

**I think I've had this
feeling of déjà-vu before!**

**Making the most of a
structural id database**

ACD Labs, Cambridge Symposium

27th September 2016

Steve Thomas

How do I handle knowledge at the rate it is being generated today?



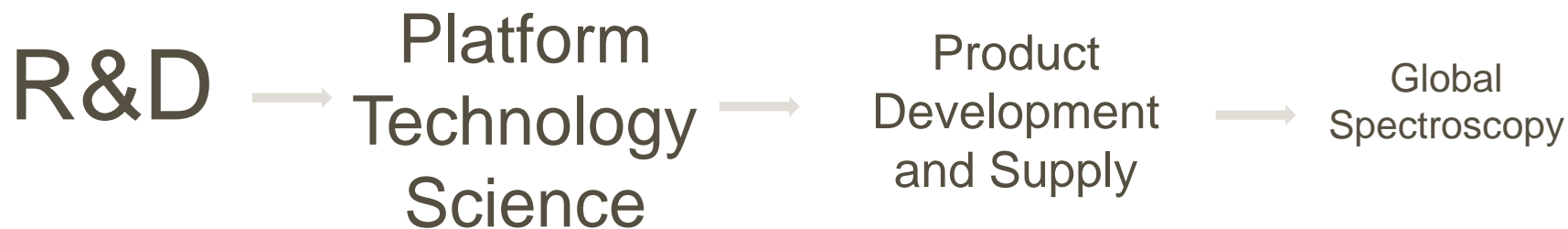
How do I best share my knowledge with my colleagues and gain access to theirs?

- Challenges in my research area
 - Data jigsaw
- Why we cannot rely on memory
 - Staff turnover
- Building a database
 - Building a data cube!
 - Metadata
- Embed and Grow
- Uptake and review
 - AAR
- Benefits
 - Accuracy and time
- Spread the word

David Jack Centre for R&D, Ware



1898 - Allen and Hanburys,
formerly Plough Court
Pharmacy (est. 1715) built on
the site of the old mill at Ware,
Hertfordshire UK



Metabolite ID



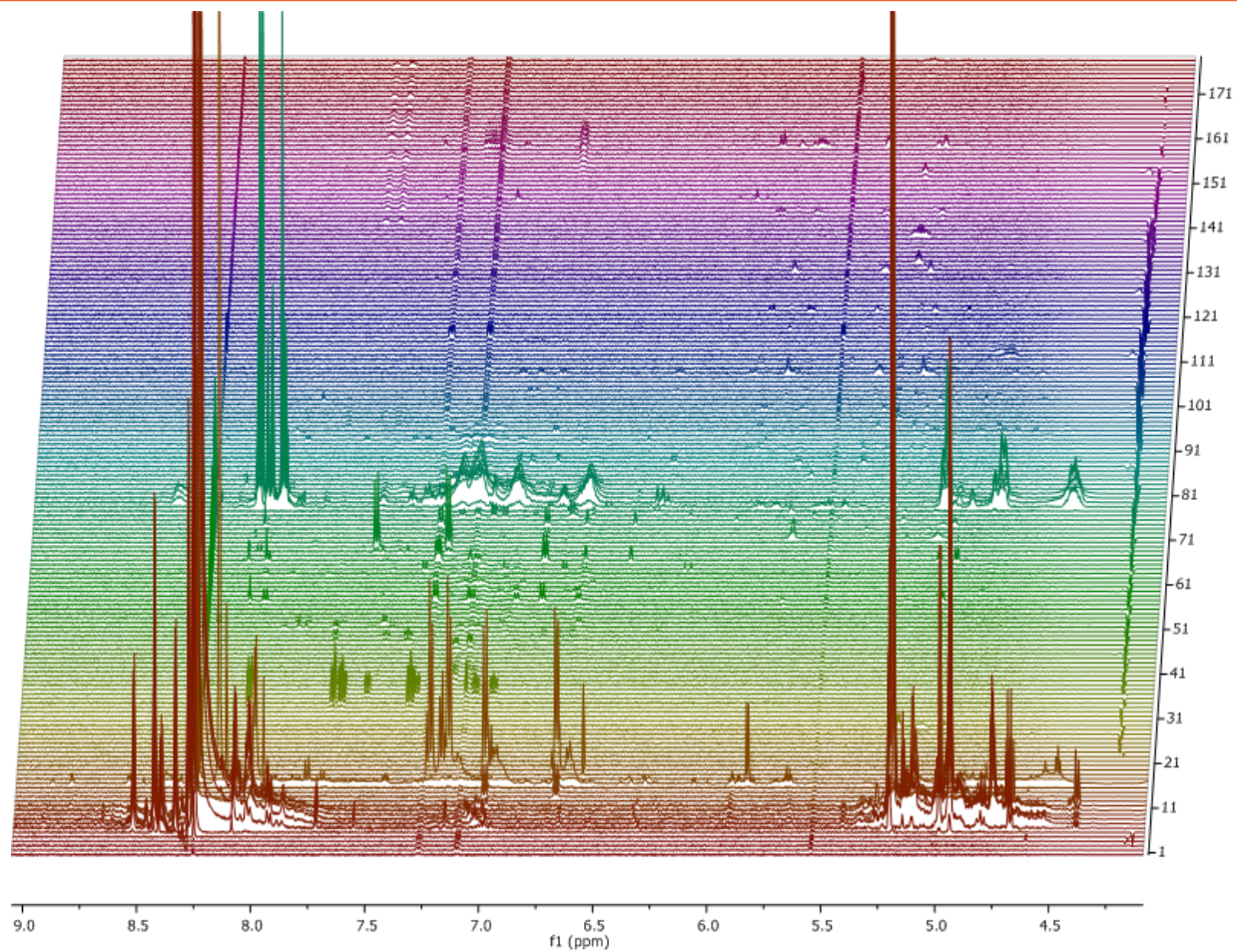
Blood



Urine



Bile



We are generating data faster than ever, how can we hope to efficiently use legacy knowledge?

The implications of passing a unsafe drug into the clinic are severe.

Getting it wrong is not an option.



What's on our side?

- Top end equipment
- Experience
- Historical data
- Ability to smell a structural alert from 20 yards!

Historical data storage



Study Number: Investigative Name: Steve Thomas Date:
Signature:

All data files have been reviewed and the data relevant to the report have been printed.

Peak ID	RT (min)	Proposed Structure	[M-H] ⁻ (m/z)	Diagnostic Fragment Ions (m/z) [†]	¹ H NMR Chemical Shifts (ppm) [‡]
Glucosylated Acid (5VA)	3.2		435 For Ion 452 (N ⁺ adduct)	312: 112 (F1) 301: 310 - H ₂ O (F2) 215: 115 (F3) 152: 112 (F4) 115: 115 (F5) 65: 65 (F6) 52: 52 (F7)	a- 0.20 b- 1.01 c- 1.10 d- 5.20 e- 2.02 f- 2.48 g- 1.12 h- 5.52 i- 6.01 j- 5.93 k- 2.44 l- 0.94 m- 1.75 n- 2.35 o- 1.43 p- 1.59, 1.27 q- 3.73 r- 1.63 s- 4.13 t- 2.41, 2.31

Agreed by:
Page 1 of 6

Date:
NA_TechDev_081

Study Number: Investigative

Peak ID	RT (min)	Proposed Structure	[M-H] ⁻ (m/z)	Diagnostic Fragment Ions (m/z) [†]	¹ H NMR Chemical Shifts (ppm) [‡]
P Glucosylated Acid	3.3		435 (P) C ₂₁ H ₃₁ O ₆ Theory: 435.2747 Found: 435.2749 Diff: 0.5 ppm.	310: F1 215: F3 152: F4 115: F5 65: F6 52: F7	a- 0.20 b- Obscured c- 1.10 d- 5.20 e- 2.02 f- 2.48 g- 1.12 h- 5.54 i- 6.01 j- 5.94 k- Obscured l- 0.94 m- Obscured n- Obscured o- Obscured p- Obscured q- 3.73 r- Obscured s- 4.12 t- Obscured
M8 Hydration, dioxetone	3.7		435 (P-32+18) C ₂₁ H ₃₁ O ₆ Theory: 435.2751 Found: 435.2770 Diff: 3.9 ppm.	300: F1+3(O) + 2(H) 247: F3 + 2(O) 115: F5 65: F6	NA

