Chemometrics and model fitting in analytical chemistry

By

Matthew James Foot

This thesis is submitted in fulfilment of the requirements for the degree of Doctor of Philosophy

Department of Chemistry, Materials and Forensic Science University of Technology, Sydney

2005

Certificate of Authorship / Originality

I certify that the work in this thesis has not been previously submitted for a degree nor has it been submitted as part of requirements for a degree except as fully acknowledged within the text.

I also certify that the thesis has been written by me. Any help that I have received in my research work and the preparation of the thesis itself has been acknowledged. In addition, I certify that all the information sources and literature used are indicated in the thesis.

Signature of Candidate

Production Note: Signature removed prior to publication.

Acknowledgements

I would like to thank my principal supervisor Dr. Philip Maynard who stepped in as my supervisor two and a bit years into my project.

I would also like to thank my co-supervisor Associate Professor Les Kirkup. Les was always there providing help and support, and constantly challenging me to try and be a better scientist. Les's knowledge of experimental design and data analysis, as well as all the little tricks with Excel has been very useful throughout my time as a postgraduate student.

I would also like to thank my former principal and now unofficial supervisor Dr. Mary Mulholland. It was Mary who started me off down the path of research and helped steer me through the early part of this project. I am incredibly thankful that Mary made me write papers early on in my thesis especially at the end of my first year. Mary has continued to be very helpful even after leaving UTS and I am grateful that she gave up her time for me.

I greatly appreciate the help provided by Dr Peter Ghosh, who kindly gave me some samples used in my project and gave me some direction. I would also like to thank Susan Shimmon who showed me the lab at INR. I would also like to thank Ronald Shimmon who acted as a go-between for Dr Ghosh and me as well as being my friend and helping me with various questions throughout my time here.

I am constantly grateful for the friendship and support of Anthea Lloyd-Jones. Anthea has been a great support throughout my time as a research student, helping keep me informed about what happening and being there to bounce ideas off when needed. Anthea has also been an ear to listen to my woes for the last three and one half years, and for this I thank her greatly. My fellow postgraduates are a bunch of champions and champion Uno players. Since moving into the office with them my life has been much more fun and much less stressful here at UTS. The Uno world championship gives me a bright spot to the day even when all things are going bad. So thanks heaps to Alison, Katherine, Sonia, Lisa, Bec, Tristan, Mark and Garry. I would also like to thank Sarka Prochazka, who helped me greatly when I started on this PhD road.

I would also like to thank Louise for being a great support since we met. Thanks for letting me stay at your place, and thanks for getting me out and doing things these last three years. Love you lots.

Without the help and support of my mum and dad, I would have never made it through these last three years. Indeed I thank them for getting me through university from when I started. I'd also like to say thanks to my brother; he didn't do all that much but he's my brother and he would feel left out if I didn't mention him.

List of publications

Some of the work presented in this thesis has been published in the following refereed journal articles

- Foot, M., M. Mulholland, and L. Kirkup, *Classification of the biopolymer* sodium pemtosan polysulfate by infrared spectroscopy. Chromatographia, 2003. 58(1/2): p. 343-348.
- Kirkup, L., M. Foot, and M. Mulholland, *Comparison of equations describing* band broadening in high-performance liquid chromatography. Journal of Chromatography A, 2004. 1030(1-2): p. 25-31.
- Foot, M. and M. Mulholland, *Classification of chondroitin sulfate A, chondroitin sulfate C, glucosamine hydrochloride and glucosamine 6 sulfate using chemometric techniques.* Journal of Pharmaceutical and Biomedical Analysis, 2005. 38(3): p. 387-407.

Abstract

The aims of this project are to investigate the ability of advanced mathematical techniques and their contribution to the analysis of complex situations in analytical chemistry. The project falls into two areas. The first is the use of chemometrics to classify glycosaminoglycans (GAGs) such as chondroitin sulfates and glucosamines, substances that are being investigated for their potential use in the treatment of arthritis symptoms. This work is then expanded to the classification of novel anti-arthritis agents from different manufactures. The second part of this project looked at fitting different chromatographic band broadening models to real data. This work attempted to provide greater understanding of the processes involved in band broadening.

