

Analytical methods for heterogeneous bio- drugs

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Overview

- Chemometrics
- Glycosaminoglycans/heparin

- 1. Principal component analysis of heparin ^1H NMR spectra**
- 2. Two-dimensional correlation spectroscopy and two-dimensional correlation spectroscopic filtering of heparin ^1H NMR spectra**

Chemometrics

- Chemometrics is the science of extracting information from chemical systems by data-driven means - [Wikipedia](#).
- Extracting patterns from complicated data sets.
- Adding value to data.
- Transforming data in to information.
- R - <http://www.R-project.org/>

Glycosaminoglycans

- Heparin / Heparan Sulfate

Involved in:

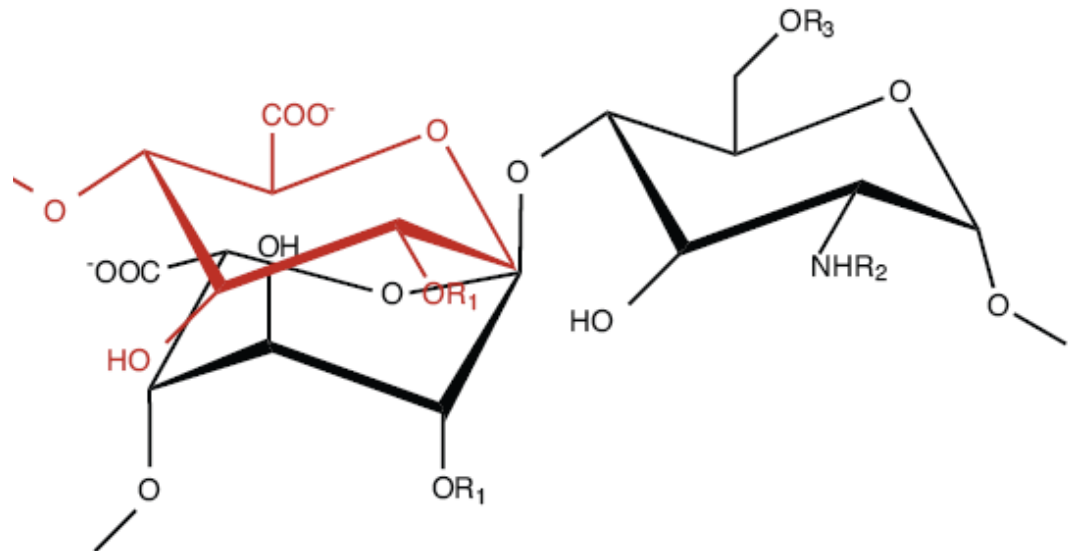
- Development
- Diseases - cancer/neurodegenerative

• Its role is governed by protein-interactions; ~ 300 known at present - 1000s predicted.

- Conformation
- Sequence
- Cation

- Heparin is the largest consumed pharmaceutical product in terms of mass, 400 - 700 million pigs per year!

- The product has evolved, heparin has been depolymerised to low molecular weight heparins



1. PCA of heparin ^1H NMR spectra

A library of heparin sample should consist of:

- Intrinsically diverse samples, covering the heterogeneity of heparin.
- It will be composed of what is considered to be “heparin” at that time and place. Samples should agree with the regulators requirements.
- As the library grows the definition of heparin will change.
- There will never be a “correct”, “complete” and “final” library - it will always be in flux.

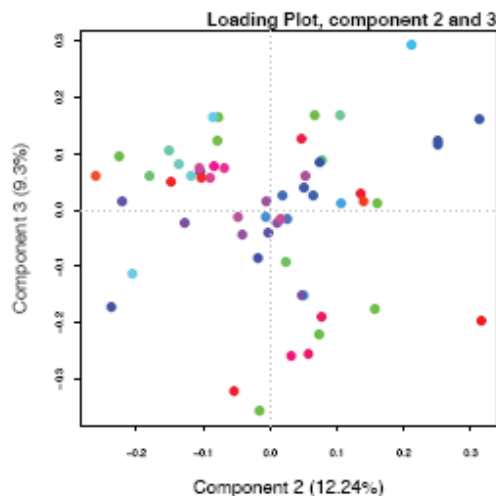
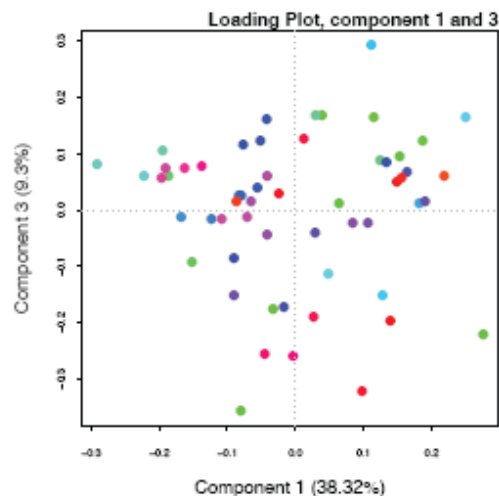
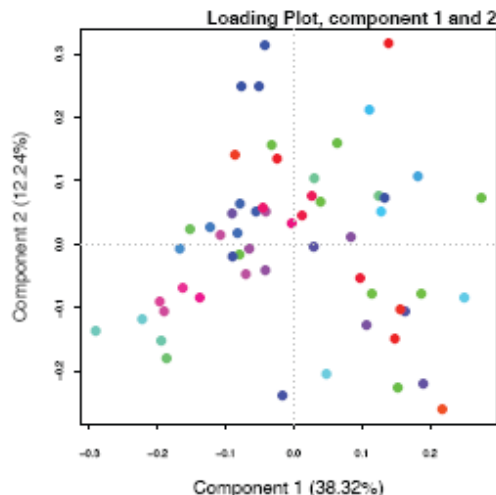
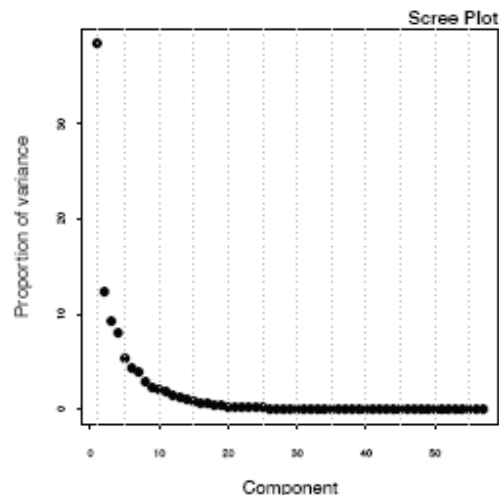
1. PCA of heparin ^1H NMR spectra