Page 2 of 6

Slm/vstathn_11

Study Number: Investigative

Peak ID	RT (min)	Proposed Structure	[M-H] ⁻ (m/z)	Diagnostic Fragment Ions (m/z) [†]	¹ H NMR Chemical Shifts (ppm) [‡]
M8 Hydration, dioxetone	3.9		435 (P-32+18) C ₂₁ H ₃₁ O ₆ Theory: 435.2751 Found: 435.2770 Diff: 3.9 ppm.	302: F1+3(O) + 2(H) 351: m/z 350 - H ₂ O 323: m/z 320 - 2H ₂ O 273: 273 (F3) 247: F3 + 2(O) 229: m/z 247 - H ₂ O 115: F5 65: F6 52: F7	a- 0.78 b- 1.91 c- 1.09 d- 5.20 e- Obscured f- Obscured g- 1.10 h- 3.91 i- 5.93 j- 3.83 k- Obscured l- 0.78 m- Obscured n- Obscured o- Obscured p- Obscured q- 3.05 r- 1.52 s- 4.02 t- Obscured, 2.30 Spectrum in ACh/D2O

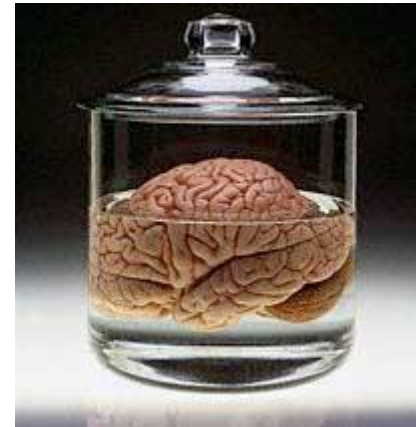
Study Number: Investigative

Peak ID	RT (min)	Proposed Structure	[M-H] ⁻ (m/z)	Diagnostic Fragment Ions (m/z) [†]	¹ H NMR Chemical Shifts (ppm) [‡]
M10 Lactonisation, oxidation, dehydrogenation, glucosylation	5.5		507 (P-18+14+178) C ₂₁ H ₃₁ O ₆ Theory: 507.2754 Found: 507.2764 Diff: 1.5 ppm.	431: glucose 318: F1 + (O) + 2(H) - (H ₂ O) 175: 112: glucosylated acid ions 115: F5 65: F6	a- 0.90 b- Obscured c- 1.13 d- 5.40 e- Obscured f- Obscured g- 1.15 h- 5.59 i- 6.05 j- 5.94 k- Obscured l- 0.95 m- Obscured n- Obscured o- Obscured p- Obscured q- Obscured r- Obscured s- Obscured t- Obscured Gluc anomeric: 5.02



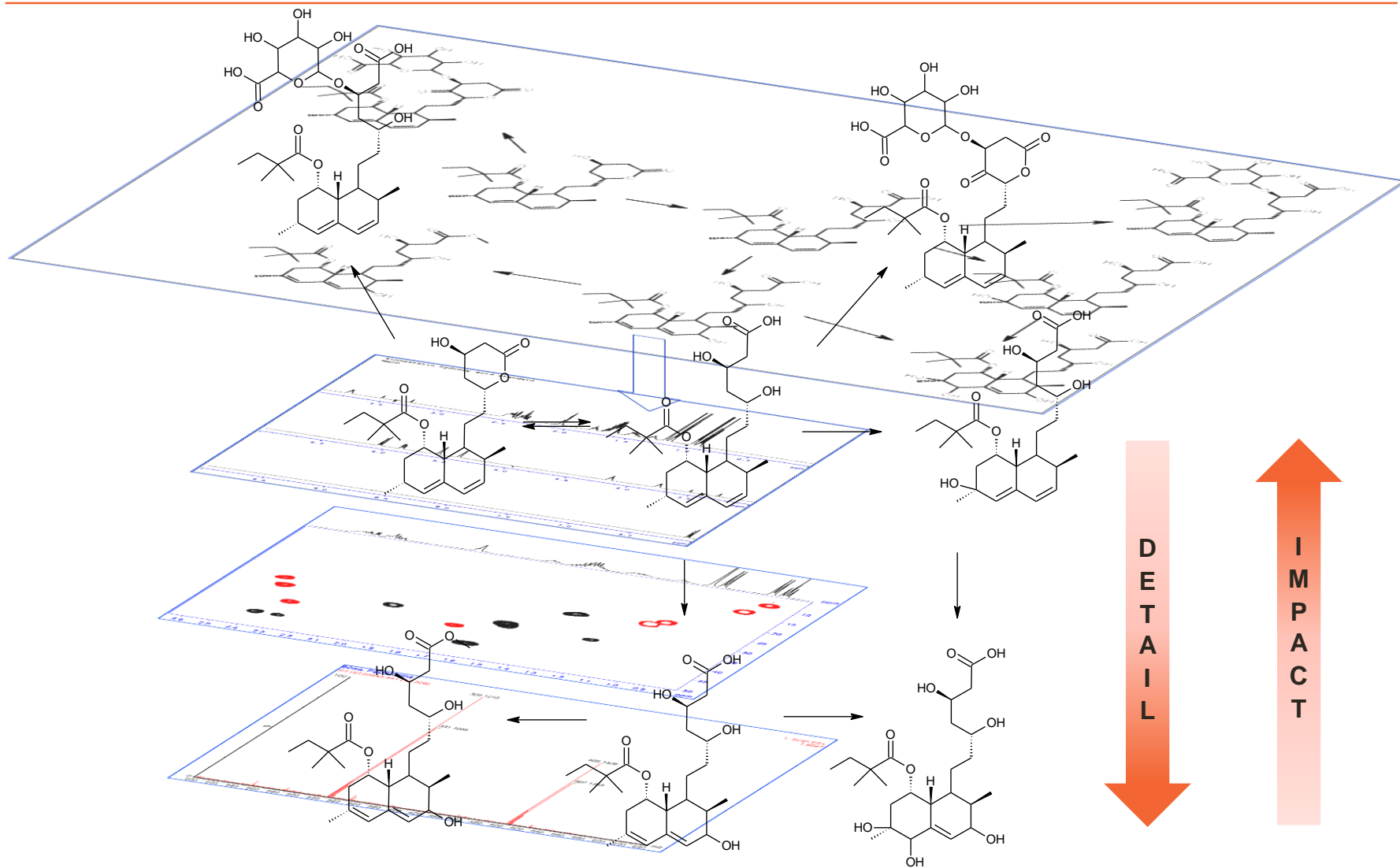
Grand wizard of metabolism –
Frank

GSK employee:
Late Jurassic - Feb 2009



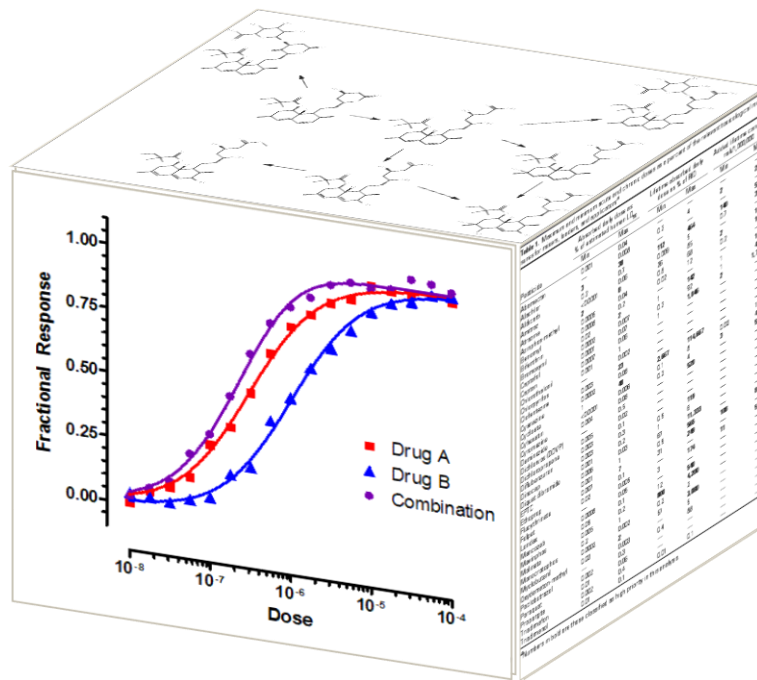
Contingency plan on Frank's
retirement!

