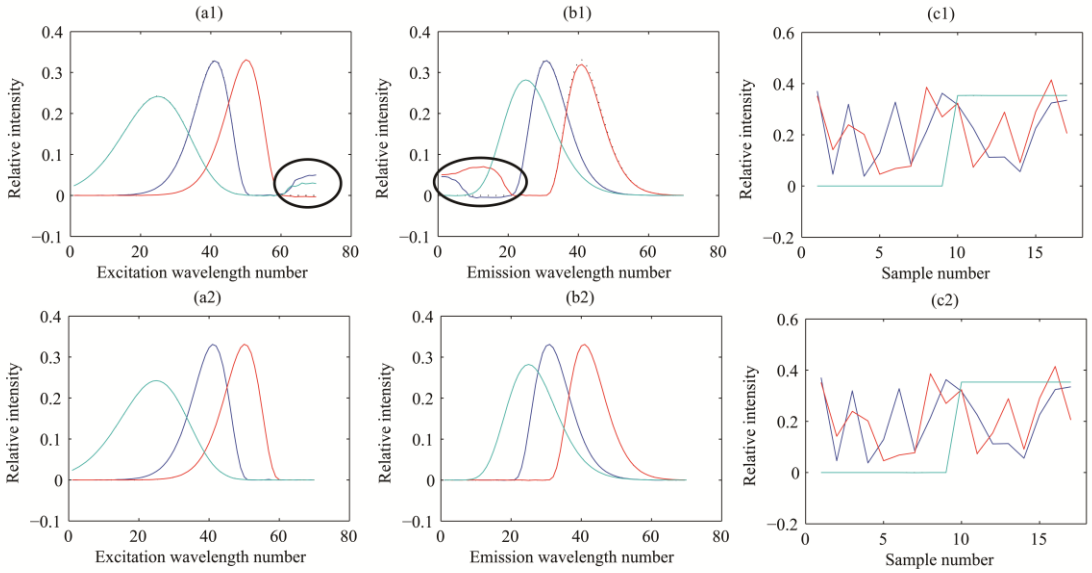

Fig. 7 Normalized resolved (solid line) and actual (dotted line) profiles of the simulated data with the large bandwidth of Rayleigh scattering: (a1)-(b1)-(c1) for IMV-PARAFAC; (a2)-(b2)-(c2) for TDR-PARAFAC.

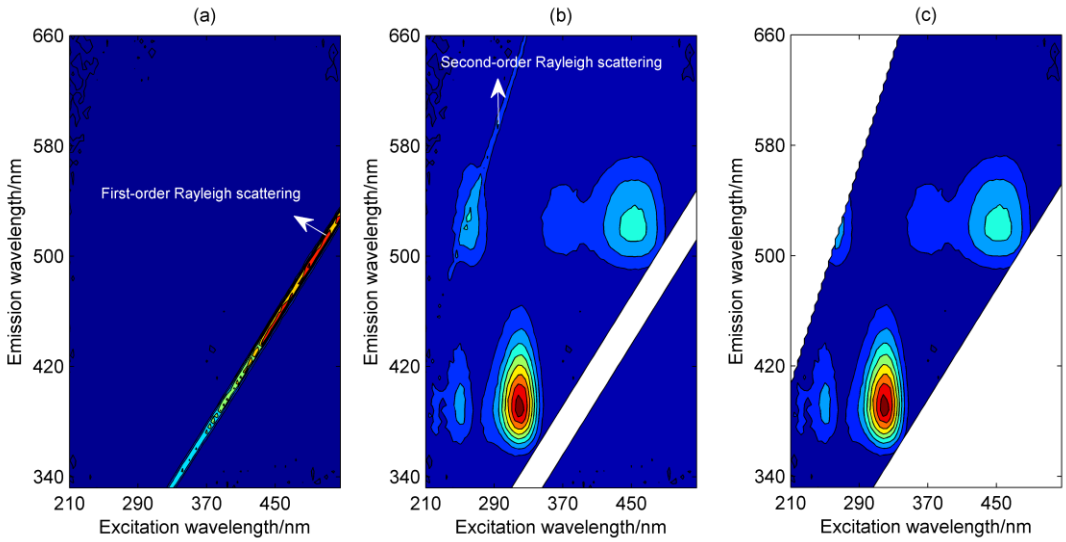

Fig. 8 EEMs of the 7th calibration sample from the real data set I: (a) the original one; (b) the first-order Rayleigh scattering region is substituted by missing; (c) the EEM is treated by IMV-PARAFAC.