Principal component analysis

- Explorative multivariate technique - **PCA can be used to explore the heparin library.**
- Generates a number of independent features (components), that explains the variation within the dataset.
- PCA reduces a dataset to a lower number of components, greatly simplifying it.
- A linear combination of components can be used to reconstruct any member of the dataset used in the analysis.
- PCA can be used to find outliers within a dataset - heparin samples contaminated with OSCS?

An example - A library of bona fide heparin samples.

1. PCA of heparin 1H NMR spectra

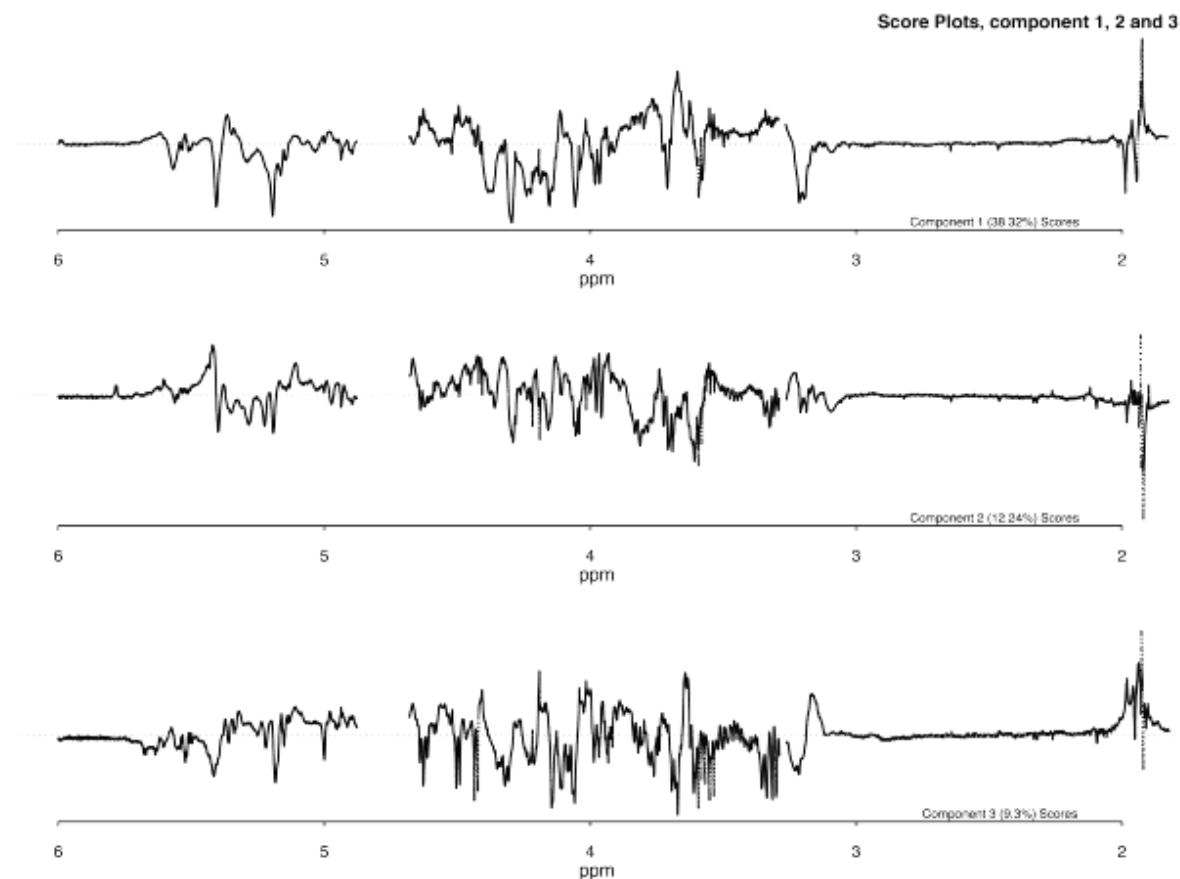


- Library of 57 *bona fide* heparin samples, which comply with EDQM regulations.
- 4 components explain over 70% of the variation within the dataset.

R:- rNMR package used to Import Bruker NMR spectra directly. Data is normalised for area, mean centered and Pareto scaled. PCA is performed using the princomp function.

