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[aabc@abc.org.br](mailto:aabc@abc.org.br)

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## Green method by diffuse reflectance infrared spectroscopy and spectral region selection for the quantification of sulphamethoxazole and trimethoprim in pharmaceutical formulations

FABIANA E.B. DA SILVA<sup>1</sup>, ÉRICO M.M. FLORES<sup>2,4</sup>, GRACIELE PARISOTTO<sup>2</sup>,  
EDSON I. MÜLLER<sup>2</sup> and MARCO F. FERRÃO<sup>3,4</sup>

<sup>1</sup>Departamento de Farmácia, Universidade Federal do Pampa, Campus Uruguaiana,  
Br 472, Km 07, Prédio 700, 97500-970 Uruguaiana, RS, Brasil

<sup>2</sup>Departamento de Química, Universidade Federal de Santa Maria, Campus Camobi, Avenida Roraima 1000,  
Cidade Universitária, Bairro Camobi, Prédio 18, Sala 2107, 97105-900 Santa Maria, RS, Brasil

<sup>3</sup>Departamento de Química Inorgânica, Universidade Federal do Rio Grande do Sul,  
Av. Bento Gonçalves, 9500, 91501-970 Porto Alegre, RS, Brasil

<sup>4</sup>Instituto Nacional de Ciência e Tecnologia de Bioanalítica/INCT-Bioanalítica, Cidade Universitária  
Zeferino Vaz, s/n, Bairro Barão Geraldo, Caixa Postal 6154, 13083-970 Campinas, SP, Brasil

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### ABSTRACT

An alternative method for the quantification of sulphamethoxazole (SMZ) and trimethoprim (TMP) using diffuse reflectance infrared Fourier-transform spectroscopy (DRIFTS) and partial least square regression (PLS) was developed. Interval Partial Least Square (*i*PLS) and Synergy Partial Least Square (*si*PLS) were applied to select a spectral range that provided the lowest prediction error in comparison to the full-spectrum model. Fifteen commercial tablet formulations and forty-nine synthetic samples were used. The ranges of concentration considered were 400 to 900 mg g<sup>-1</sup> SMZ and 80 to 240 mg g<sup>-1</sup> TMP. Spectral data were recorded between 600 and 4000 cm<sup>-1</sup> with a 4 cm<sup>-1</sup> resolution by Diffuse Reflectance Infrared Fourier Transform Spectroscopy (DRIFTS). The proposed procedure was compared to high performance liquid chromatography (HPLC). The results obtained from the root mean square error of prediction (RMSEP), during the validation of the models for samples of sulphamethoxazole (SMZ) and trimethoprim (TMP) using *si*PLS, demonstrate that this approach is a valid technique for use in quantitative analysis of pharmaceutical formulations. The selected interval algorithm allowed building regression models with minor errors when compared to the full spectrum PLS model. A RMSEP of 13.03 mg g<sup>-1</sup> for SMZ and 4.88 mg g<sup>-1</sup> for TMP was obtained after the selection the best spectral regions by *si*PLS.

**Key words:** chemometrics, diffuse reflectance infrared Fourier transform spectroscopy, green analytical method, high performance liquid chromatography, interval partial least squares (*i*PLS), synergy partial least squares (*si*PLS).

### INTRODUCTION

Quantitative analysis of pharmaceutical samples by spectroscopy is typically accomplished by univariate regression methods. Infrared (IR) spectroscopy

is generally only able to provide qualitative and semi-quantitative analysis of pharmaceutical samples due to deviations from Beer's law as a result of instrument and sample effects. However, the developments of reliable FTIR instrumentation and strong computerized data-processing capabilities have greatly improved the

Correspondence to: Marco Flôres Ferrão  
E-mail: [marco.ferrao@ufrgs.br](mailto:marco.ferrao@ufrgs.br)

performance of quantitative IR work. Thus, modern infrared spectroscopy has gained acceptance as a reliable tool for quantitative analysis (Settle 1997). Different accessories with diffuse or attenuated reflectance operating in mid-infrared and reflectance or transmittance mode operating in near infrared enabled the analysis of samples in many different forms such as solutions, powders and intact tablets (Kipouros et al. 2006, Armenta et al. 2005, Boyer et al. 2006, Silva et al. 2009, 2012, Ferreira et al. 2013). In some instances, previous sample treatment is unnecessary and the results are obtained in real time (Lin et al. 2006). Quantitative analysis involving infrared spectroscopy has been applied to pharmaceutical samples in association with multivariate methods (Bunaciu et al. 2010). Partial Least Square (PLS) regression is the most popular multivariate calibration technique to build prediction models using spectroscopic signals (Lavine and Workman 2010). This association is very important now, since infrared spectroscopy technology may be a quick, non-destructive and environmentally friendly method in comparison to traditional analyses methods. In addition, this procedure is considered low time-consuming and requires only few milligrams of sample (Ferrão and Davanzo 2005). There are a whole series of problems in quantitative analysis for which multivariate calibration is appropriate, such as treatment for spectra with strong band overlapping. However, some spectral regions may contain information due to other analytes, non-modeled interferences, background variations and interactions, which degrade model accuracy (Hemmateenejad et al. 2007).