This classification work used different infrared spectroscopy techniques to analyse the molecules to which the classification systems were applied. Fourier Transform Infrared spectroscopy (FTIR), diffuse reflectance spectroscopy (DRIFTS) and Attenuated Total Reflectance spectroscopy (ATR) were evaluated for the classification of the chondroitin sulfates and glucosamines. The use of different spectral regions and derivative spectra were evaluated for their effect on the classification of the samples. It was found that FTIR coupled with derivative spectrums below 2000 cm⁻¹ provided the best classification of these molecules.

The classification of sodium pentosan polysulfate was then considered using methods developed in the classification of chondroitin sulfates and glucosamines. Samples of the same material made by different manufacturers were provided to see if classification methods could distinguish them. Transmission spectroscopy coupled with the chemometric methods similar to those used for the classification of chondroitin sulfate and glucosamines, were able to discriminate the samples by manufacturer and partially discriminate the samples by batch.

The second part of this thesis looks at fitting models to data as opposed to building classification models from data. This section looks at band broadening models in liquid chromatography followed by gas chromatography and finally looking at model fitting generally with some theoretical data. In this section a new model for band broadening in liquid chromatography is proposed. This model was found to be better able to predict band broadening behaviour in liquid chromatography at high flow rates. This model was then applied to gas chromatography; however it was found that previously published models best fit the data. The theoretical analysis highlighted the need for high quality data in order to draw conclusions about the model. It was also found that post column processes had the greatest effect on the band broadening.

Overall it was found that these advanced analytical techniques would be able to significantly improve the analysis of Glycosaminoglycan type compounds and provide further understanding of the band broadening process in liquid chromatography.

Table of contents

Acknowledgements	i
List of publications	.iii
Abstract	.iv
Table of contents	.vi
List of figures	.ix
List of tablesx	ciii
Chapter 1: Modelling and model fitting in analytical chemistry	1
1 Modelling and model fitting in chemistry	2
1.1 Multivariate analysis	2
1.2 Chemometrics	4
1.3 Computers and software	5
1.4 Chemometric Techniques	5
1.4.1 Exploratory data analysis, data reduction and principal components	
analysis. 5	
1.4.1.1 Principal components analysis	6
1.4.1.2 Hierarchical cluster analysis (HCA)	11
1.4.2 Pattern Recognition	12
1.4.2.1 Linear Discriminant Analysis	14
1.4.2.2 Soft Independent Modelling of Class Analogies (SIMCA)	17
1.4.2.3 Validation of pattern recognition models	19
1.5 Non-linear regression and model selection	19
1.5.1 Regression analysis	19
1.5.2 Model selection criteria	22
1.5.2.1 Akaike Information Criterion	23
1.5.2.2 Bayesian (Schwarz) Information Criterion	24
1.6 References	25
Chapter 2 : Glycosaminoglycans use and analysis	35
2 Glycosaminoglycans: use and analysis	36
2.1 Current Treatments	37
2.1.1 Pharmaceuticals	37
2.1.1.1 Corticosteroids	37
2.1.1.2 Non steroidal anti-inflammatory drugs (NSAIDs)	38
2.1.2 Natural products and remedies	38
2.1.3 Surgery	40
2.2 Glycosaminoglycans	40
2.2.1 Analysis of Glycosaminoglycans	42
2.2.1.1 Spectroscopy	43
2.2.1.2 Separations	48
2.2.1.3 Other techniques	54
2.3 References	55
Chapter 3: Classification of chondroitin sulfate A, chondroitin sulfate C,	
glucosamine hydrochloride and glucosamine 6 sulfate, using chemometrics and	
different infrared techniques	67