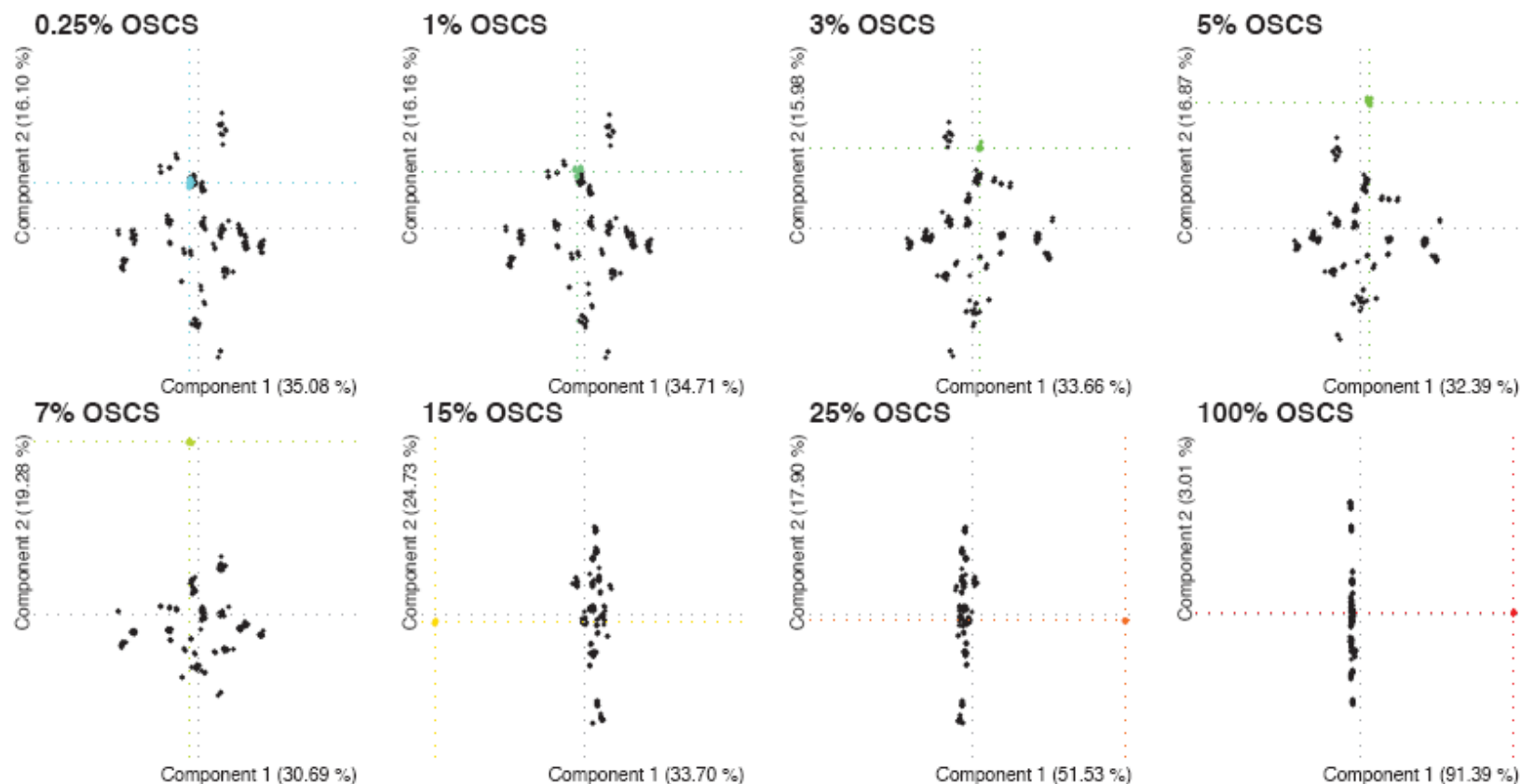
1. PCA of heparin ^1H NMR spectra

- Scores - spectral features extracted by PCA.



1. PCA of heparin 1H NMR spectra

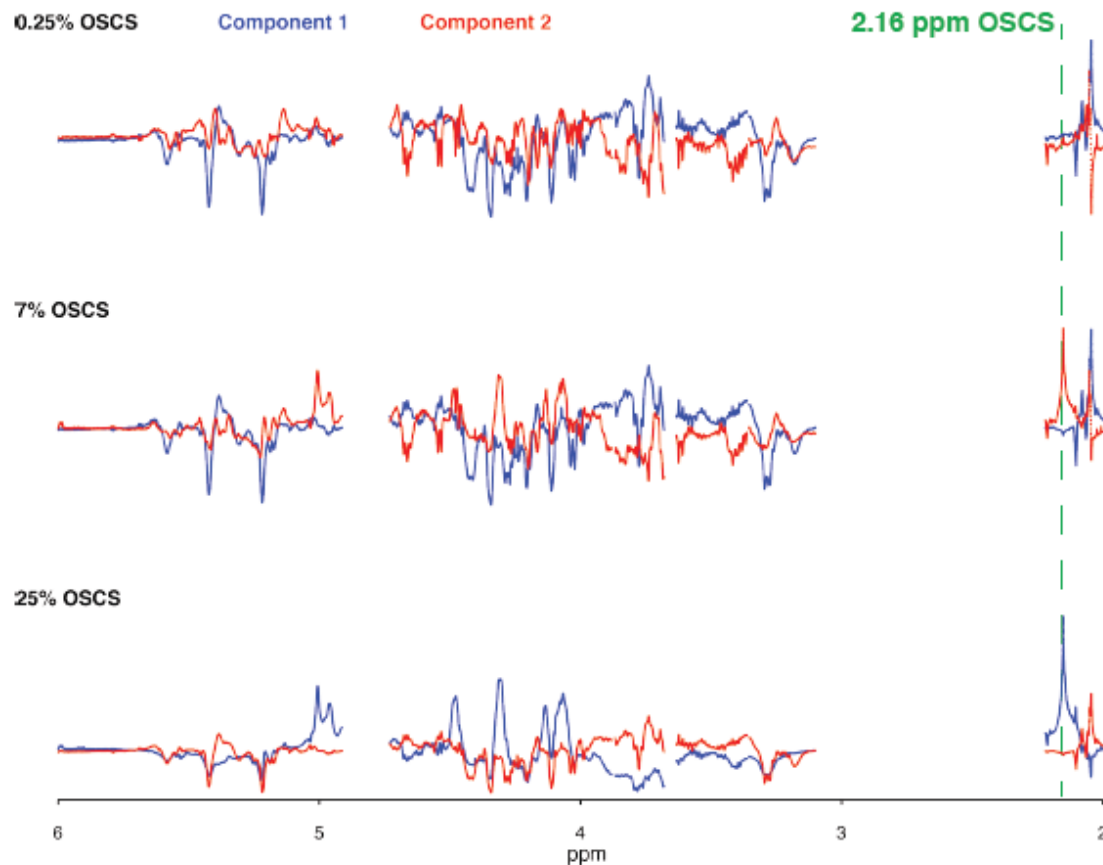
- Heparin contaminated with OSCS.