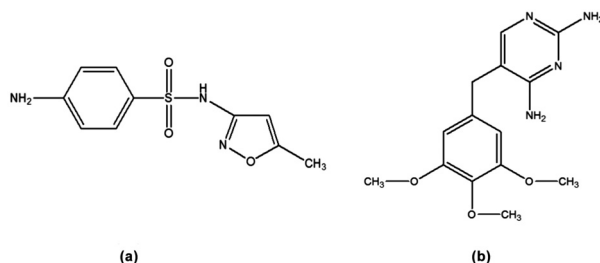
Recent applications have been published showing that spectral region selection using appropriate algorithms can significantly improve the performance of these full-spectrum calibration techniques, avoiding non-modeled interferences and building a well-fitted model (Lee et al. 2012, Nørgaard et al. 2005, Friedel et al. 2013). In practice,

multivariate regression model optimization is based on the identification of a complete data subset that will produce the lowest prediction error (Chen et al. 2008). Several approaches have been proposed for selection of optimal set of spectral regions for multivariate calibration such as genetic algorithms, interval PLS (iPLS) and synergy PLS (siPLS) (Silva et al. 2009, Friedel et al. 2013, Leardi and Nørgaard 2004, Navea et al. 2005, Bogomolov and Hachey 2007, Menezes et al. 2014, Ruschel et al. 2014). Interval PLS allows the construction of models with a spectral interval, and Root Mean Square Error of Cross Validation (RMSECV) values can be used as the criterion to evaluate the prediction ability of this interval. However, the exclusion of intervals with higher RMSECV values can cause the loss of useful information. Thus, advanced regression algorithms like siPLS can be applied to find favorable interval combinations for calibration. Spectroscopy procedures involving multivariate calibration have received increasingly wider applications in pharmaceutical analysis (Bodson et al. 2006, Blanco et al. 2007, Garcia-Reiriz et al. 2007, Müller et al. 2011, Li et al. 2012, Ferreira et al. 2013). However, mid-infrared (MIR) in combination with multivariate calibration is underutilized in pharmaceutical analysis in comparison to other spectroscopic techniques (Lundstedt-Enkel et al. 2006, Moros et al. 2007).

One of the most interesting pharmacological groups that can be analyzed involving multivariate calibration methods are the antimicrobial compounds. These compounds are usually pharmaceuticals combined and, prior to be analyzed, require a separation step. Sulphamethoxazole (SMZ) is a sulfonamide used in combination with trimethoprim (TMP) in a single pharmaceutical product to treat infections such as bronchitis, middle ear infection, urinary tract infection, and traveler's diarrhea (O'Neil 2006). The structural formulas of the sulphamethoxazole and trimethoprim are shown in Figure 1. Quantification

of SMZ and TMP in pharmaceutical preparations has been described using the spectrophotometric method based on red-colored product formation by diazotization of sulphonamides (Nagaraja et al. 2002), the flow injection systems (Tomšů et al. 2004), high performance liquid chromatography (Akay and Ozkan 2002, Goulas et al. 2014), second derivative spectrophotometry (Granero et al. 2002), adsorptive stripping voltammetry (Carapuça et al. 2005) and multivariate methods (Ni et al. 2006, Cordeiro et al. 2008).

Pharmacopoeial methods list HPLC as the official assay procedure for quality control in pharmaceutical preparations (USP 2007). In the present work, DRIFTS quantification of commercial tablets containing SMZ and TMP were presented. Interval Partial Least Square (iPLS) and Synergy Partial Least Square (siPLS) were applied to select a spectral range that provided the lowest prediction error in comparison to the full-spectrum model.



**Figure 1** - Sulphamethoxazole (A) and trimethoprim (B) structural formulas.

## MATERIALS AND METHODS

### MATERIALS AND SAMPLE PREPARATION

SMZ (batch 22960805) and TMP (batch 200504246) bulk drugs were purchased from Henrifarma (São Paulo, Brazil) and used for the preparation of synthetic samples. Forty-nine formulations (named synthetic samples) containing SMZ (400 to 900 mg g<sup>-1</sup> range), TMP (80 to 240 mg g<sup>-1</sup> range) and diluent (starch and magnesium stearate (99:1)) were prepared in laboratory, as shown in Table I. Fifteen formulations of commercial tablets (400 and 80

mg of SMZ and TMP per tablet, respectively) from nine manufactures (named commercial samples) were purchased from local drugstore or acquired by means of donation from pharmaceutical industries. SMZ and TMP certified reference materials were acquired from Brazilian Pharmacopoeia (batches 1010 and 1011 for SMZ and TMP, respectively). Methanol, acetonitrile and triethylamine were HPLC grade. For building of the clusters by hierarchical cluster analysis (HCA), the Euclidian distance and incremental linkage for were used. To carry out the HCA Pirouete<sup>®</sup> (Infometrix) software was used. For the selection of the calibration and the validation sets was employed The calibration set was constructed with thirty- two synthetic samples and nine commercial samples and the prediction set was constructed using seventeen synthetic samples and six commercial samples. Synthetic and commercial samples were prepared by powder mixing in a cryogenic mill Spex Certiprep (model 6750 Freezer Mill, Metuchen, EUA). A time period of 2 min was enough to mix each sample, which was ground up to particle sizes smaller than 80 µm.

**TABLE I**

**Synthetic samples used in calibration and prediction sets.**

Samples	SMZ (mg g <sup>-1</sup> )	TMP (mg g <sup>-1</sup> )	Excipients (mg g <sup>-1</sup> )
1 <sup>c</sup>	400	120	480
2 <sup>c</sup>	400	140	460
3 <sup>c</sup>	400	160	440
4 <sup>c</sup>	400	180	420
5 <sup>c</sup>	400	200	400
6 <sup>c</sup>	400	240	360
7 <sup>c</sup>	600	80	320
8 <sup>c</sup>	600	120	280
9 <sup>c</sup>	600	140	260
10 <sup>c</sup>	600	160	240
11 <sup>c</sup>	600	180	220
12 <sup>c</sup>	600	200	200
13 <sup>c</sup>	600	240	160
14 <sup>c</sup>	700	80	220
15 <sup>c</sup>	700	120	180
16 <sup>c</sup>	700	140	160

TABLE I (continuation)