3 Classifica	tion of chondroitin sulfate A, chondroitin sulfate C, glucosamin	ie
hydrochloride	and glucosamine 6 sulfate, using chemometrics with different in	nfrared
techniques		
3.1 Intro	duction	
3.2 Expe	erimental	71
3.2.1	Chemicals and reagents	71
3.2.2	Transmission spectroscopy	71
3.2.3	DRIFTS	72
3.2.4	ATR	72
3.2.5	Data analysis	72
3.3 Resu	Ilts and Discussion	73
3.3.1	Spectroscopy	73
3.3.1.1	Chondroitin sulfate A and chondroitin sulfate C	75
3.3.1.2	Glucosamine hydrochloride and glucosamine 6 sulfate	75
3.3.2	Chemometrics	76
3.3.2.1	Transmission spectroscopy	76
3.3.2.2	DRIFTS	
3.3.2.3	ATR	
3.4 Cond	clusions	
3.5 Refe	rences	
Chapter 4 : C	lassification of the biopolymer sodium pentosan polysulfate	by
Fourier transf	form infrared spectroscopy	
4 Classifica	tion of the biopolymer sodium pentosan polysulfate by Fourier	transform
infrared spectre	oscopy (FTIR)	
4.1 Intro	duction	
4.2 Expe	erimental	116
4.2.1	Chemicals and reagents	
4.2.2	Instrumentation	116
4.2.3	Data Analysis	
4.3 Resu	Ilts and Discussion	
4.3.1	Spectroscopy	117
4.3.2	Principal components analysis	
4.3.3	Linear discriminant analysis	
4.3.4	SIMCA	
4.4 Conc	clusions	
4.5 Refe	rences	
Chapter 5 : Fi	itting band broadening equation in chromatography	
5 Fitting ba	nd broadening equations in chromatography	
5.1 Anal	ytical Chromatography	
5.1.1	Columns	
5.1.2	Detectors	
5.2 Band	l broadening	
5.2.1	Kinetic rate theory of chromatography	
5.2.2	More than just van Deemter	
5.3 Why	model band broadening equations?	
5.4 Expe	erimental	
5.4.1	Chemicals and reagents	145

5.4.2	HPLC analysis	
5.4.3	GC analysis	
5.4.4	Theoretical Analysis	147
5.4.5	Data Analysis	147
5.5 R	esults and Discussion	
5.5.1	HPLC	
5.5.2	GC	
5.5.3	Theoretical Data	
5.6 C	onclusions	
5.7 R	eferences	
Chapter 6	Conclusions	
6 Conclu	isions and recommendations	
6.1 C	lassification systems	
6.2 M	lodel fitting	
6.3 Fi	urther Work	

List of figures

Figure 1.1: A score plot of a FTIR data set showing the first two principal components plotted orthogonally to each other. The different coloured points represent different samples. This data has been mean centered
Figure 1.2: A loadings plot of a principal component extracted from mid infrared FTIR data. The loading is plotted against the variables of that data set
Figure 1.3: A dendrogram
Figure 2.1: Common monosaccharide components of Glycosaminoglycans
Figure 2.2: Chondroitin sulfate A with the N-acetylagalactosamine ring sulfated in the 4 position joined to D-glucoronic acid
Figure 2.3 Aggrecan: An example of a cartilage proteoglycan which contains both chondroitin sulfate and keratin sulfate
Figure 3.1: Chondroitin sulfate A
Figure 3.2: Chondroitin sulfate C
Figure 3.3: Glucosamine hydrochloride (left) and glucosamine 6 sulfate (right)70
Figure 2.4. The transmission spectra of alloggaming (sulfate (tap left), alloggaming
hydrochloride (top right), chondroitin sulfate A (bottom left) and chondroitin sulfate C (bottom right)
Figure 3.4: The transmission spectra of glucosamine o suffate (top feft), glucosamine hydrochloride (top right), chondroitin sulfate A (bottom left) and chondroitin sulfate C (bottom right)
Figure 3.4: The transmission spectra of glucosamine o suffate (top feft), glucosamine hydrochloride (top right), chondroitin sulfate A (bottom left) and chondroitin sulfate C (bottom right) Figure 3.5: First two principal components extracted from the full spectrum. The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C, The green circles represent glucosamine hydrochloride, and the blue circles represent glucosamine 6 sulfate. 77 Figure 3.6: Loadings plot from the first principal component extracted from the raw spectrum 77
Figure 3.4: The transmission spectra of glucosamine 6 suffate (top fielt), glucosamine hydrochloride (top right), chondroitin sulfate A (bottom left) and chondroitin sulfate C (bottom right) Figure 3.5: First two principal components extracted from the full spectrum. The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C, The green circles represent glucosamine hydrochloride, and the blue circles represent glucosamine 6 sulfate. 77 Figure 3.6: Loadings plot from the first principal component extracted from the raw spectrum 77 Figure 3.7: Loadings plot from the second principal component extracted from the raw spectrum 78
Figure 3.4: The transmission spectra of glucosamine 6 suffate (top feff), glucosamine hydrochloride (top right), chondroitin sulfate A (bottom left) and chondroitin sulfate C (bottom right)