- Heparin contaminated with 7% OSCS can be clearly differentiated .**

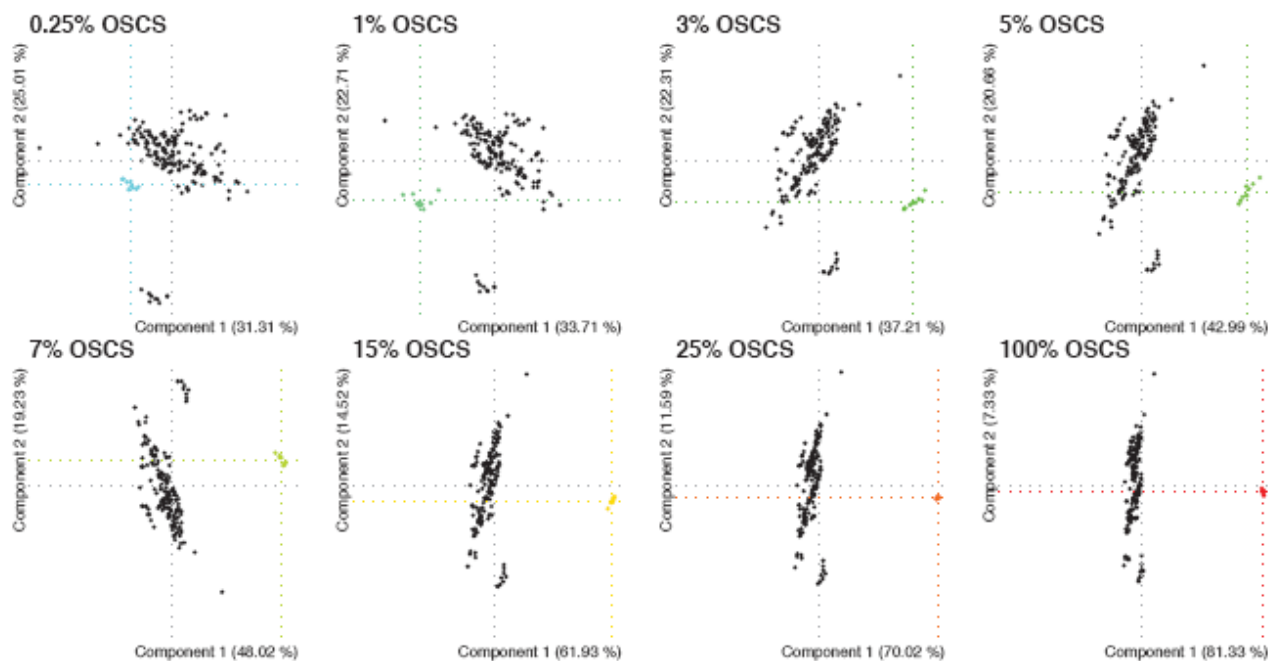
1. PCA of heparin ^1H NMR spectra

- N-acetyl signal of OSCS at 2.16 ppm is the primary diagnostic signal.



1. PCA of heparin ¹H NMR spectra

- OSCS has a *free signal* at 2.16 ppm. By selecting these data, sensitivity can be improved - **heparin contaminated with 1% OSCS is differentiable.**



Rudd TR, *et al.* (2011) **Construction and use of a library of bona fide heparins employing ¹H NMR and multivariate analysis**, *Analyst*, 136, 1380.

1. PCA of heparin ^1H NMR spectra

Conclusions

- “Heparin” has no conventional definition, but a statistical one.
- The pragmatic definition of heparin takes the form of a library of ^1H NMR spectra.
- PCA can be used to explore the heparin library/definition.
- A library of heparin ^1H NMR spectra can be used to differentiate a heparin sample contaminated with 7% OSCS - full spectrum.
- Selecting the spectral region can increase the limit of detection for OSCS, with samples containing 1% OSCS differentiable - N-acetyl region, OSCS signal at 2.16 ppm.

2. 2D-COS/2D-COS-f

Two-dimensional correlation spectroscopy (2D-COS):

Orthodox 2D-COS is the correlation of a set of linearly perturbed spectra, the sample can be mechanically or chemically perturbed.

Noda *et al.* 2000 Appl. Spectrosc.

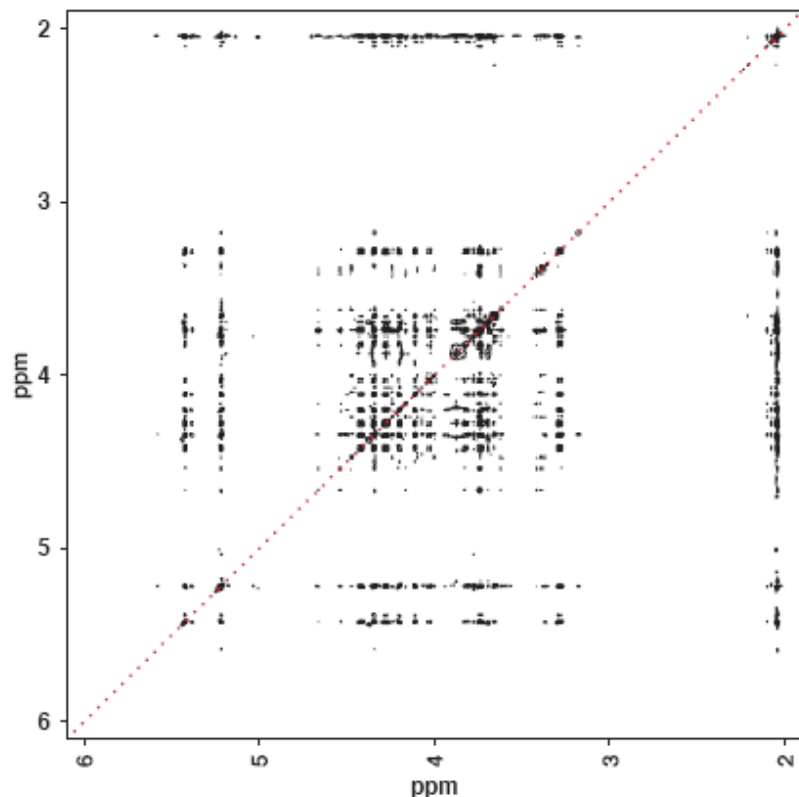
$$\text{2D-COS spectrum} = \text{Covariance matrix} = 1/(n-1)XX^T$$

Linear algebra formalisation Šašić *et al.* 2000 J. Phys. Chem. B

A variation of this idea has been used for Metabolomics, instead of using a covariance matrix a correlation matrix is used, (STOCSY - Cloreac *et al.* 2005 Anal. Chem.).