Samples	SMZ (mg g <sup>-1</sup> )	TMP (mg g <sup>-1</sup> )	Excipients (mg g <sup>-1</sup> )
17 <sup>c</sup>	700	160	140
18 <sup>c</sup>	700	200	100
19 <sup>c</sup>	700	240	60
20 <sup>c</sup>	800	80	120
21 <sup>c</sup>	800	120	80
22 <sup>c</sup>	800	140	60
23 <sup>c</sup>	800	160	40
24 <sup>c</sup>	800	180	20
25 <sup>c</sup>	800	200	0
26 <sup>c</sup>	850	80	70
27 <sup>c</sup>	850	120	30
28 <sup>c</sup>	850	140	10
29 <sup>c</sup>	850	150	0
30 <sup>c</sup>	900	80	20
31 <sup>c</sup>	900	90	10
32 <sup>c</sup>	900	100	0
33 <sup>p</sup>	500	125	375
34 <sup>p</sup>	500	175	325
35 <sup>p</sup>	500	220	280
36 <sup>p</sup>	650	100	250
37 <sup>p</sup>	650	150	200
38 <sup>p</sup>	650	175	175
39 <sup>p</sup>	650	220	130
40 <sup>p</sup>	750	100	150
41 <sup>p</sup>	750	125	125
42 <sup>p</sup>	750	150	100
43 <sup>p</sup>	750	175	75
44 <sup>p</sup>	750	220	30
45 <sup>p</sup>	825	100	75
46 <sup>p</sup>	825	125	50
47 <sup>p</sup>	825	175	0
48 <sup>p</sup>	875	100	25
49 <sup>p</sup>	875	125	0

<sup>c</sup>synthetic samples used in calibration set.<sup>p</sup>synthetic samples used in prediction set.

## APPARATUS AND SOFTWARE

A Nicolet Magna 550 spectrometer (Nicolet Instrument Co., Madison, WI) was used for all the experiments. All spectra were recorded from 4000 cm<sup>-1</sup> to 600 cm<sup>-1</sup> with 16 scans and spectral resolution of 4 cm<sup>-1</sup>. This instrument was equipped with an EasiDiff<sup>®</sup> diffuse reflectance sampling accessory (Pike Technologies Inc., USA). For DRIFTS data

acquisition, 34.0 ± 0.3 mg of solid sample was placed onto the accessory and its spectrum was recorded without any dilution in KBr (Wu et al. 2010). For the background spectrum, we used only KBr grade spectroscopic. For each sample, three spectra were acquired and the average spectrum was used for building the multivariate models.

Data were handled using Matlab software 6.5 version (The Math Works, Natick, USA). For PLS multivariate calibration models, the “PLS Toolbox” 2.0 version was used (Eigenvector Technologies, Manson, USA). The *i*Toolbox for Matlab was used for the variable selection and the multivariate model development (Nørgaard et al. 2000). Software program was run on an IBM-compatible Intel Pentium 4 CPU 3 GHz and 2 Gbytes RAM microcomputer. The spectral band was divided into 10, 25 and 50 intervals for evaluation of the models generated from *i*PLS and *si*PLS algorithms. The differential compaction degree and particle size may lead to baseline variations and artefacts because of physical light scattering, therefore, multiplicative scatter correction (MSC) was employed to reduce this scattering effect. The spectra of samples were preprocessed by mean centering. A statistical F test ( $\alpha = 0.5\%$ ) was introduced in order to show if there were significant differences between prediction errors of the constructed models.

## HPLC REFERENCE METHOD

SMZ and TMP content was carried out using HPLC procedure according to the method described in the United States Pharmacopoeia (USP 2007). This procedure was chosen as reference and it was performed with a HPLC system consisting of Agilent 1100 Series system. Commercial tablets were finely powdered. A mass corresponding to 160 mg of sulphamethoxazole and 32 mg trimethoprim for each formulation was accurately weighed and dissolved in 100 mL of methanol. The sample preparations were subjected to sonication using an ultrasonic bath for fifteen minutes. An aliquot of 5

mL of each sample was added to 50 mL volumetric flasks and the mobile phase was used to complete the volume. All these determinations were performed in triplicate for synthetic and commercial samples.

#### MULTIVARIATE ANALYSIS

Multivariate chemometric methods were applied to obtain quantitative information from the measurements. Partial Least Square Regression was applied to DRIFTS data to build calibration models, enabling prediction of SMZ and TMP amounts in pharmaceutical preparations. The Root Mean Square Error (RMSE) was calculated according to the equation 1 (Geladi et al. 2004):

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{n}} \quad (1)$$

Where:  $\hat{y}_i$  is the predicted value for the test set sample  $i$ ,  $y_i$  the measured value for the test set sample  $i$ , and  $n$  is the number of observation in the tested set. Root Mean Square Error of Cross-Validation was used to evaluate the error of the proposed calibration models and to select the number of latent variables. Root Mean Square Error of Prediction (RMSEP) was used to evaluate the prediction ability between different PLS models (Brereton 2003). Performance of the obtained calibration models was checked through relative Standard Error of Prediction (RSEP) as calculated by:

$$RSEP = \sqrt{\frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{\sum_{i=1}^n (y_i)^2}} \times 100 \quad (2)$$

Where:  $\hat{y}_i$  is the predicted value for the test set sample  $i$ ,  $y_i$  the measured value for the test set sample  $i$ . The  $i$ PLS models were built with the spectrum divided into 10, 25 and 50 intervals. The  $i$ PLS routine generated graphical information indicating

the optimal number of latent variables used in each interval model, and RMSECV values. In this case, the subinterval that presented the lowest RMSECV values was selected. Synergy PLS models were constructed with the spectrum set divided into 10, 25 and 50 intervals and combinations from two to five intervals. The combined subintervals that presented the lowest RMSECV values were selected. The systematic error ("bias") and the Standard Deviation of Validation (SDV) were calculated from equations 3 and 4, respectively (ASTM E1655-05 2005):

$$bias = \frac{\sum_{i=1}^n (y_i - \hat{y}_i)}{n} \quad (3)$$

$$SDV = \sqrt{\frac{\sum_{i=1}^n [(y_i - \hat{y}_i) - bias]^2}{n - 1}} \quad (4)$$

Thereafter, the t-test was applied, according to equation 5 (ASTM E1655-05 2005):

$$t_{sist} = \frac{|bias| \sqrt{n}}{SDV} \quad (5)$$

The systematic error was not considered significant for the  $t_{sist}$  values lower than critical value at  $\alpha = 0.05$  and  $df = n-1$ .

