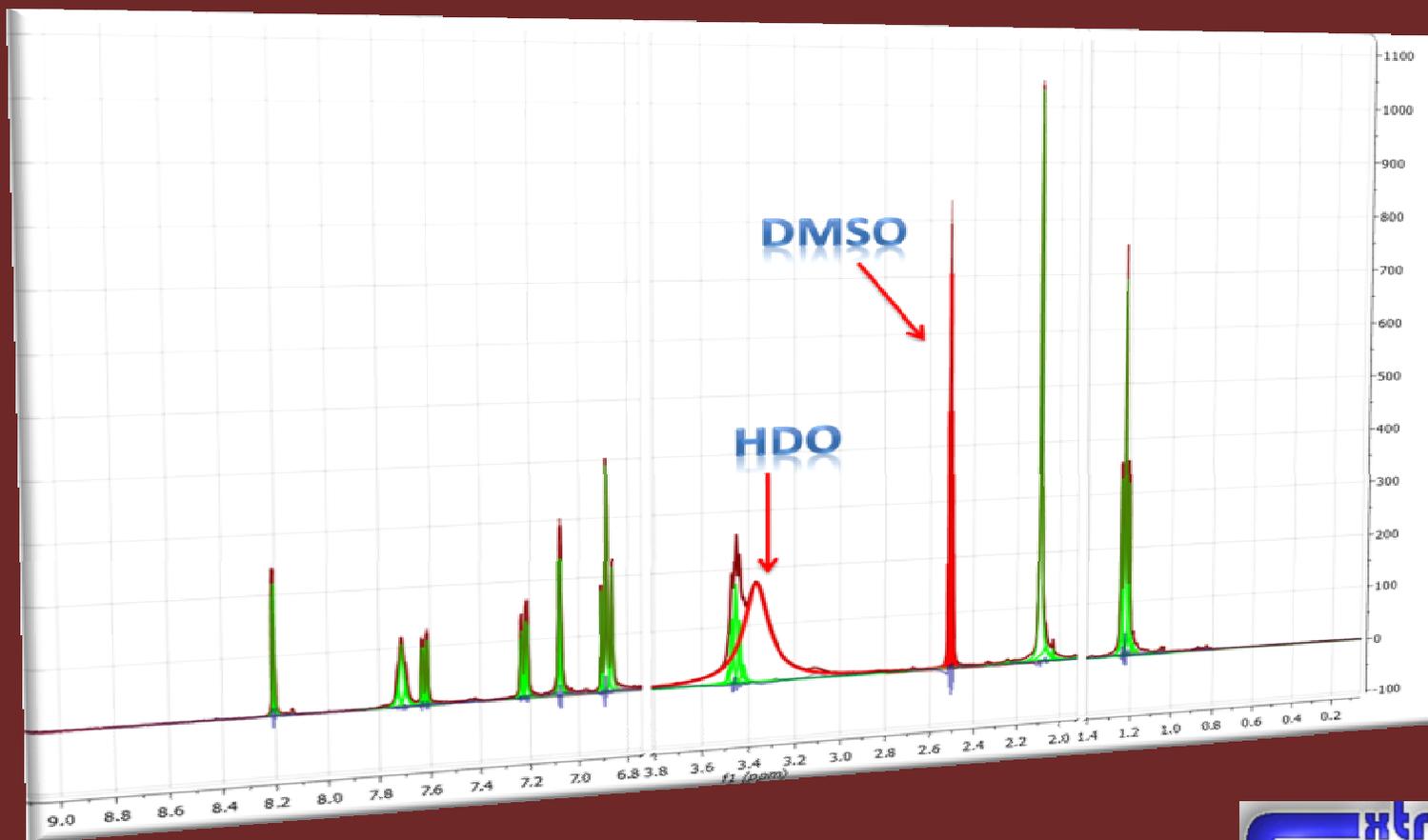


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## Automatic Solvent Recognition wizard: example of an AI at work