Drill down from a biotransformation map



Not a database, a data cube

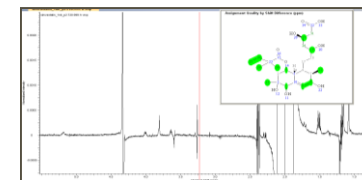
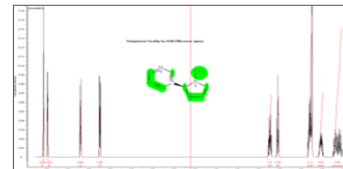
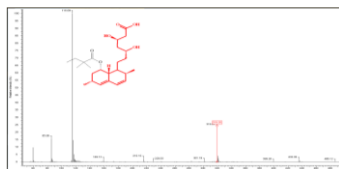
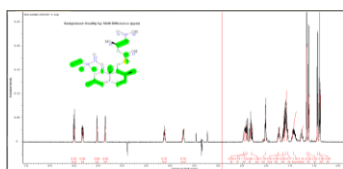
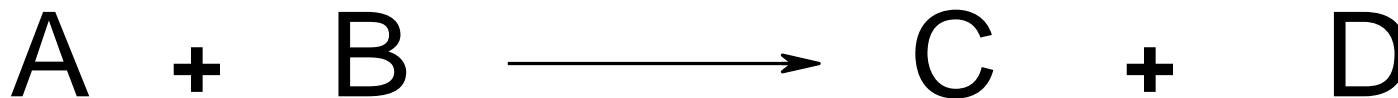
Search from any point of interest



Variety of customers leads to a wide range of ideas as to which data is most important.

Initially designed as a tool for synthetic chemists:

- CFE allows users to database reactions
- Links to data supporting structure assignments
- Structures searchable
 - “Has this been made before?”
- Data searchable
 - “What have I made?”

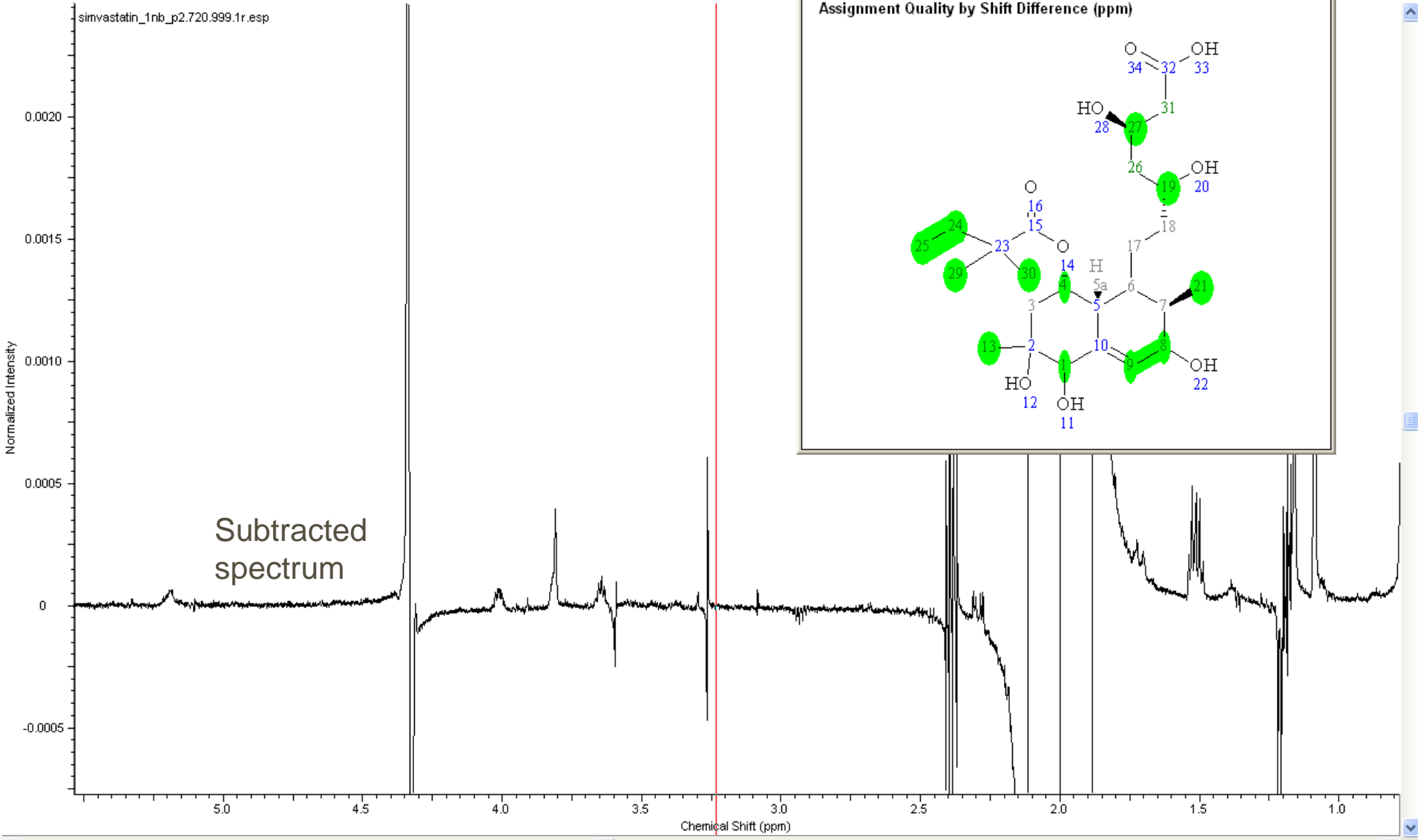


To be of use in metabolism, the system must cope with 50+ products?

Your workflows?

1. How easy is it to get the data into the database?
 2. Can it help us move away from relying on the power of memory to solve tricky problems if seen before and gain access to other associated information?
 3. Can we speed up the process of interpretation?
 4. Can we have greater confidence in the elucidations and structural ID?
 5. Can it help us avoid mistaken elucidations?
 6. Will the proposed solution offer advantages in communication of data?
-

simvastatin_1nb_p2.720.999.1r.esp



Subtracted spectrum

User data entry form



How to ensure your data is easily found.

Auto triggered on update.

Fully customisable

- Auto fill e.g. Date
- Combiboxes
- Radio (choice)
- Mandatory entry
- Free text

UK BDD Spectral Data form

Compound Number GSK1234567	Biological Matrix Plasma	Biotransformation 1 Oxidation
Study number CEDD_01	Species Human	Biotransformation 2 [Empty]
Date 10/27/2014	Sex Male	Biotransformation 3 [Empty]
Program Project 1	Analyst Steve T.	Biotransformation 4 [Empty]
Peak ID M1	Data Type NMR	
Molecule type Metabolite	Instrument NMR b	
Retention Time (min) 7.6	# of exchangeables (from H/D) [Empty]	
Data Mode <input checked="" type="radio"/> Initial Characterization <input type="radio"/> Confirmation		
Comments 74% DRM		