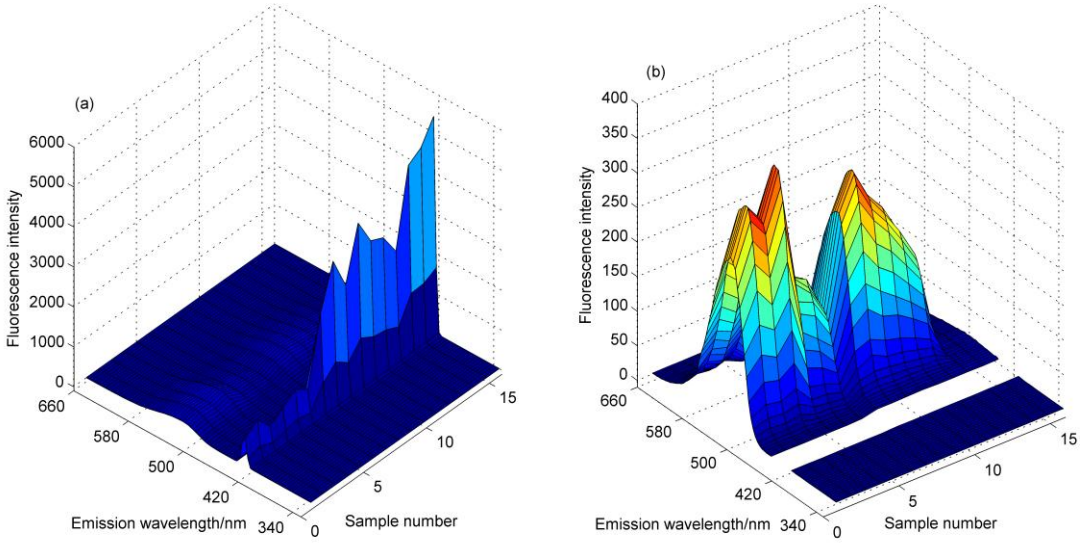

Fig. 9 The landscapes of $\mathbf{X}_{i..}$ (i=55) in the real data set I: (a) the original one; (b) its Rayleigh scattering region is substituted by missing.