Stan Sykora, Carlos Cobas,  
Felipe Seoane, Pablo Monje, Esther Vaz, et al



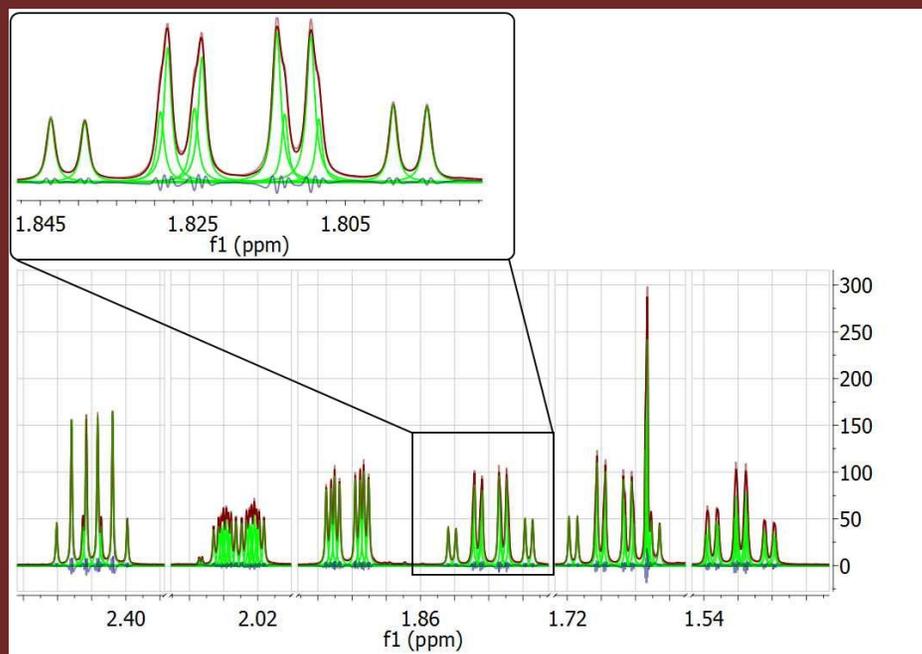
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## GSD – Global Spectral Deconvolution

f-domain algorithm which automatically decomposes sets of superposed *Lorentzians* and *near-Lorentzians* and ends up in a

### GSD Peaks List

**GSD is a standard feature of Mnova,**  
subject to continuous development



GSD has been born in 2008

and presented in detail at several meetings in 2009 and 2010



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## GSD Peaks Editing

Peaks editing brings in  
**specific NMR know-how**  
by **classifying** of the peaks in an GSD List

GSD Peaks

Report Copy Set Flags Select Peaks Reveal Peaks Setup

Resolution: 1.00 [Normal]; Refinement: 2; AutoEdit: yes

	ppm	Width	Height	Area	Type	Flags
5	9.247	0.972	7.571	99.762	Compound	Weak
6	<b>9.226</b>	<b>0.866</b>	<b>946.878</b>	<b>10952....</b>	<b>Compo...</b>	<b>None</b>
7	<b>9.222</b>	<b>1.004</b>	<b>1151.325</b>	<b>13926....</b>	<b>Compo...</b>	<b>None</b>
8	<b>9.217</b>	<b>0.950</b>	<b>1018.984</b>	<b>11608....</b>	<b>Compo...</b>	<b>None</b>
9	<b>9.214</b>	<b>1.287</b>	<b>1059.235</b>	<b>17003....</b>	<b>Compo...</b>	<b>None</b>
10	9.196	4.133	25.819	1114.023	Impurity	Weak + Labile
11	8.850	1.461	6.746	111.421	Impurity	Weak





# GSD Peaks Editing Modes

- ✓ Manual: Always accessible
- ✓ Automatic: An optional GSD feature always used in ASV

The screenshot displays the GSD Peaks software interface. The main window shows a table of peaks with columns for ppm, Width, Height, Area, and Flags. The 'AutoEdit' checkbox in the GSD Settings dialog is highlighted with a red box. The GSD Peak Flags dialog is open, showing a dropdown menu for 'Type' with options: Impurity, Compound, Artifact, Impurity, Solvent, S. Reference, and Q. Reference.