Results obtained by DRIFTS for SMZ and TMP quantification in commercial tablets were compared with the interval permitted by Brazilian Pharmacopoeia (93-107% declared value).

## RESULTS AND DISCUSSION

### SELECTION OF CALIBRATION AND VALIDATION SAMPLES

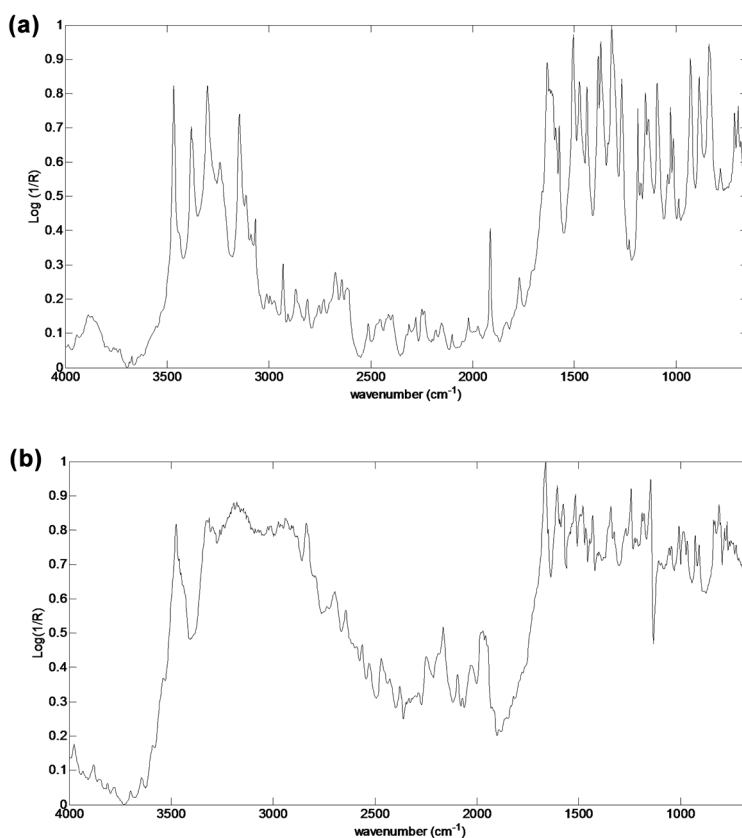
The variations in the formulations could impose quite a challenge for the development of the universal model. Although the drugs in the tablets are the same, the types and amounts of excipients

in their formulations can vary considerably as per manufacturer products. If careful considerations are made when selecting the representative calibration sample set that will cover these variations, the universal model should be achievable. A Hierarchical Cluster Analysis (HCA) was then performed for a representative calibration and prediction sets for different samples (synthetic and commercial samples).

#### FULL-SPECTRUM PLS MODEL

Figure 2 shows the SMZ and TMP spectra used for the preparation of the synthetic samples. These

spectra show signals (SMZ signals: N-H stretch 3482, 3395 and 3315  $\text{cm}^{-1}$ , =C-H stretch 3160  $\text{cm}^{-1}$ , overtone aromatic p-disubstituted 1771  $\text{cm}^{-1}$ , C=N stretch isoxazole ring 1634  $\text{cm}^{-1}$ , C=C aromatic stretch 1475  $\text{cm}^{-1}$ , O=S=O stretch 1317 and 1189  $\text{cm}^{-1}$ , C-H aromatic p-disubstituted 840  $\text{cm}^{-1}$ ; TMP signals: N-H stretch 3475 and 3319  $\text{cm}^{-1}$ , C-H stretch 2935 and 2848  $\text{cm}^{-1}$ , C=C aromatic stretch 1480  $\text{cm}^{-1}$ , C-O stretch 1243 and 1046  $\text{cm}^{-1}$ , C-H aromatic substituted 838  $\text{cm}^{-1}$ ) corresponding to the aromatic rings (in this case heteroaromatic) for the pharmaceutical compounds used.



**Figure 2** - DRIFTS spectra of sulphamethoxazole (A) and trimethoprim (B).

Initially, in order to have a measurement of the quality of the variable selection algorithms, as well as the effects that pretreatment, models were built using DRIFTS full-spectrum information. Full-spectrum PLS models were obtained with

fourteen and eight latent variables for spectra with or without pretreatment, and results are shown in Tables II and III. Through RMSEP value was calculated for the accuracy of the results obtained with DRIFTS technique.

**TABLE II**  
**Statistical results to *i*PLS calibration models and full-spectrum PLS model without pretreatment for the SMZ.**

Model SMZ	VN <sup>a</sup>	Intervals	LVs <sup>b</sup>	RMSECV SMZ (mg g <sup>-1</sup> )	R <sup>2</sup> <sub>cal</sub>	RMSEPSMZ (mg g <sup>-1</sup> )
PLS	1764	all	14	24.16	0.985	21.12
<i>i</i> PLS10	175	9	9	26.74	0.964	27.44
<i>i</i> PLS25	70	17	7	28.81	0.834	33.12
<i>i</i> PLS50	34	34	5	30.09	0.716	33.21

<sup>a</sup>VN: total number of variables.

<sup>b</sup>LVs: latent variables.