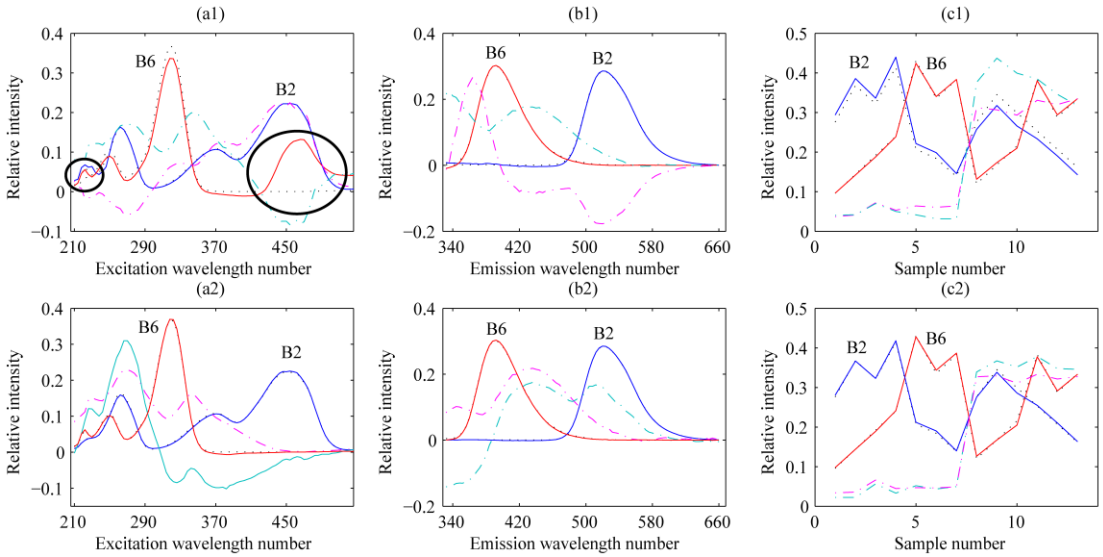

Fig. 10 Normalized resolved (solid line) and actual (dotted line) profiles in the real data I: (a1)-(b1) for IMV-PARAFAC; (a2)-(b2) for TDR-PARAFAC. Dash-dotted lines represent the resolved spectra profiles of interferents.

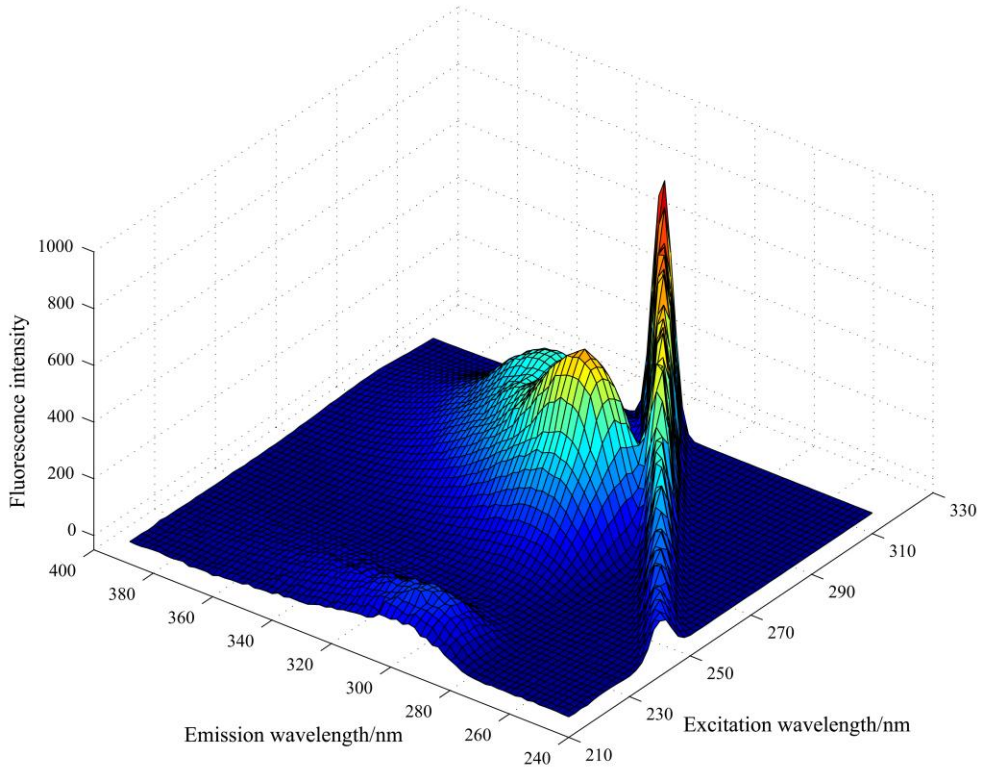

Fig. 11 The landscape of the calibration sample 5 in the real data set II.