**GSD Settings**

Settings

Refinement Level  
Ref. 1 ( 2 fitting cycles )

Resolution

High  
 Normal  
 Low  
 Custom 1.00

Additional Refinement

Splittings

Auto edit

Set as Default  
Restore

**GSD Peak Flags**

Peak: 9.214

Type: Solvent

Flags:

OK  
Cancel

ppm	Width	Height	Area	Flags
5	9.247			one
6	9.226			one
7	9.222			one
8	9.217			one
9	9.214	1.287	003....	Compo... None

AutoEdit does not exclude subsequent manual peaks editing  
(transparently followed by PostEdit)



# The GSD Auto-Edit algorithm: what is it up to

- ✓ Reference peaks recognition
- ✓  $^{13}\text{C}$  satellites recognition (where possible)
- ✓ Solvent peaks recognition (primary and secondary)
- ✓ Labile peaks recognition
- ✓ J-coupling multiplets recognition
- ✓ Impurity peaks recognition
- ✓ Weak peaks labeling





# GSD Auto Editing results

## Peak Types:

pt\_Compound,  
pt\_Artifact,  
pt\_Impurity,  
pt\_Solvent,  
pt\_SReference,  
pt\_QReference

## Peak Flags:

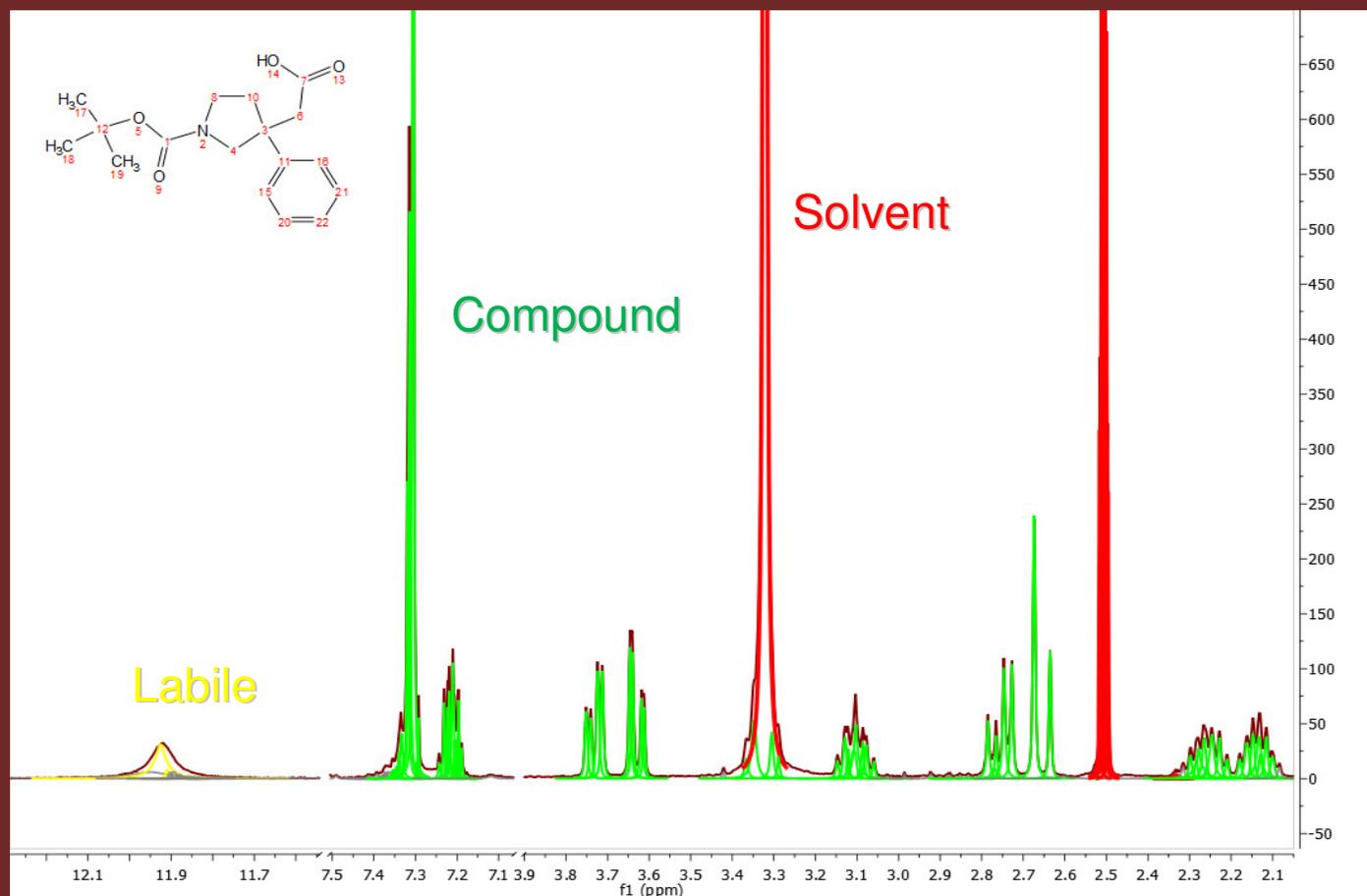
pf\_SetByUser  
pf\_Hidden  
pf\_Weak  
pf\_C13Satellite  
pf\_Rotational  
pf\_Labile  
pf\_HasC13Sats