**TABLE III**  
**Statistical results to *i*PLS calibration models and full-spectrum PLS model for the SMZ.**

Model SMZ	VN <sup>a</sup>	Intervals	LVs <sup>b</sup>	RMSECV SMZ (mg g <sup>-1</sup> )	R <sup>2</sup> <sub>cal</sub>	RMSEPSMZ (mg g <sup>-1</sup> )
PLS	1764	all	8	23.29	0.999	16.99
<i>i</i> PLS10	175	9	9	21.74	0.979	20.91
<i>i</i> PLS25	70	17	2	27.46	0.954	31.85
<i>i</i> PLS50	34	34	2	29.86	0.634	34.21

<sup>a</sup>VN: total number of variables.

<sup>b</sup>LVs: latent variables.

When the results with and without pretreatment were compared, the number of latent variables increase for the models without pretreatment. The RMSECV and RMSEP values also increased for the models without pretreatment. These results demonstrate the necessity of pretreatments of the spectral data to build a multivariate regression models. On this basis in other tables will be presented only the results that employ them preprocessed spectral data.

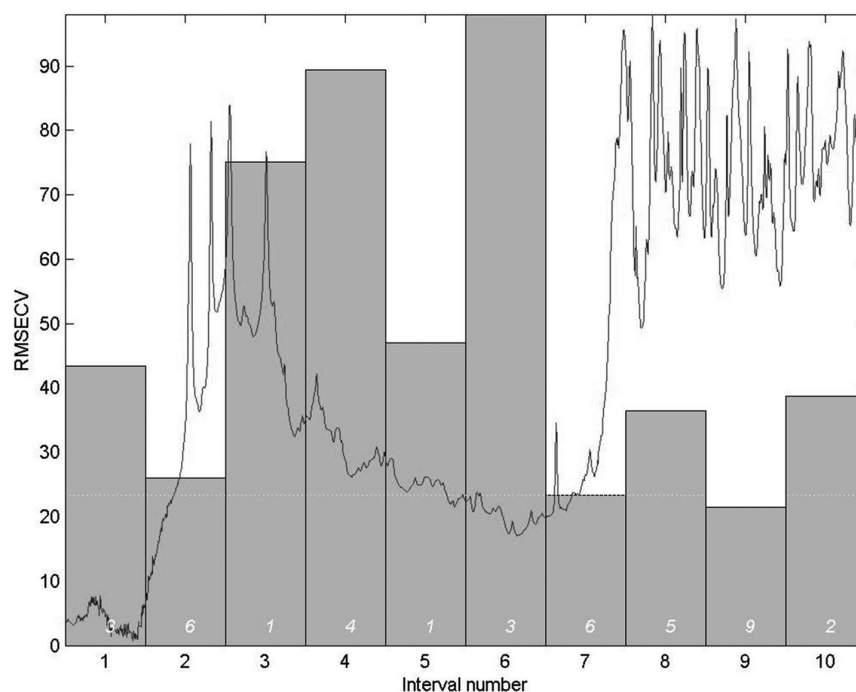
#### SULPHAMETHOXAZOLE *i*PLS MODELS

The principle behind the interval PLS algorithm is to split the spectrum into smaller equidistant regions and develop models for each subinterval. Thereafter, the subintervals RMSECV are compared to full-spectrum RMSECV values. The results are shown in Table III.

Interval PLS plots RMSECV values for each interval selected and the RMSECV values for the full-spectrum model using eight latent variables are shown in Figure 3. Interval of number 9 for model PLS with 10 intervals (*i*PLS10) produced

the lowest RMSECV but did not produce RMSEP lower than the full-spectrum PLS model. Problems associated with overfitting were present in this model, which led to higher errors than the ones generated by the global model. This fact can be due to the lack of robustness of these models which, despite producing RMSECV in the same order as the global model, did not have enough information to build models with low prediction errors (Faber and Rajkó 2007). It is possible that the most important spectral information for the regression are not contiguous. In this case the selection of a single range is insufficient, leading to increased error in prediction (Friedel et al. 2013). Moreover, the calibration using the full spectrum may include non-informative spectral regions making the obtained model more vulnerable to noise. In this case, a judicious selection of spectral regions would improve the predictive ability of the PLS model (Lee et al. 2012). Therefore, variable selection by *si*PLS was implemented to verify if the combination of more than one interval would result in models with better predictive capacity.





**Figure 3** - Cross-Validated Prediction Errors (RMSECV) values for full-spectrum model and interval models (bars) for the SMZ determination using PLS and iPLS algorithms (dotted line and numbers above interval numbers refer to full-spectrum RMSECV and latent variables used in each model, respectively).

#### SULPHAMETHOXAZOLE *si*PLS MODELS

The *si*PLS algorithm principle is to split the data set into a number of intervals (variable-wise) and to calculate all possible PLS model combinations of two, three or more intervals. Thereafter, the combined subinterval RMSECV is compared to

full-spectrum RMSECV values. The spectrum was divided into 10, 25 or 50 intervals combined in up to 5 subintervals. The best results were achieved when the spectrum was split into ten intervals and the intervals of number 6, 7 and 10 were selected, as shown in Table IV. For this *si*PLS model, results showed good correlation between

**TABLE IV**  
Statistical results to *si*PLS calibration models and full-spectrum PLS model for the SMZ.

Model SMZ	VN <sup>a</sup>	Intervals	LVs <sup>b</sup>	RMSECV SMZ (mg g <sup>-1</sup> )	R <sup>2</sup> <sub>cal</sub>	RMSEP SMZ (mg g <sup>-1</sup> )
PLS	1764	all	8	23.29	0.988	16.99
<i>si</i> PLS10	350	6 and 8	7	14.97	0.997	13.25
<b><i>si</i>PLS10*</b>	<b>525</b>	<b>6, 7 and 10</b>	<b>4</b>	<b>15.28</b>	<b>0.996</b>	<b>13.03</b>
<i>si</i> PLS10	700	3, 6, 7 and 9	10	13.79	0.999	23.43
<i>si</i> PLS10	875	1, 5, 6, 8 and 9	7	15.06	0.997	13.57
<i>si</i> PLS25	140	15 and 20	7	13.16	0.995	27.86
<i>si</i> PLS25	210	15, 20 and 22	6	13.75	0.996	22.88
<i>si</i> PLS50	70	30 and 39	5	16.32	0.974	25.43
<i>si</i> PLS50	105	30, 34 and 47	6	12.60	0.990	17.86