OK Cancel

Screen space and unknowns

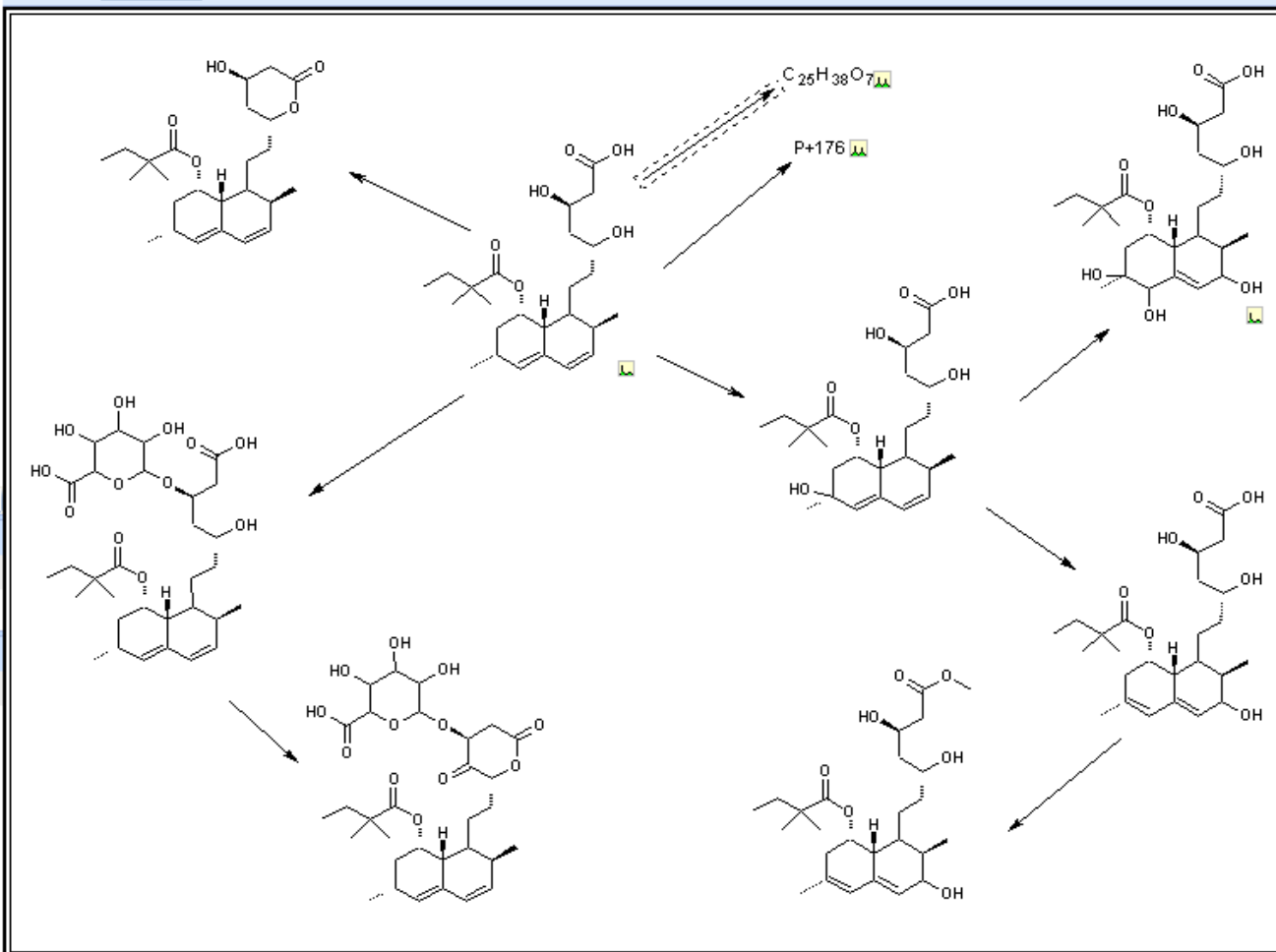


Database View Record Search Reaction Lists Options ACD/Labs Help

LOCAL REMOTE

Fit All

Metabolite Entry form



No spectrum

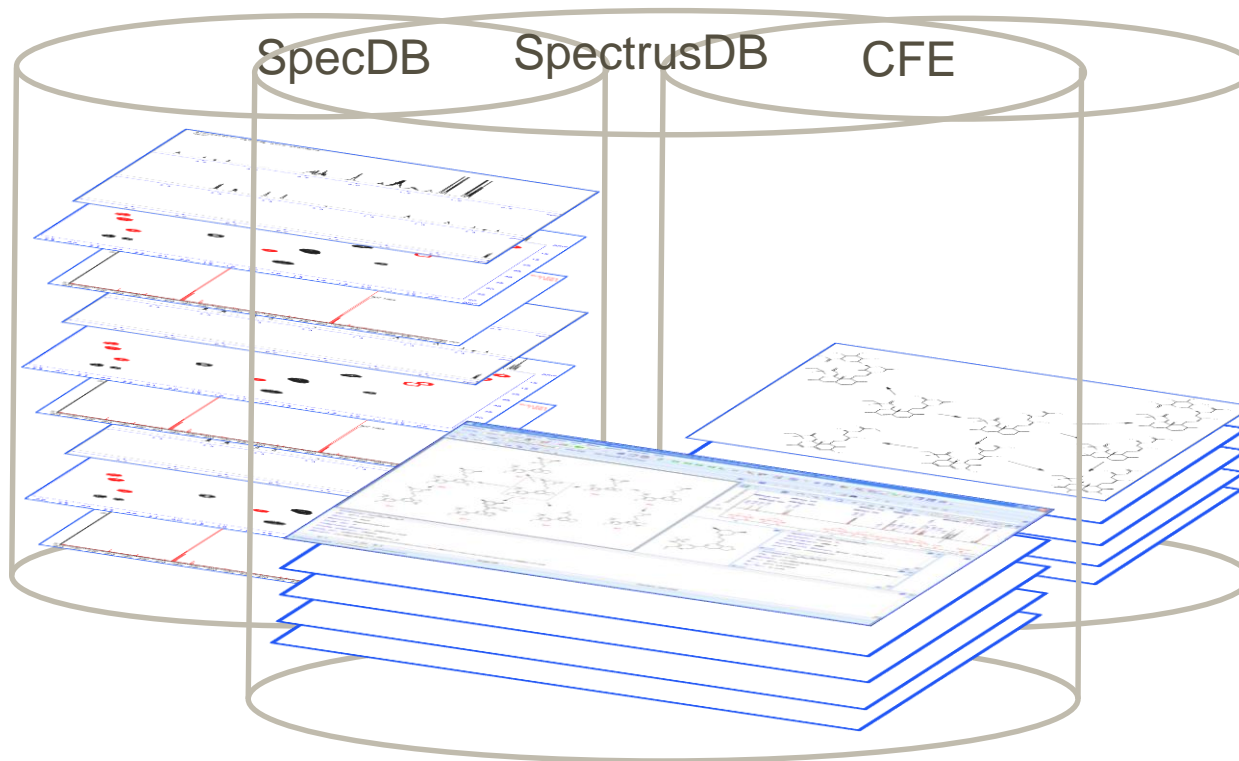
Reaction Mass Difference: 13.9793 Da (-H₂, +O)