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## What can one do with the Edited Peaks List

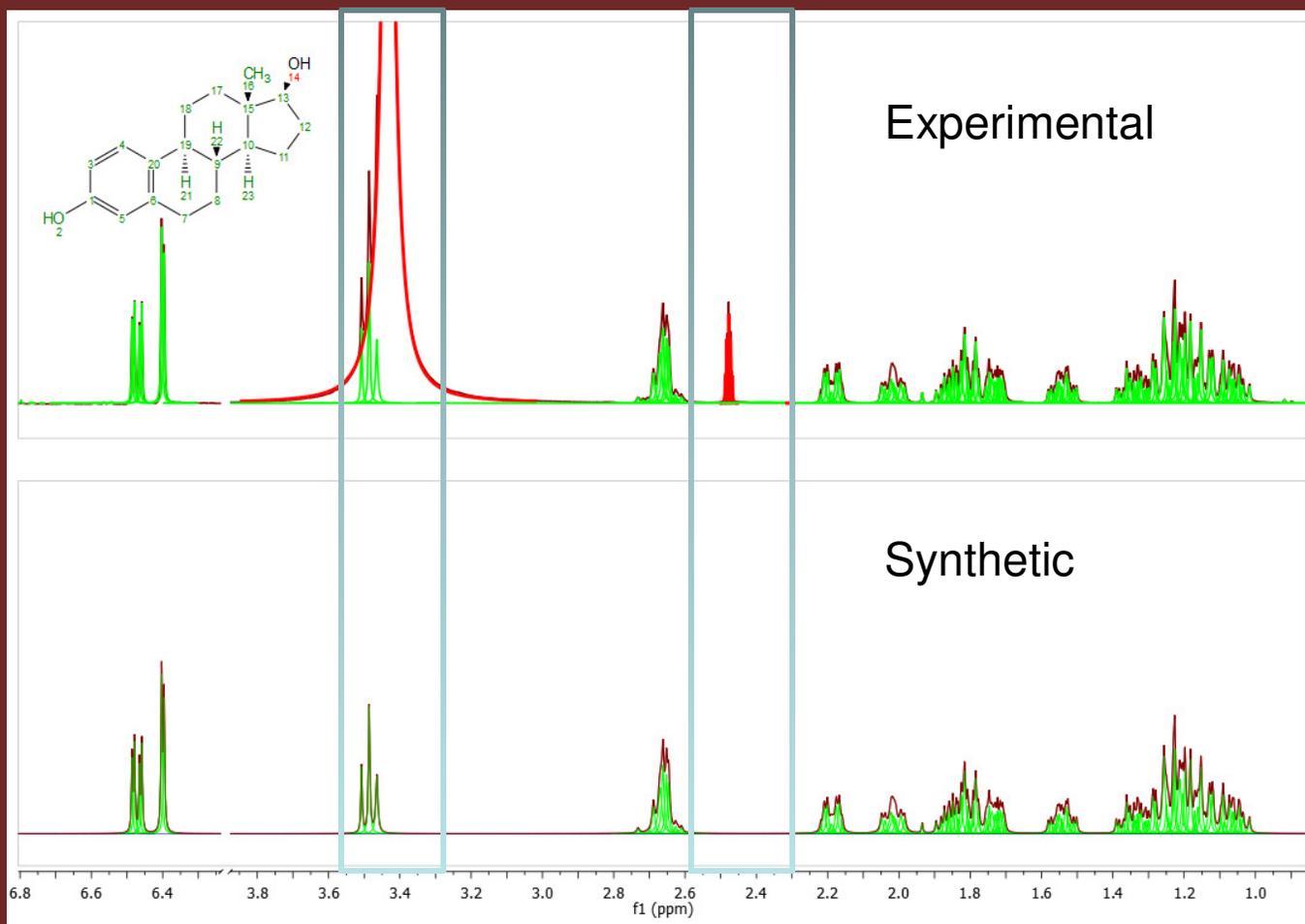
a) Color-labeled peak plots of the edited peaks

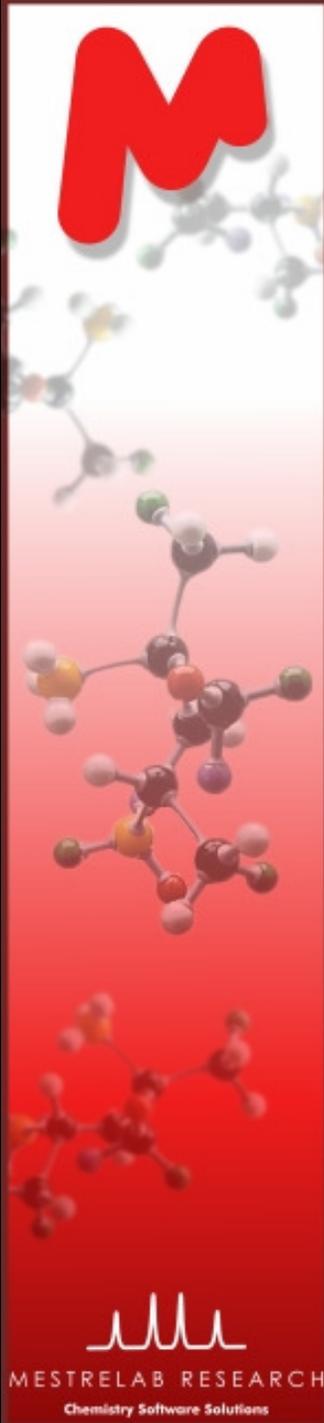




# What can one do with the Edited Peaks List

b) Synthetic spectra of any desired category of peaks





## What can one do with the Edited Peaks List ?

c) Good editing is an essential pre-requisite of ...