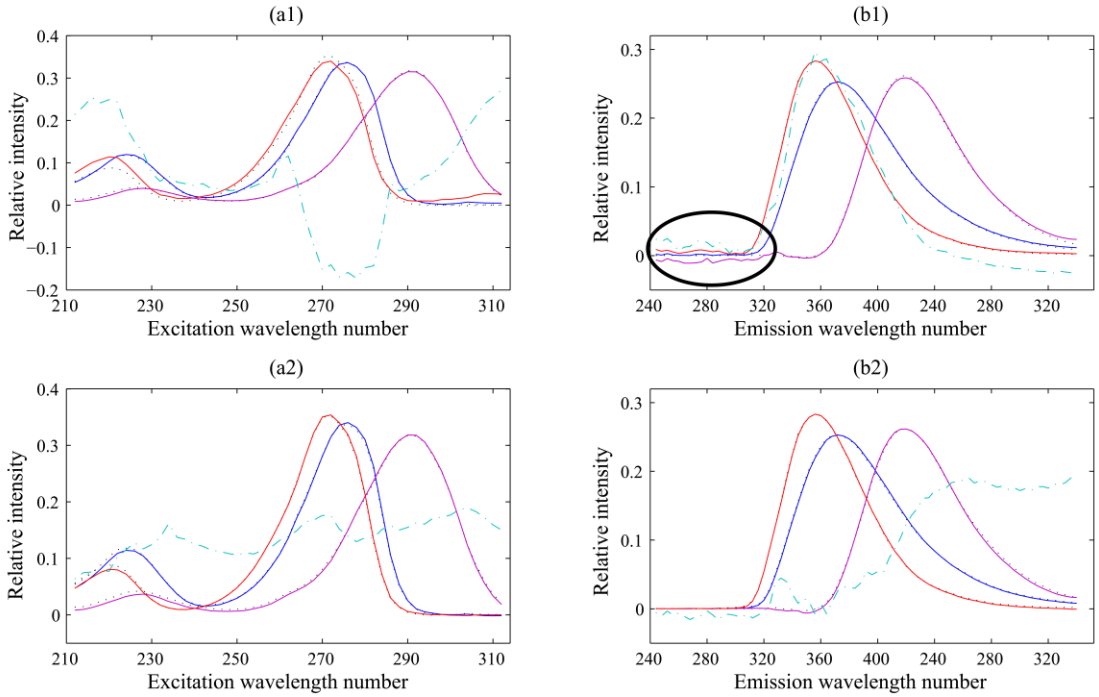

Fig. 12 Normalized resolved (solid line) and actual (dotted line) profiles in the real data II: (a1)-(b1) for IMV-PARAFAC; (a2)-(b2) for TDR-PARAFAC. Dash-dotted lines represent the resolved spectra profiles of interferents.

Table 1. Results from IMV-PARAFAC and TDR-PARAFAC in the real data set I.

Test Sample	Vitamin B2/ ng mL^{-1}			Vitamin B6/ ng mL^{-1}		
	Actual	IMV-PARAFAC	TDR-PARAFAC	Actual	IMV-PARAFAC	TDR-PARAFAC
1	120	105.4	118.6	134	147.5	140.3
2	150	130.6	146	187.6	194.8	186.2
3	130	109.1	123.1	241.2	235.8	227.8
4	110	95.7	109.4	428.8	426.9	419.9
5	90	77.6	89.9	321.6	330.2	324.1
6	70	57.9	69.2	375.2	376.2	371
Average Recovery/%		85.8±2.0	98.2±1.9		102.4±4.4	99.3±3.4
RMSEP/ng mL^{-1}		17.5	3.6		8.3	8.1

Table 2. Results from IMV-PARAFAC and TDR-PARAFAC in the real data set II.

Test Sample	Phenol/μg ml^{-1}			Resorcinol/μg ml^{-1}			Hydroquinone/μg ml^{-1}		
	Actual	IMV-PARAFAC	TDR-PARAFAC	Actual	IMV-PARAFAC	TDR-PARAFAC	Actual	IMV-PARAFAC	TDR-PARAFAC
1	0.232	0.230	0.236	1.013	1.022	1.026	0.300	0.317	0.307
2	0.697	0.689	0.701	1.182	1.093	1.090	–	–	–
3	–	–	–	–	–	–	0.400	0.427	0.416
4	0.116	0.115	0.114	0.506	0.438	0.444	0.700	0.700	0.690
5	0.349	0.340	0.340	–	–	–	–	–	–
6	0.581	0.580	0.588	0.675	0.663	0.652	0.200	0.220	0.207
7	0.813	0.786	0.784	–	–	–	0.500	0.501	0.491
8	–	–	–	0.844	0.790	0.785	–	–	–
Average Recovery/%		98.5±1.2%	99.2±2.2%		94.3±5.6%	94.1±5.1%		104.6±4.4%	101.3±2.7%
RMSEP/ng mL^{-1}		0.011	0.011		0.044	0.045		0.013	0.008