Script Information: CFE record does not contain data

Enzyme: CYP3A4

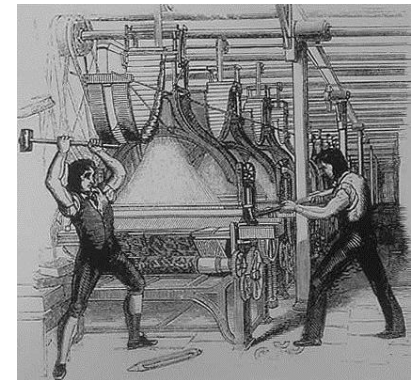
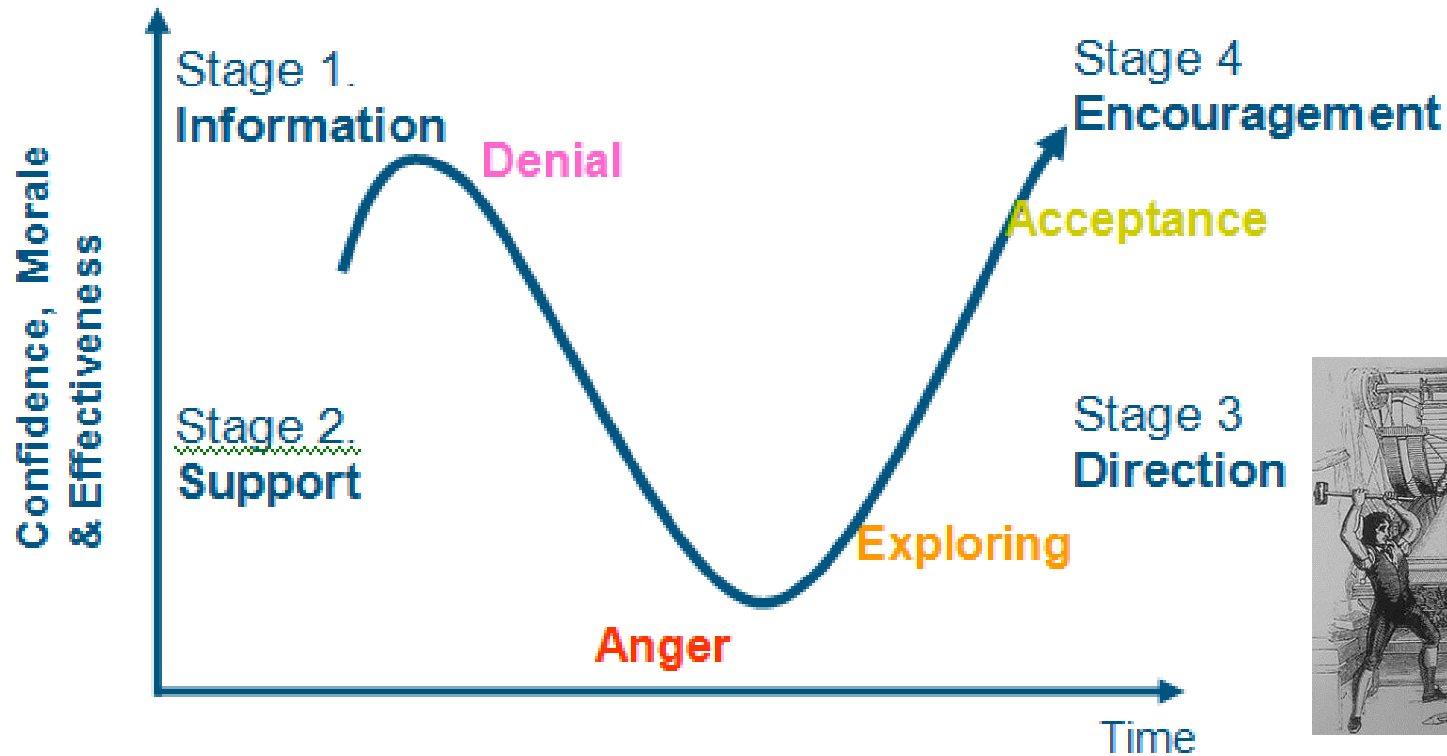
Category	Formula	FW
Scheme		
Reaction 1		
Product 1	C ₂₅ H ₃₈ O ₇	450.5660

Merger of ACD/Chemfolder and ACD/SpecDB



ACD/Spectrus Processor and ACD/Chemfolder Enterprise now together as a single Spectrus Database.

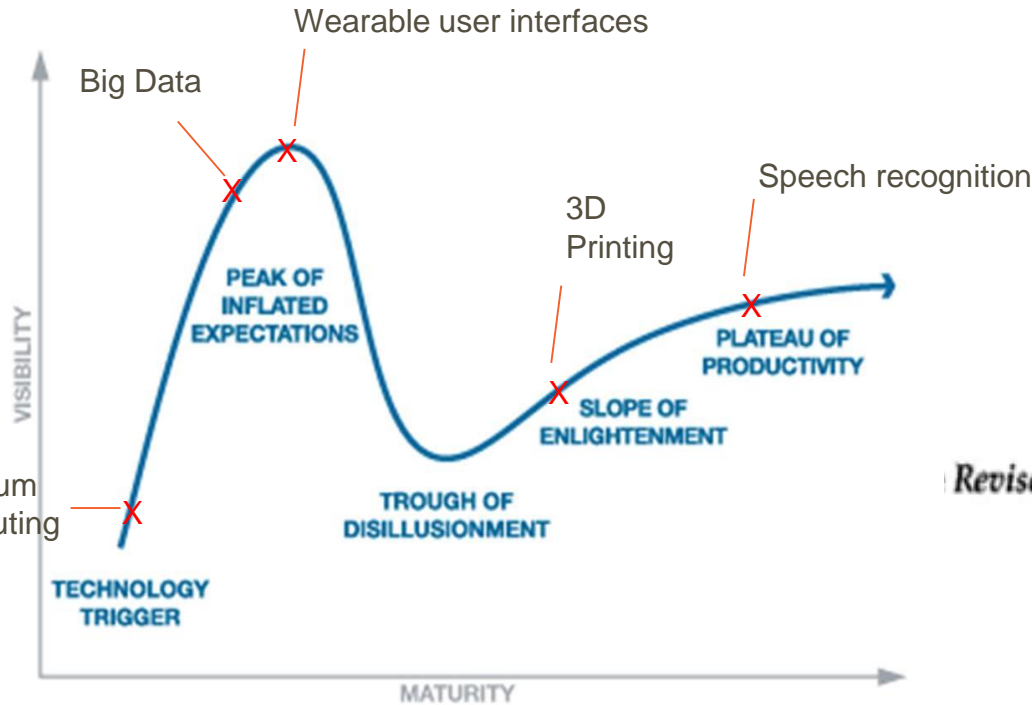
Change management curve



Looking to the past

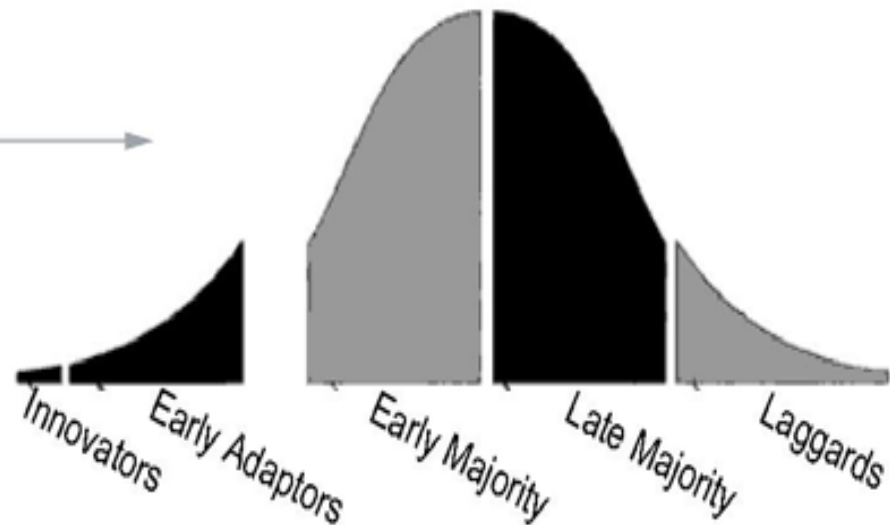
Looking to the future

Momentum and speed bumps



“The most frequent point of failure is the chasm between early adopters ‘*The visionaries*’ and early majority, ‘*The pragmatists*’.” John Trigg

Revised Technology Adoption Life Cycle



Gartner “Hype cycle”

Expectations of novel technology over time

Scripting 1. - Map comparison



#ID	Structure	Species	Compound Number	Study number
130		Human	ACD001	S0001
146		Dog	ACD001	S0001
177		Rat	ACD001	S0001

Safety cover?