... **ASV !**

Automatic Structure Verification



# Solvent recognition

Possibly the most important and tricky part of **AutoEdit**

## **Human solvent recognition:**

Based on a few imperfect rules and lots of intuition

## **Automatic solvent recognition:**

Based on a long list of imperfect scoring tests

## **Primary and secondary solvent signals:**

Primary solvent recognition is relatively easy

Secondary solvent signals (water) often present problems

## **Basic development rule:**

How the hell does Tony know that this peak belongs to solvent !!!

(if you ask him, he does not know)



# Solvent description

```
DWORD SdFlags; // See the FFP_Flags enum in EbPeaks.h
// Main Multiplet:
REAL Shift; // typical main multiplet shift value
REAL ShiftLoPpm; // low limit of main multiplet in ppm
REAL ShiftHiPpm; // high limit of main multiplet in ppm
DWORD Npeaks; // number of main peaks (may not be 0)
REAL JHz; // coupling constant
REAL Pweights[5]; // array of relative weights of the peaks
// Satellite Peaks:
REAL SatWeight; // satelites relative weight (0.011 or 0)
REAL JSatHz; // satelites coupling constant
REAL SatShiftPpm; // satelites relative isotope shift
// Associated Multiplet:
DWORD Npeaks2; // number of peaks (may be 0)
REAL Weight2; // relative weight (typical)
REAL ShiftPpm2; // relative isotope shift
REAL JHz2; // coupling constant
REAL Pweights2[5]; // array of relative weights of the peaks
```





# Solvent descriptors

Typically, a solvent entry in Mnova contains two Solvent Descriptors:

- One for the **primary solvent** peaks and
- One for the **secondary solvent** peaks (usually water)

However, it could contain any number of them (even a typical impurity might be nominally considered part of the solvent)

**Coming soon:**

Possibility to easily edit and add solvent description XML files.