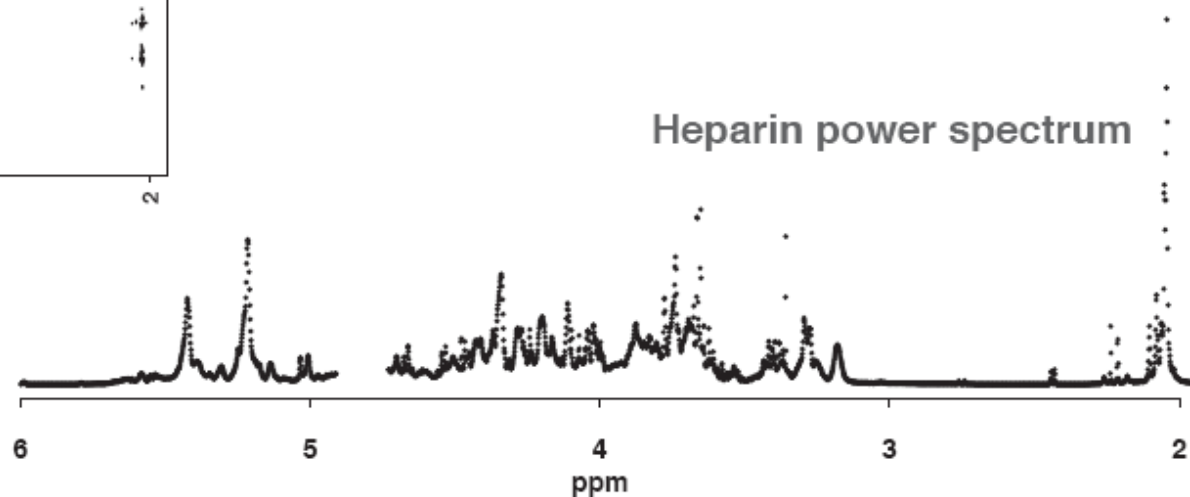
Pre-data processing is VERY important, the data is normally mean centred and then scaled (Pareto or auto scaling), data can also be normalised for area.

2. 2D-COS/2D-COS-f



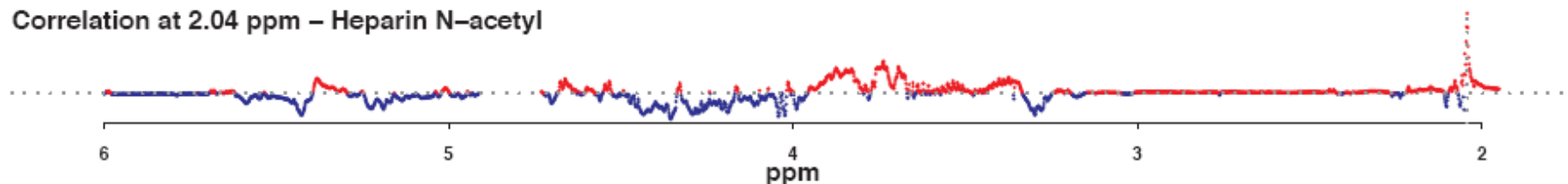
2D-COS of heparin library

- A psuedo-TOCSY spectrum is produced
- **Diagonal** - Variances of the covariance matrix - power spectrum.
- **Off-diagonal** - Covariances - cross peak correlations.

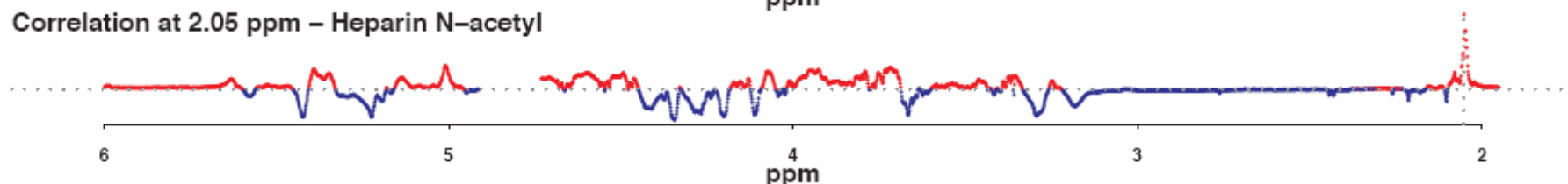


2. 2D-COS/2D-COS-f

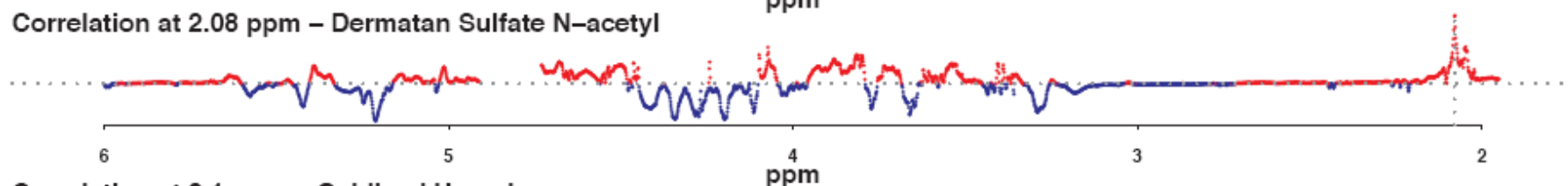
Correlation at 2.04 ppm – Heparin N-acetyl