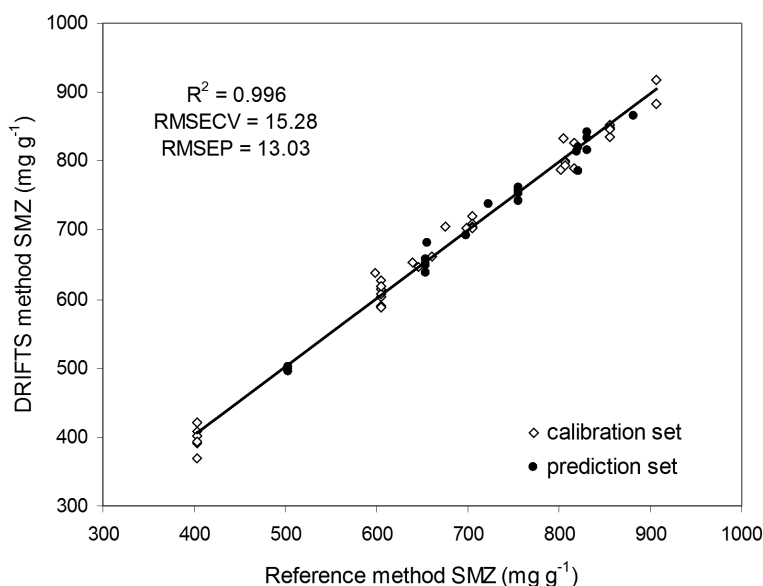
<sup>a</sup>VN: total number of variables.

<sup>b</sup>LVs: latent variables.

\*selected model.

reference and predicted values indicated by a correlation coefficient of 0.994, as shown in Figure 4. The selected intervals included the regions of  $1,960 - 2,300 \text{ cm}^{-1}$  (interval 6) and  $1,620 - 1,960 \text{ cm}^{-1}$  (interval 7). Both intervals correspond to harmonic bands by aromatic ring (Colthup et al. 1990). Interval 10 ( $600 - 939 \text{ cm}^{-1}$ ) corresponds to out-of-plane N-H bending vibration. On the whole, the combination of intervals 6, 7 and 10 by *si*PLS algorithm, reduced RMSECV and RMSEP values. Therefore, it was possible to find a narrow region for SMZ determination with small prediction errors; reduced variable numbers (525 variables compared to 1,764 used in the full-spectrum model) and reduced latent variables (4 LV compared to 8

LV used in the full-spectrum model) resulting in a more robust model with better predictive power. Average prediction results, and RMSEP for the selected *si*PLS calibration models, are shown in Table V. The *si*PLS model using intervals 6, 7 and 10 resulted in low Relative Standard Error of Prediction (RSEP = 1.77%), suggesting that the method used is accurate as also shown in Table V. The errors calculated for the prediction samples showed random behavior as shown by this model with insignificant systematic error ( $\text{bias} = 1.77$  and  $t_{\text{sist}} < t_{\text{crit}}$ ). For a subset of commercial samples, no significant trend was observed ( $\text{bias} = 1.29$  and  $t_{\text{sist}} < t_{\text{crit}}$ ), which shows that the systematic error for the model may be considered insignificant.



**Figure 4** - Reference HPLC values versus predicted SMZ values for *si*PLS model using intervals 6, 7 and 10 and 4 latent variables.

**TABLE V**  
Results of average prediction values for the better *si*PLS models.

Samples	SMZ		TMP	
	Reference HPLC method ( $\text{mg g}^{-1}$ )	DRIFTS method ( $\text{mg g}^{-1}$ )	Reference HPLC method ( $\text{mg g}^{-1}$ )	DRIFTS method ( $\text{mg g}^{-1}$ )
1 <sup>s</sup>	503.59	499.04	175.73	169.99
2 <sup>s</sup>	503.59	500.52	220.91	217.80
3 <sup>s</sup>	654.67	650.59	100.41	93.37
4 <sup>s</sup>	654.67	657.72	150.62	159.36
5 <sup>s</sup>	654.67	638.90	220.91	222.82

TABLE V (continuation)

Samples	SMZ		TMP	
	Reference HPLC method (mg g <sup>-1</sup> )	DRIFTS method (mg g <sup>-1</sup> )	Reference HPLC method (mg g <sup>-1</sup> )	DRIFTS method (mg g <sup>-1</sup> )
6 <sup>S</sup>	755.38	762.19	100.41	101.08
7 <sup>S</sup>	755.38	758.25	175.72	181.46
8 <sup>S</sup>	755.38	753.49	220.91	233.02
9 <sup>S</sup>	830.92	834.03	100.41	95.66
10 <sup>S</sup>	830.92	842.28	125.52	123.70
11 <sup>S</sup>	830.92	815.18	175.72	181.70
12 <sup>S</sup>	881.28	864.70	125.52	119.89
13 <sup>C</sup>	698.12	692.53	145.10	135.51
14 <sup>C</sup>	655.30	680.68	129.00	133.64
15 <sup>C</sup>	722.95	737.63	141.83	138.71
16 <sup>C</sup>	819.79	813.22	155.44	144.41
17 <sup>C</sup>	820.66	819.38	156.23	160.23
18 <sup>C</sup>	820.88	786.49	155.60	152.63
19 <sup>S</sup>	503.59	494.30	125.52	123.16
20 <sup>S</sup>	654.67	648.13	175.72	183.65
21 <sup>S</sup>	755.38	741.58	125.52	126.30
22 <sup>S</sup>	755.38	741.60	150.62	157.76
23 <sup>S</sup>	881.28	865.27	100.41	101.02
RMSEP (mg g <sup>-1</sup> )		13.03		4.88
RSEP (%)		1.77		3.16