Rat and dog data for illustrative purposes only

Scripting 1. - Map comparison



ACD/ChemFolder Enterprise: Database Window - [C:\ACD\GSK_COMPARE.CFD]

Database View Record Search Reaction Lists Options ACD/Labs Help

LOCAL REMOTE 92%

WW SID Unique Metabolite Metabolite Matrix Report

Formula: C₂₁H₂₂Cl₂N₄O₄
FW: 465.3298
Compound Number: ACD001
Study number: S0001
Peak ID: M04
Species: Human
Matrix: Bile;Faeces
Link_ID: ACD001_S0001_M04
UniqueMetabolite: Unique

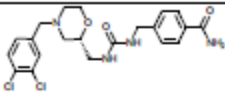
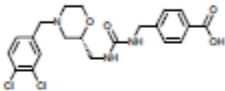
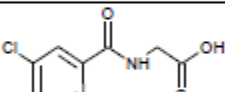
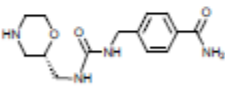
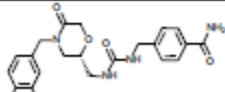
Reaction Mass ...	Compound Num...	Study number	Species	Matrix
	ACD001	S0001	Human	
-157.969 Da (-C ₇ H)	ACD001	S0001	Human	Plasma,Urine
	ACD001	S0001	Human	Urine
-203.1422 Da (-C ₁)				
	ACD001	S0001	Human	Bile;Plasma,Urine
0.984 Da (-HN, +O)				
	ACD001	S0001	Human	Faeces;Plasma
13.9793 Da (-H ₂ ,				

ID: 130 A: 1/2 B: 5 Last Updated: 30/10/2013 15:32 Single DB

1-ChemSketch 2-Database

Scripting 2. - Matrix report



Peak ID	Link_ID	Structure	Bile	Faeces	Plasma	Urine
P	ACD001_S0001_P		ND	ND	X	X
M01	ACD001_S0001_M01		ND	X	X	ND
M02	ACD001_S0001_M02		X	ND	X	X
M03	ACD001_S0001_M03		ND	ND	ND	X
M04	ACD001_S0001_M04		X	X	ND	ND

Scripted table in word summarising where each metabolite was found

Outreach – disseminating the knowledge



Peak ID	RT (min)	Proposed Structure	Mass (m/z)	Diagnostic Fragment Ions (m/z)	¹ H NMR Chemical Shifts (ppm)
0			M [H ₂] (accurate): 485.2910 M [H ₁] (nominal): 485		18 - 0.82 23 - 0.82 25 - 1.13 12 - 1.36 22 - 1.55 24 - 1.65 26 - 1.77 4 - 2.02 10α - 2.24 10β - 2.30 29α - 2.39 16 - 3.80 3 - 3.96 7 - 4.13 1 - 4.81 4 - 5.27 8 - 5.55
			M [H ₂] (accurate): 83.0440 M [H ₁] (nominal): 83		
			M [H ₂] (accurate): 115.0970 M [H ₁] (nominal): 115		
			M [H ₂] (accurate): 137.1215 M [H ₁] (nominal): 137		
			M [H ₂] (accurate): 213.1510 M [H ₁] (nominal): 213		

Avoid “Silo” mentality

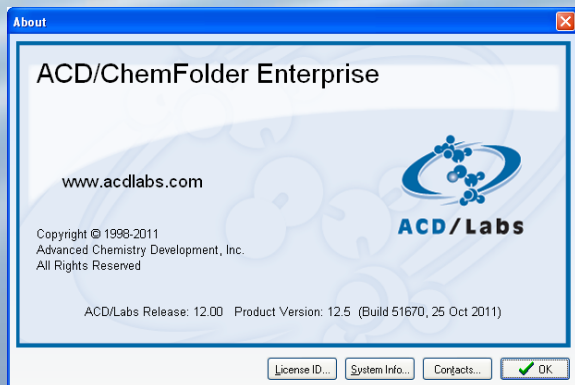
- Users typically used to facile, free access will not want access restricted by logistics or cost.
- Without barriers our data will reach everyone it can help



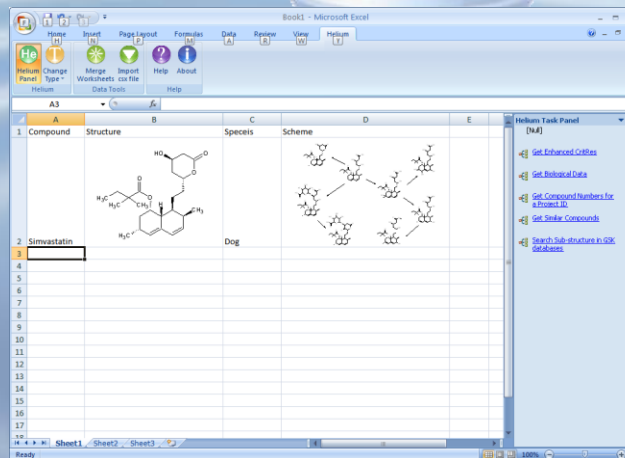
Dissemination strategies



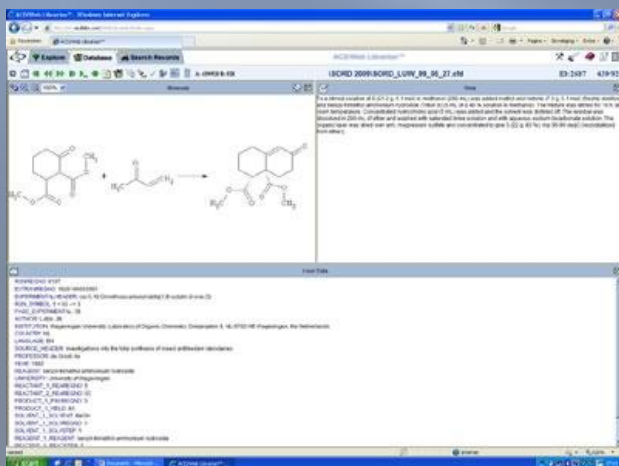
Local super users



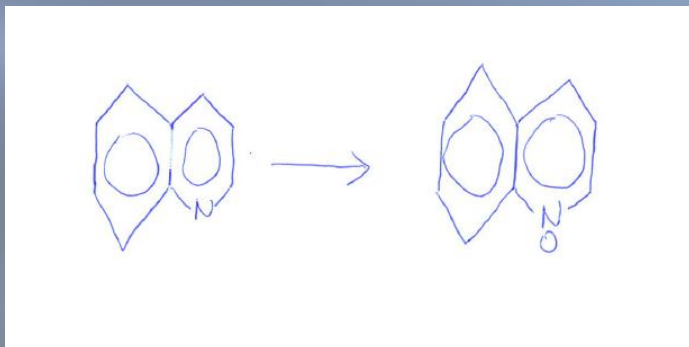
Helium



ACD/Web Librarian



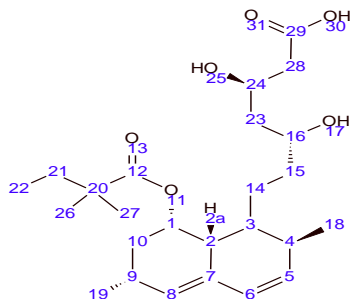
Requests!



Scripting 3. – Automated reporting (scripting)



Peak ID P
Retention Time 8.6 min
Mol Weight: 436.3



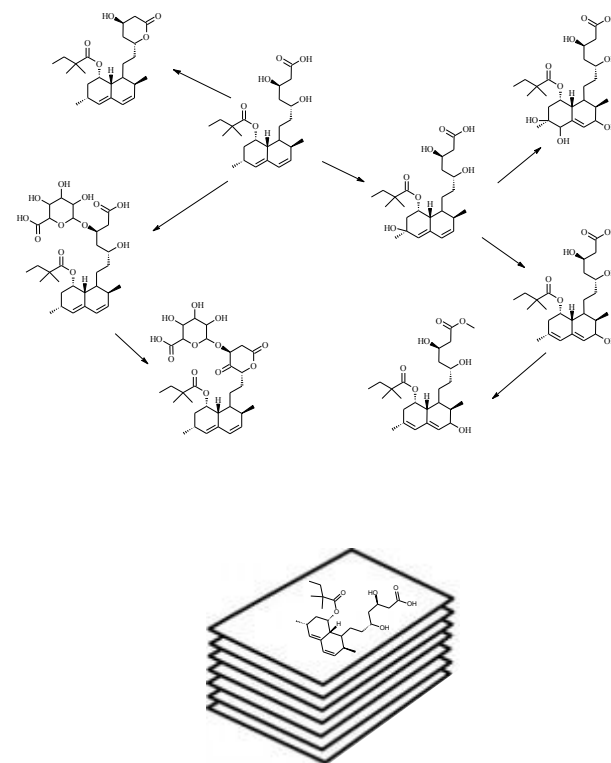
Formula	m/z Calc.	Difference (Da)	m/z Exp.
C25H39O6	435.2752	-0.1155	435.1597

¹H NMR:

Atom	Exp. Shift (ppm)	Atom	Exp. Shift (ppm)
18	0.94	4	2.31
19	1.12	9	2.35
15	1.16	2a	2.41
27	1.16	28	2.45
26	1.16	28	2.46
15	1.27	16	3.74
10	1.43	24	4.13
23	1.43	1	5.36
23	1.57	8	5.53
21	1.61	5	5.83
14	1.61	6	6.01
21	1.66		
3	1.74		
10	2.02		