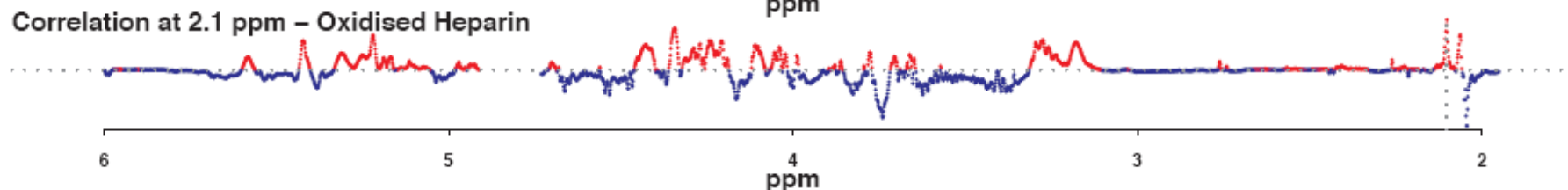
Correlation at 2.05 ppm – Heparin N-acetyl



Correlation at 2.08 ppm – Dermatan Sulfate N-acetyl



Correlation at 2.1 ppm – Oxidised Heparin



Reveals library contents

2. 2D-COS/2D-COS-f

2D-COS-Filtering: Effectively a 2D-COS difference spectrum between the reference heparin library and a test heparin sample.

$$\text{2D-COS-F spectrum} = 1/(n_{\text{lib+Test Sample}}-1)(X_{\text{lib+Test Sample}} X_{\text{lib+Test Sample}}^T) - 1/(n_{\text{lib}}-1)(X_{\text{lib}} X_{\text{lib}}^T)$$

- Auto-correlations between signals from the heparin samples in the reference library and heparin test sample.
- Subtraction removes correlated heparin signals, leaving 'alien' features.

Library

- The library is a reference definition for the conventionally undefinable heparin.
- The library encompasses the natural variation within pharmaceutical heparin.

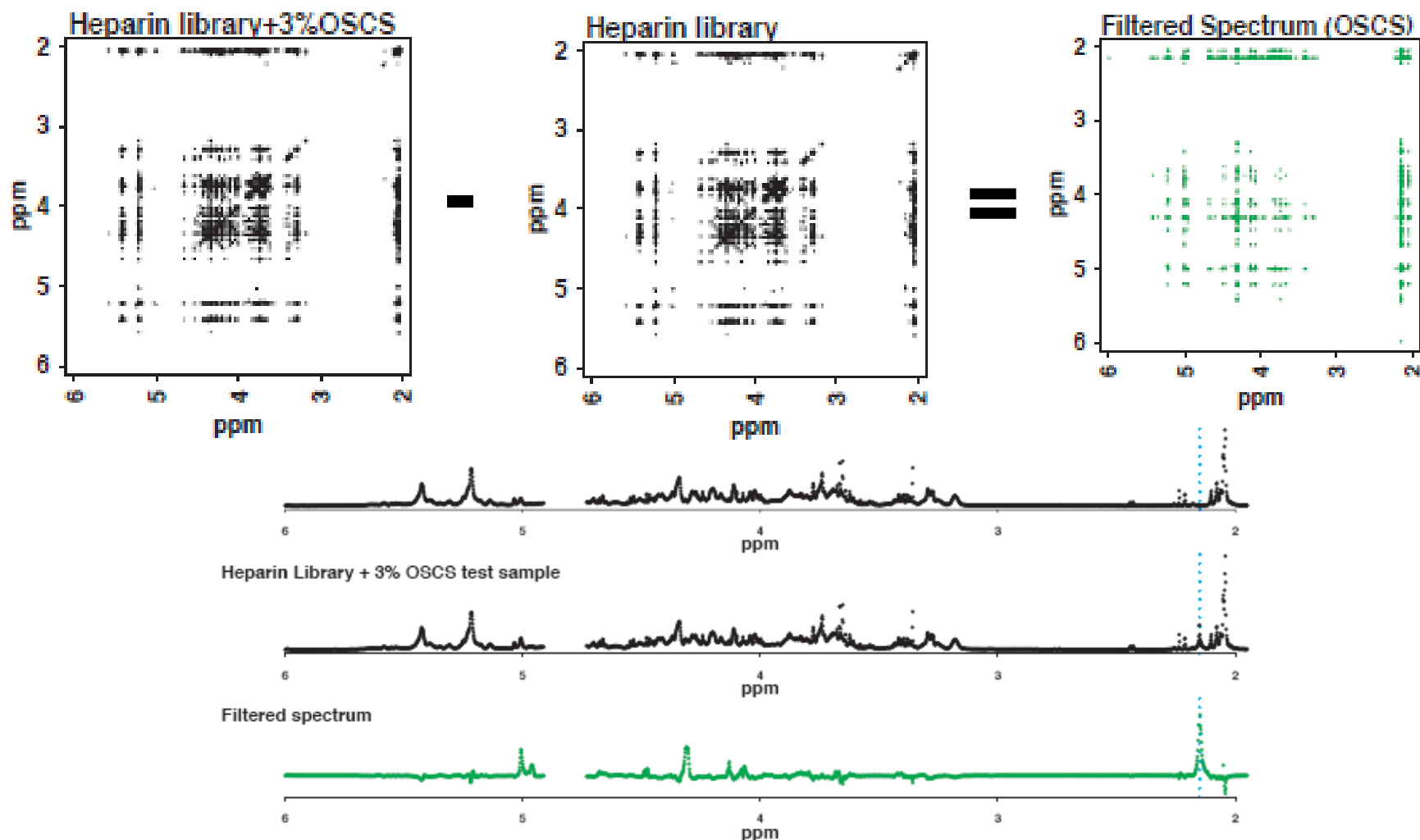
2. 2D-COS/2D-COS-f

2D-COS-Filtering Procedure:

1. Measure ^1H NMR spectra - the same conditions!
2. Import data in to R [no other programmes are available... ;-)]: <http://www.R-project.org/>.
3. Cut data - water signal, other signals can be removed - solvents.
4. Normalise for area.
5. Mean centre.
6. Pareto Scale, scale to the square root of the standard deviation. **van der Berg et al. 2006 BMC Genomics - Good scaling reference.**
7. Determine the covariance matrix of the reference heparin library [A].
8. Determine the covariance matrix of the reference heparin library with the test sample added [B].
9. B-A - plot the data...