represent chondroitin sulfate C, The green circles represent glucosamine hydrochloride, and the blue circles represent glucosamine 6 sulfate
Figure 3.10: First two principal components extracted from the first difference spectrum below 2000 cm ⁻¹ . The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C, The green circles represent glucosamine hydrochloride, and the blue circles represent glucosamine 6 sulfate
Figure 3.11: Dendrogram created from the first three principal components of the full spectrum showing the clustering of the glucosamine hydrochloride (gluhcl), chondroitin sulfate A (CSA), chondroitin sulfate C (CSC) and the glucosamine 6 sulfate (G6S)81
Figure 3.12: Dendrogram of the first three principal components above 2000 cm ⁻¹ showing the clustering of the glucosamine hydrochloride (gluhcl), chondroitin sulfate A (CSA), chondroitin sulfate C (CSC) and the glucosamine 6 sulfate (G6S)
Figure 3.13: First three principal components extracted from the raw DRIFTS spectra The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C, The green circles represent glucosamine hydrochloride, and the blue circles represent glucosamine 6 sulfate
Figure 3.14: Loadings plot for principal component 2
Figure 3.15: Score plot of principal component 2 vs. principal component 3 extracted from the first difference DRIFTS spectra above 2000 cm ⁻¹ . The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C, The green circles represent glucosamine hydrochloride, and the blue circles represent glucosamine 6 sulfate
Figure 3.16: Loadings plot of principal component 3
Figure 3.17: Dendrogram obtained using only principal component 2 and principal component 3 showing the clustering of the glucosamine hydrochloride (GH), chondroitin sulfate A (CA), chondroitin sulfate C (CC) and the glucosamine 6 sulfate (GS)
Figure 3.18: An ATR spectrum of chondroitin sulfate A
Figure 3.19:3d score plot of ATR raw spectrum. The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C and the green circles represent glucosamine hydrochloride
Figure 3.20: PC2 vs. PC3 score plot from ATR data. The black squares represent chondroitin sulfate A, the yellow squares represent chondroitin sulfate C and the green circles represent glucosamine hydrochloride
Figure 3.21: Raw spectra dendrogram showing the clustering of the glucosamine hydrochloride (GH), chondroitin sulfate A (CA) and chondroitin sulfate C (CC) 100

Figure 3.22: First difference dendrogram glucosamine hydrochloride (GH), chondroitin sulfate A (CA) and chondroitin sulfate C (CC)
Figure 4.1: The repeating unit of NaPPS [2]111
Figure 4.2: A typical near infrared spectrum of NaPPS118
Figure 4.3: A typical mid infrared spectrum of NaPPS118
Figure 4.4: %RSD plots from the near infrared spectra. The lines for each sample indicate the intra-batch variation, while the combined RSD indicates the %RSD across all samples
Figure 4.5: %RSD plots from the mid infrared spectrum. The lines for each sample indicate the intra-batch variation, while the combined RSD indicates the %RSD across all samples.
Figure 4.6: An overlay of typical MIR spectra obtained from the two manufacturers. Manufacturer A is in blue and manufacturer B is in red
Figure 4.7: A score plot of the first two principal components of the entire raw spectrum
Figure 4.8: The loadings plot for the first principal component, obtained for the full spectrum
Figure 4.9 Score plot of the first two principal components of the raw spectrum using only the region $<1800 \text{ cm}^{-1}$
Figure 4.10: Score plot of the first two principal components of the first difference spectrum
Figure 4.11: Score plot of the first two principal components of the first difference spectrum using only the region below 1800 cm ⁻¹
Figure 5.1: Derivation of H from σ^2 and L from a chromatographic peak
Figure 5.2: <i>H</i> vs. <i>u</i> data for propylparaben collected using HPLC
Figure 5.3: Residuals for unweighted fit of equation (5.7) to data in Figure 5.2
Figure 5.4: Residuals for weighted fit of equation (5.7) to data in Figure 5.2150
Figure 5.5: Propylparaben H vs. u data with equations (5.3) (5.5), (5.6) and (5.7) fitted.
Figure 5.6: Weighted residuals of equations (5.3), (5.5) and (5.7) plotted against linear velocity for propylparaben data
Figure 5.7: Plot of HETP vs. linear velocity (0.1 spectra/s)