MS Fragmentation:

Structure	m/z Exp.	Structure	m/z Exp.
	59		319
	85		435
	115		
	215		



Comments:

Success criteria



1. How easy is it to get the data into the database?

Variable e.g MassLynx ACD/Labs button,  Xcaliber, Unify

2. Can it help us move away from relying on the power of memory to solve tricky problems if seen before and gain access to other associated informatic

Search on

3. Can we sp

Ready acc

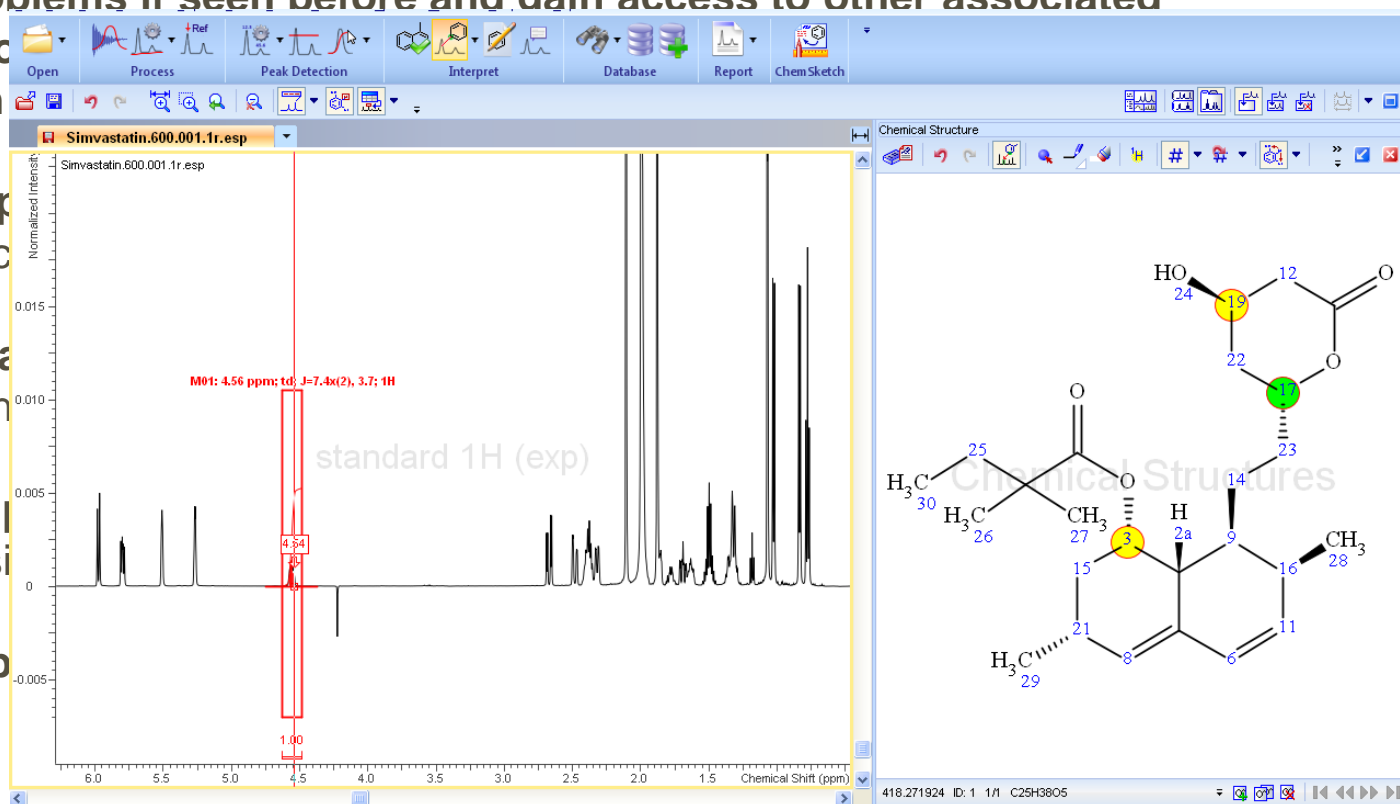
4. Can we ha

Has anyon

5. Can it help

Smart assi

6. Will the p



What went well?

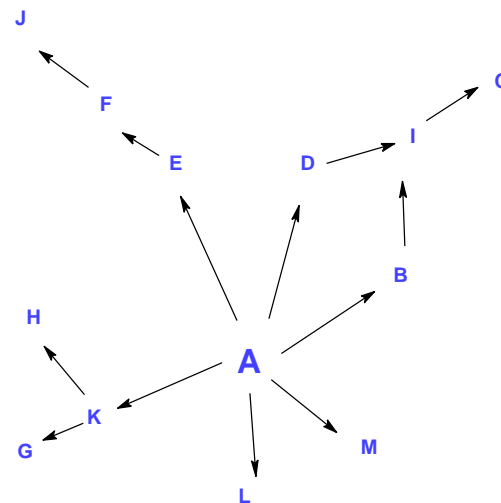
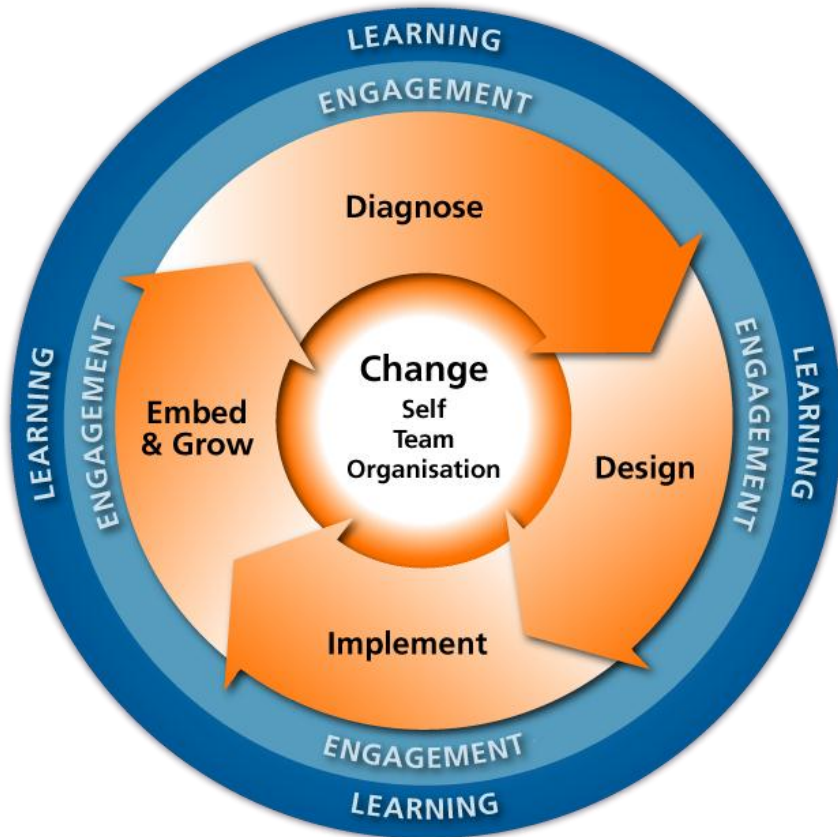
1. Communication between sites has been good on occasions
2. 1:1 training has been excellent
3. Regular up-dates
4. The database searchability is starting to show promise – some early adopters
5. Summer students – data entry (good use of resource)
6. Communicated well across boundaries and teams

What could be improved?