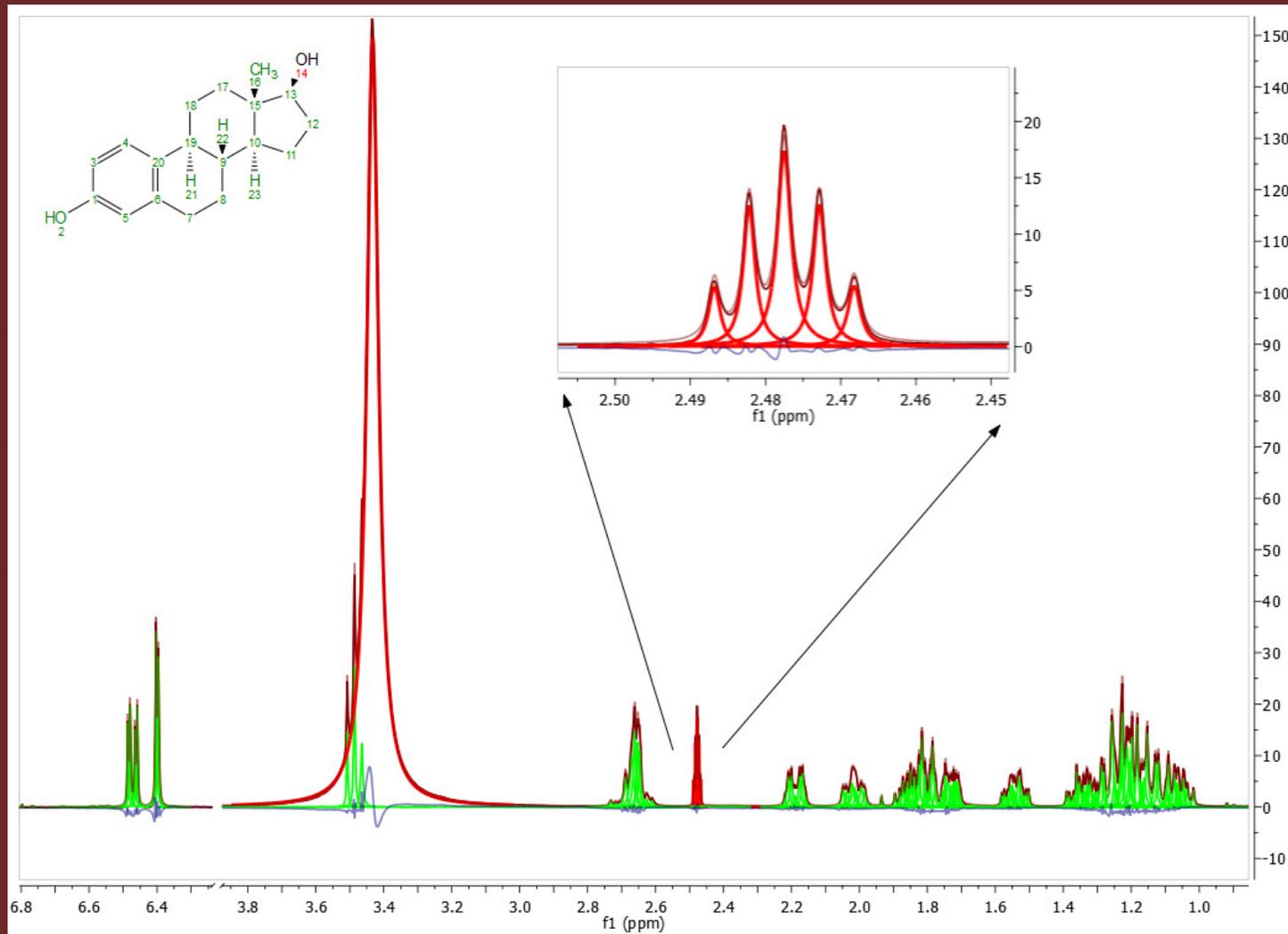
# Solvent recognition algorithm

- ✓ Look for the central peak of a solvent multiplet
- ✓ Scan all peaks in the admissible range
- ✓ Associate a full-fledged scoring system with each peak
- ✓ Scan on all of these criteria (if pertinent):
  - Position
  - Width
  - Height
  - Kurtosis
  - Presence of J-coupling multiplet peaks
    - J-HD coupling constant value
    - Relative intensities
  - Presence of  $^{13}\text{C}$  satellite peaks
    - Relative intensities
    - J-CH coupling value
    - J-CH isotope shift
  - Presence of secondary J-coupling multiplet
    - Relative intensities
    - J-HD coupling in secondary multiplet