<sup>S</sup>synthetic samples.<sup>C</sup>commercial samples.TRIMETHOPRIM *i*PLS MODELS

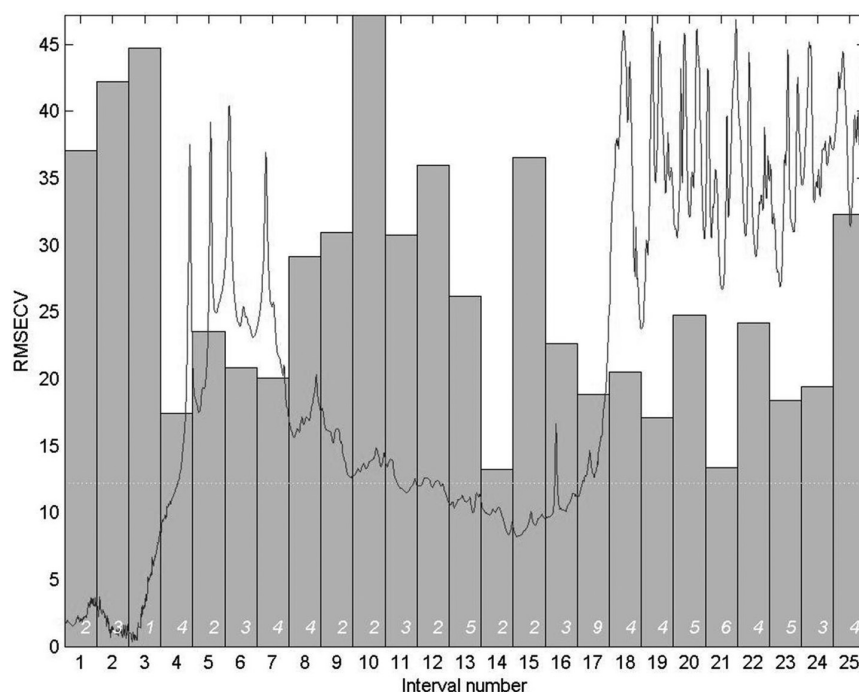
Figure 5 shows the central *i*PLS plots, the RMSECV values for each interval selected (bars) and the RMSECV values for full-spectrum model (line) using four latent variables. Table VI shows the statistical indicator for TMP *i*PLS calibration models using the spectrum subdivided into 10, 25 and 50 intervals. The models were developed from the division of the spectrum into 10 and 25 selected intervals in a similar region (941-1280 and 1110-1250 cm<sup>-1</sup>), showing that this region is sufficient to create a model for drug quantification. For these regions does not occur a significant increase in RMSECV value compared to the value of the global model, but the RMSEP value and the number of variables have been reduced. As in the previous case, *si*PLS was implemented to verify if

the combination of more than one interval would result in models with better predictive capacity.

TRIMETHOPRIM *si*PLS MODELS

The algorithm *si*PLS was implemented using the spectrum subdivided into 10, 25 or 50 intervals combined in up to 5 subintervals. Table VII shows the statistical indicators for TMP *si*PLS calibration models. The results showed a good correlation between reference and predicted values, indicated by a correlation coefficient of 0.983, as shown in Figure 6.

The lowest RMSEP value was obtained when the spectrum was split into 25 intervals and intervals 15 and 17 were combined. For this *si*PLS model, the results showed a good correlation between reference and predicted values, indicated



**Figure 5** - Cross-Validated Prediction Errors (RMSECV) values for full-spectrum model and interval models (bars) for the TMP determination using PLS and iPLS algorithms (dotted line and numbers above interval numbers refer to full-spectrum RMSECV and latent variables used in each model, respectively).

**TABLE VI**  
Statistical results to *i*PLS calibration models and full-spectrum PLS model for the TMP.

Model TMP	VN <sup>a</sup>	Intervals	LVs <sup>b</sup>	RMSECV TMP (mg g <sup>-1</sup> )	R <sup>2</sup> <sub>cal</sub>	RMSEPTMP (mg g <sup>-1</sup> )
PLS	1764	all	4	12.22	0.959	10.61
<i>i</i> PLS10	175	9	5	13.19	0.952	6.87
<i>i</i> PLS25	70	21	6	12.92	0.954	8.66
<i>i</i> PLS50	35	28	4	11.26	0.965	10.13

<sup>a</sup>VN: total number of variables.

<sup>b</sup>LVs: latent variables.

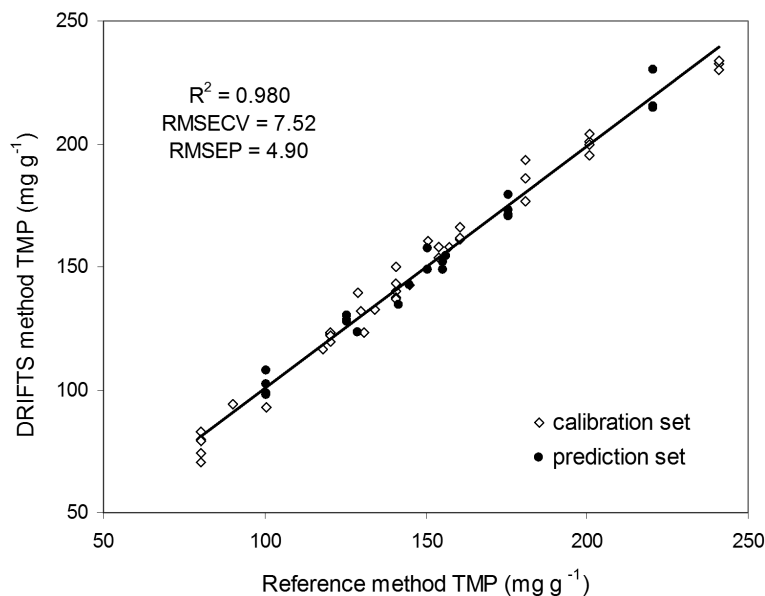
**TABLE VII**  
Statistical results to *si*PLS calibration models and full-spectrum PLS model for the TMP.