Figure 5.8: Plot of HETP vs. linear velocity (1 spectra/s)
Figure 5.9: Plot of HETP vs. linear velocity (10 spectra/s)159
Figure 5.10: Standard deviation versus flow rate for 0.1 spectra/s sample rate and 10 spectra/s sample rate
Figure 5.11: 15 ms exposure time <i>H</i> versus <i>u</i> plot161
Figure 5.12: 150 ms exposure time <i>H</i> versus <i>u</i> plot161
Figure 5.13: Standard deviation vs. flow rate for both exposure times
Figure 5.14: H verse u plot of toluene analysed by GC sampling rate 200 Hz163
Figure 5.15: Unweighted (top) and weighted (bottom) residuals for toluene from fit of equation (5.5)
Figure 5.16: Histogram of "best fit" equations at 1% noise
Figure 5.17: Histogram of "best fit" at 3% noise173
Figure 5.18 : Best fit determined by BIC at 6% noise
Figure 5.19: AIC at 9% noise

List of tables

Table 3-1: LDA on spectrum below 2000 cm ⁻¹
Table 3-2: A summary of LDA results for transmission spectroscopy
Table 3-3: Number of outliers, principal components and % variance explained for eachspectral region using raw spectra.85
Table 3-4: Class distances calculated for each spectral region using the raw spectra 86
Table 3-5: Number of outliers, principal components and % variance explained for eachspectral region using the first difference spectra
Table 3-6: Class distances calculated from each spectral region of the first difference spectra.
Table 3-7: A summary of LDA classification rates using DRIFTS spectra. 93
Table 3-8: Number of outliers, principal components and % variance extracted for each group using the DRIFTS spectra
Table 3-9: Class distances calculated for each spectral region using the DRIFTS spectra
Table 3-10: Number of outliers, principal components and % variance extracted foreach group using the first difference DRIFTS spectra
Table 3-11: Class distances calculated for each spectral region using the first difference DRIFTS spectra
Table 3-12: Cross validated LDA on the raw spectrum
Table 3-13: Cross validated LDA on the first difference spectrum
Table 3-14: Number of principal components and the % variance explained for the cross validated models
Table 3-15: Class distances calculated using the cross validated models
Table 4-1: List of samples
Table 4-2: Overall classification rate for NaPPS samples using LDA on the first three principal components. Samples were classified to the different manufacturers
Table 4-3: Classification of batches using LDA on raw spectrum below 1800cm ⁻¹ 126
Table 4-4: Classification of batches using LDA on the first difference spectra below 1800cm ⁻¹ 126

Table 4-5: Class distances calculated using the full spectral range and the spectrumbelow 1800 cm ⁻¹ for the raw spectra.127
Table 4-6: Class distances calculated using the full spectral range and the spectrum below 1800 cm ⁻¹ for the first difference spectra
Table 5-1: Parameter estimates from the weighted and unweighted fits of equations(5.3) and (5.5)-(5.7)
Table 5-2: Fitting statistics from methylparaben and propylparaben. 153
Table 5-3: Predictive ability of equations (5.3), (5.5), (5.6) and (5.7)155
Table 5-4: Different experimental conditions for investigation of source of scatter and curvature
Table 5-5: Model fitting data 158
Table 5-6: Parameter estimates for GC data at 20 Hz sampling rate
Table 5-7: Parameter estimates for GC data at 100 Hz
Table 5-8: GC parameter estimates for GC data at 200 Hz 167
Table 5-9: Fitting statistics for GC data
Table 5-10: predictive ability of the equations 170