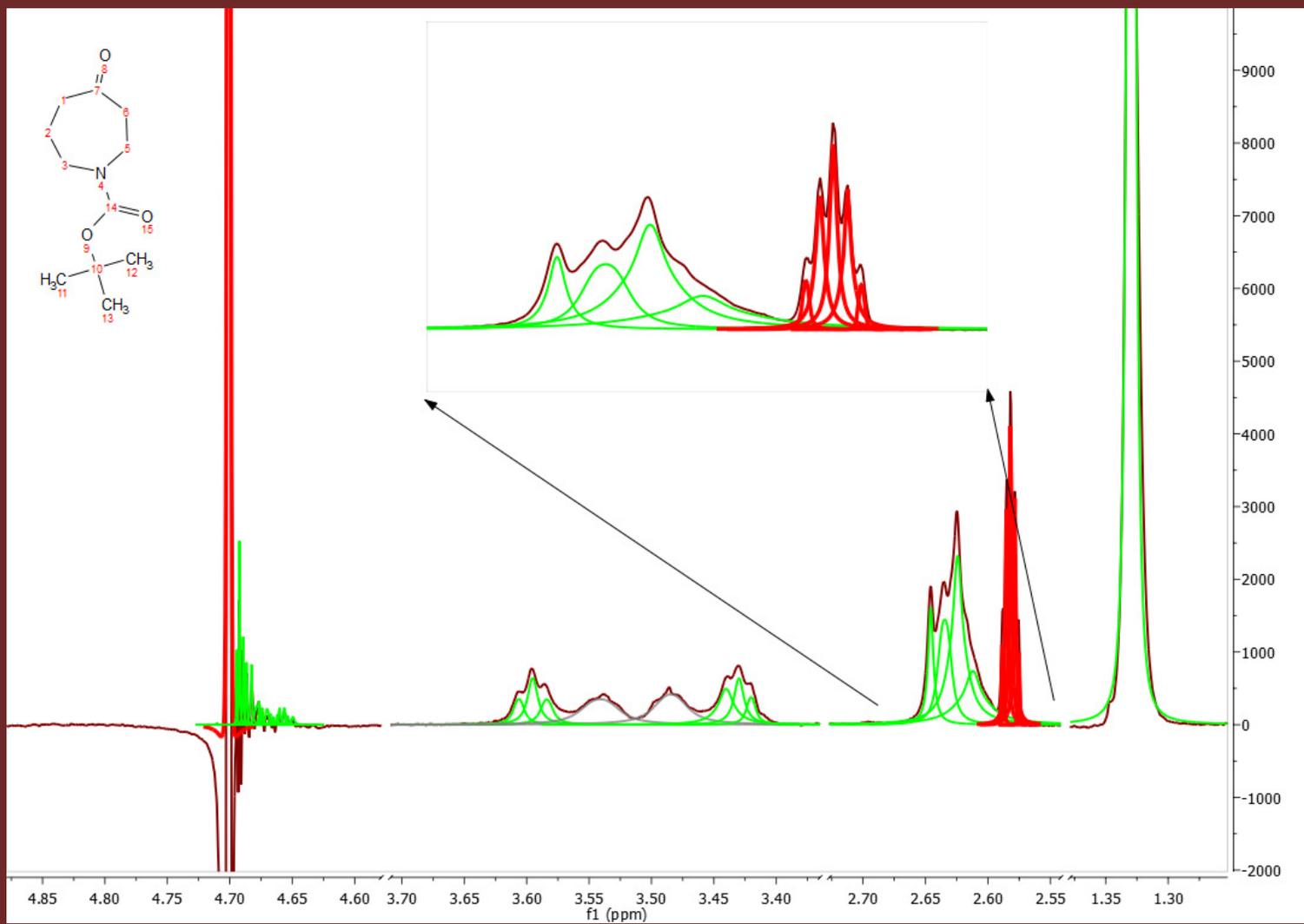
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## Some examples



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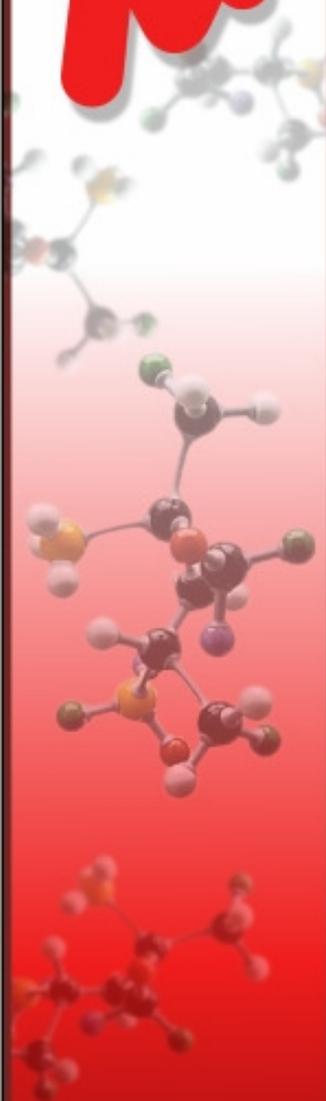
## Some examples



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Thank You for your Patience

Any Questions ?



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SMASH 2010, Portland, OR, USA

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[www.ebyte.it](http://www.ebyte.it)