Model TMP	TV <sup>a</sup>	Intervals	VLs <sup>b</sup>	RMSECV TMP (mg g <sup>-1</sup> )	R <sup>2</sup> <sub>cal</sub>	RMSEPTMP (mg g <sup>-1</sup> )
PLS	1764	all	4	12.22	0.951	10.61
siPLS10	350	6 and 10	6	9.495	0.982	7.04
siPLS10	525	6, 7 and 8	7	10.54	0.983	4.37
siPLS10	700	6, 7, 8 and 10	7	9.89	0.988	6.40
siPLS10	875	1, 4, 6, 7 and 8	9	8.92	0.989	9.14
<b>siPLS25*</b>	<b>140</b>	<b>15 and 17</b>	<b>6</b>	<b>7.52</b>	<b>0.980</b>	<b>4.90</b>
siPLS25	210	15, 17 and 18	7	8.41	0.986	5.38
siPLS50	70	21 and 31	7	8.71	0.974	7.76
siPLS50	105	20, 30 and 31	4	7.75	0.982	8.88

<sup>a</sup>VN: total number of variables.

<sup>b</sup>VLs: latent variables.

\*selected model.



**Figure 6** - Reference HPLC values versus predicted TMP values for siPLS model using 15 and 17 intervals and 6 latent variables.

by a correlation coefficient of 0.983, as shown in Figure 5. The selected intervals included the regions of 2100 to 2230 cm<sup>-1</sup> (interval 15) and 1830 to 1960 cm<sup>-1</sup> (interval 17). Both intervals include harmonic bands vibrations of the pyrimidine ring presented in structure of TMP (Colthup et al. 1990). The *si*PLS model combined intervals 15 and 17 allowing better predictive ability when compared to *i*PLS models and full-spectrum PLS model. Therefore, it was possible to find a narrow region for TMP determination with small prediction errors and reduced variable numbers. Average prediction results, RMSEP and RSEP (%) for the selected *si*PLS calibration model are shown in Table V. This *si*PLS model combining three intervals resulted in low prediction errors (RSEP = 3.16%). The systematic error obtained for the model was not significant. The errors calculated for the prediction samples showed random behavior (bias = 1.26 and  $t_{\text{sist}} < t_{\text{crit}}$ ). For a subset of commercial samples, no significant trend was observed (bias = -0.09 and  $t_{\text{sist}} < t_{\text{crit}}$ ), which shows that the systematic error for the model may be considered insignificant.

## CONCLUSIONS

Using the PLS regression algorithm combined with DRIFTS data it was possible to develop multivariate models for simultaneous determination of SMZ and TMP in commercial pharmaceutical products. Assay results, expressed as the percentage of the label claim, were found to be 95.8 to 103.9% for SMZ and 95.7 to 106.4% for TMP. These results were in agreement with the content of SMZ and TMP in powder mixtures according to the USP 30 requirements (93 to 107%) for the solid preparations. The variable selection techniques used in this work, produced models with better predictive ability compared to full-spectrum PLS models. The *si*PLS algorithm proved to be most appropriate, combining the spectral regions containing the most relevant information for each analyte quantified. The proposed method is simple, solvent-free and allows potential applications for simultaneous, fast and reliable determination of SMZ and TMP in solid pharmaceutical dosage forms.

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## RESUMO

Um método alternativo para quantificação de sulfametoxazol (SMZ) e trimetoprima (TMP), empregando espectrometria por refletância difusa no infravermelho por transformada de Fourier (DRIFTS) e regressão por mínimos quadrados parciais (PLS) foi desenvolvido. Regressão por mínimos quadrados parciais por intervalo (*i*PLS) e por sinergismo de intervalos (*si*PLS) foram aplicadas para selecionar as faixas espectrais que produziram modelos com menores erros na previsão, em comparação ao modelo que emprega todo o espectro. Quinze comprimidos de formulações comerciais e quarenta e nove amostras sintéticas foram usados. As faixas de concentração consideradas foram de 400-900 mg g<sup>-1</sup> para o SMZ e de 80-240 mg g<sup>-1</sup> para a TMP. Os espectros por refletância difusa no infravermelho por transformada de Fourier (DRIFTS) foram adquiridos na faixa 600-4000cm<sup>-1</sup> com resolução de 4 cm<sup>-1</sup>. O presente procedimento foi comparado com cromatografia líquida de alta eficiência (HPLC). Os resultados obtidos para os erros quadráticos médios de previsão (RMSEP), durante a validação dos modelos para as amostras de sulfametoxazol (SMZ) e trimetoprima (TMP) usando *si*PLS, demonstram que esta abordagem trata-se de uma técnica válida para análise quantitativa de formulações farmacêuticas. Os modelos de regressão, obtidos a partir dos intervalos selecionados pelo algoritmo, apresentaram menores erros quando comparados ao modelo PLS global. Para as melhores regiões selecionadas pelo *si*PLS, Os valores RMSEP de 13,03 mg g<sup>-1</sup> para SMZ e de 4,88 mg g<sup>-1</sup> para TMP foram obtidos a partir da seleção das melhores regiões espectrais pelo *si*PLS.

**Palavras-chave:** quimiometria, espectrometria por refletância difusa no infravermelho por transformada de Fourier, metodologia ambientalmente amigável, cromatografia

líquida de alta eficiência, mínimos quadrados parciais por intervalo (*i*PLS), mínimos quadrados parciais por sinergismo de intervalos (*si*PLS).

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