2. 2D-COS/2D-COS-f

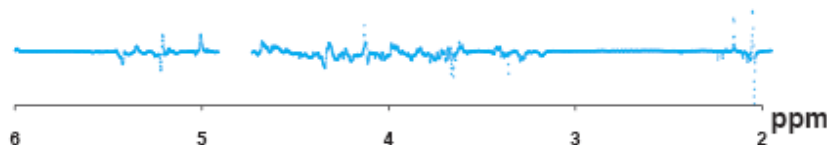
OSCS contamination of heparin



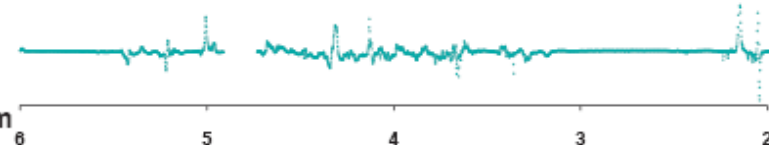
2. 2D-COS/2D-COS-f

OSCS contamination of heparin

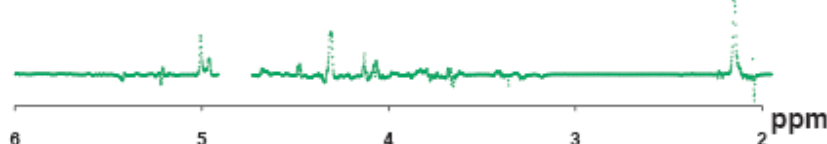
0.25% OSCS



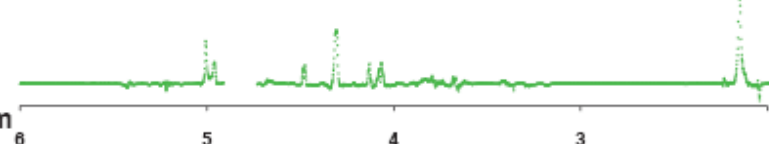
1% OSCS



3% OSCS



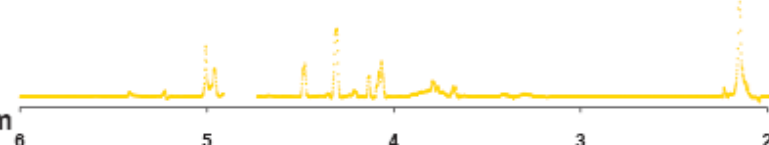
5% OSCS



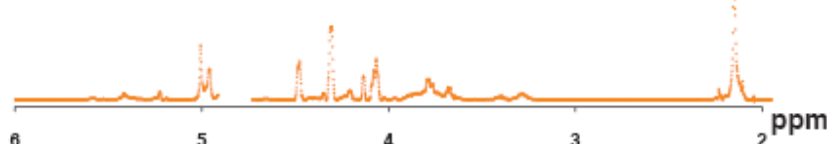
7% OSCS



15% OSCS



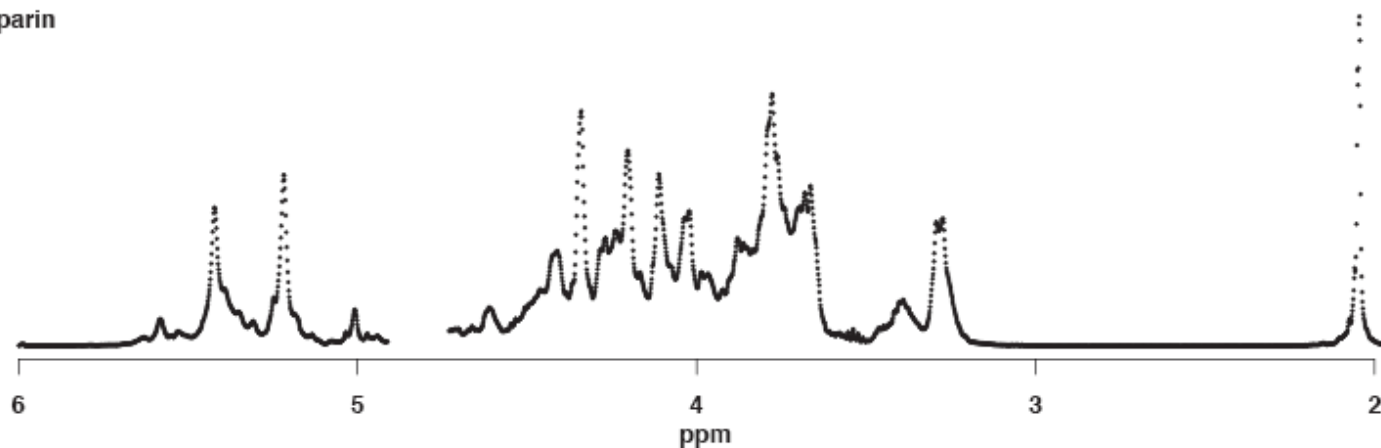
25% OSCS



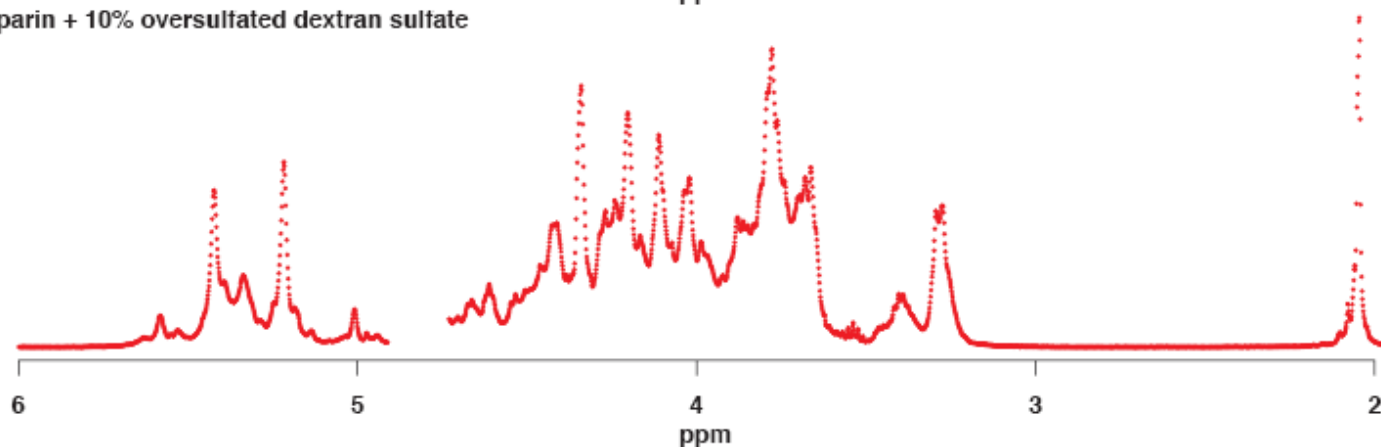
2. 2D-COS/2D-COS-f

- Oversulfated Dextran Sulfate - example of an economically relevant contaminant
- No N-acetyl signals - all other signals are within heparin signals

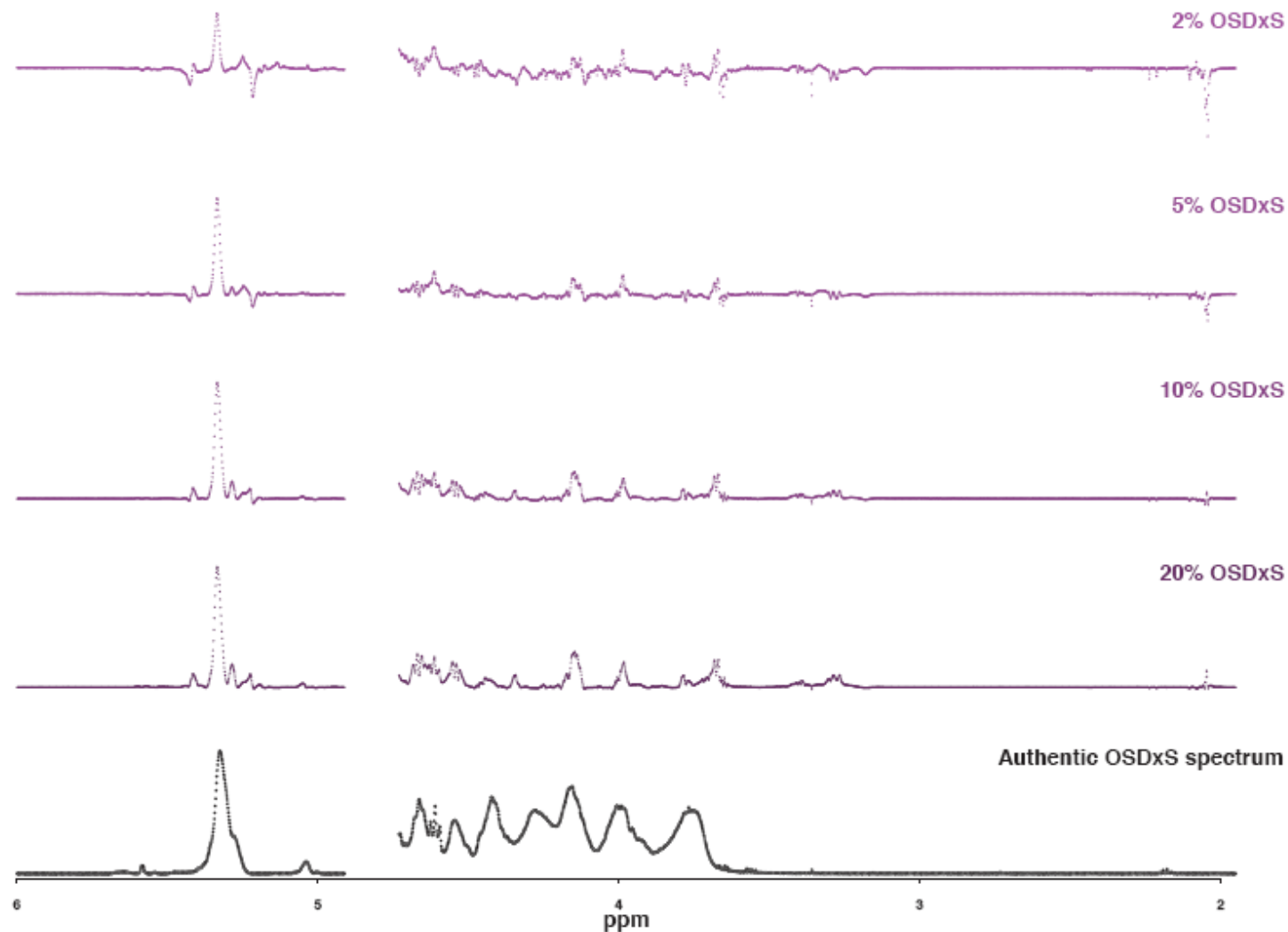
Heparin



Heparin + 10% oversulfated dextran sulfate



2. 2D-COS/2D-COS-f



2. 2D-COS/2D-COS-f

- 2D-COS filtering is a means of visualising signals which are under a complicated spectrum.
- The technique relies on having a library of reference samples to filter out signals from the test sample.
- In this circumstance the library is a definition of the polydisperse carbohydrate heparin.
- 2D-COS filtering can detect signals from compounds that do not have N-acetyl signals, which would be hidden under the mass of heparin signals.
- 2D-COS filtering can be used to visualise OSCS signals from samples contaminated with as little as 0.25 % and 2% oversulfated dextran sulfate.

Final Remarks

- **2D-COS - a means of visualising signals under complicated spectra.**
- **Employs library approach to define heterogeneous product**
- **Sensitive detection of samples with separate NMR signals and those without**
- **Applicable to any heterogeneous compounds, natural products, industrial products etc**

Acknowledgements

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Heparin, spectroscopy and chemometric analysis

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Any Questions?



Heparin, spectroscopy and chemometric analysis