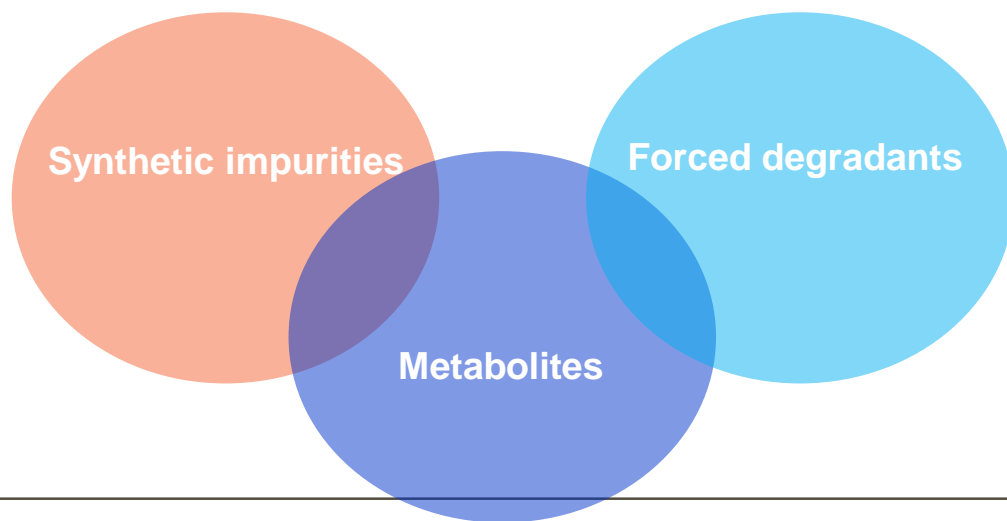
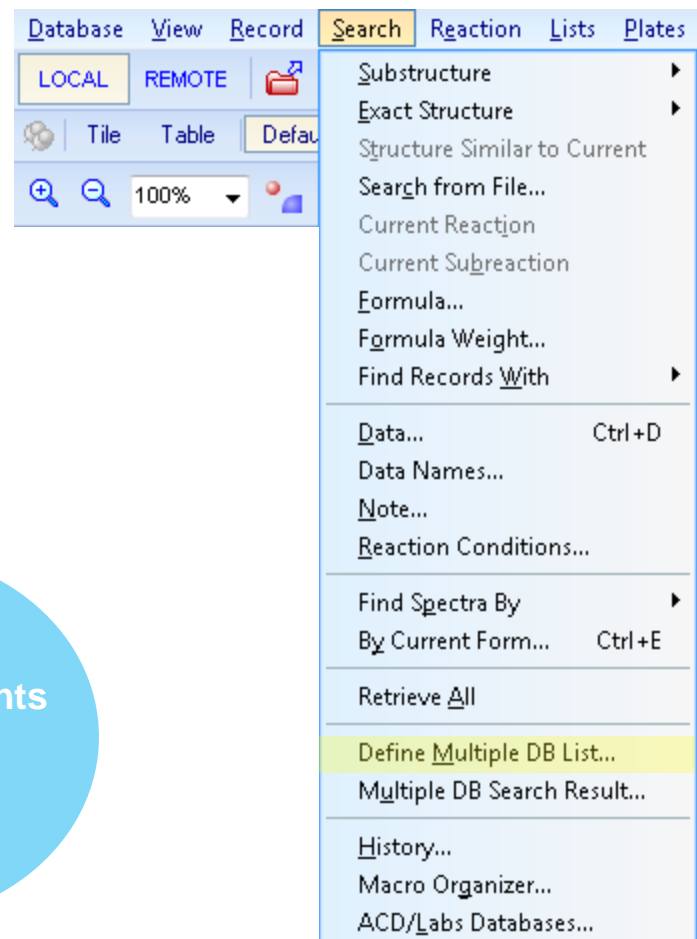
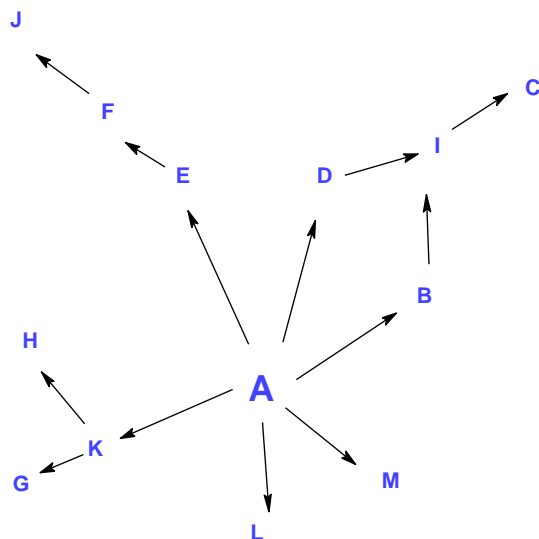
1. **Communication** between sites has been poor on occasions
2. **Training guide** is obsolete - needs up-dating (seen as vital)
3. “Our site didn’t have a training guide, or at least weren’t aware one existed “(**communication**)
4. Lack of **training** has hindered uptake
5. Clarity and visibility on business rules (**communication**)
6. Lack of energy at times – felt like lost momentum , because Spectrus upgrade was looming
7. Not easy to enter data - lack of **training** options?
8. Issues with processing software (automatic assignment) when looking at real metabolites
9. Same for MS (duplication)
10. Big issue with re-learning (as long time gaps between use) – comes back to provision of adequate **training** guide
11. Uncertainty about Spectrus – when, where and how (**communication**)
12. Better visibility to a project plan – when, where, how and who (**communication**)
13. **Training** set/tutorial should be available
14. Reporting and exporting issues – more energy in this space
15. Clarity around met id data reporting e.g. in report Appendix
16. Inconsistent message from ACD – different viewpoints from different ACD experts/sales folk?

Spread the word

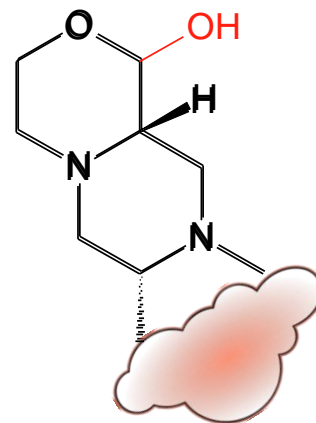
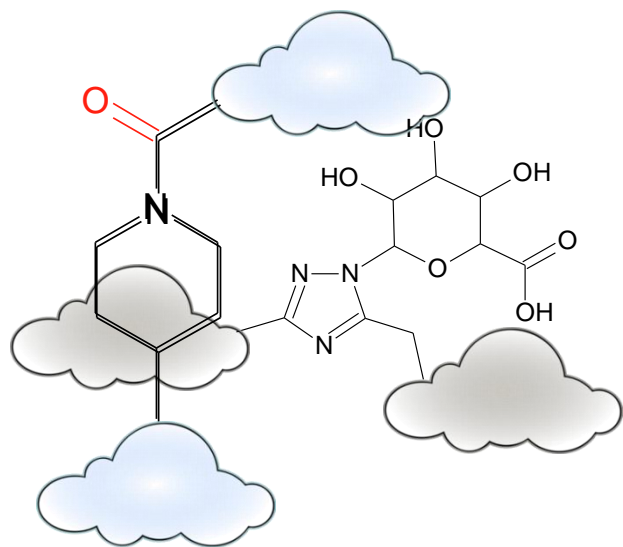
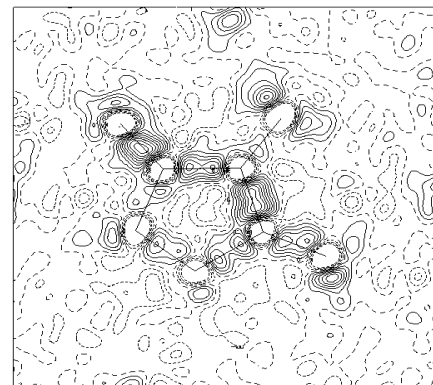
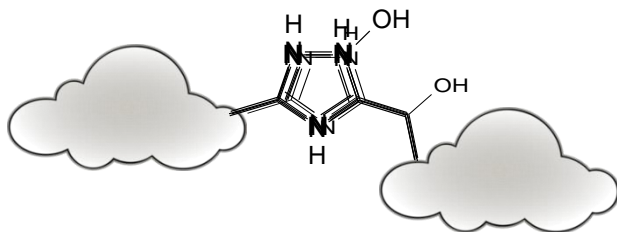
- Other groups facing similar challenges



Working across boundaries



Synergy – Metabolism and Degradation



Summary



- Get everyone on-board. Community of empowered users.
 - Training, user guides
 - Hooks

 - Valuable way to store, search and share sets of related molecules
 - Body (metabolites)
 - Environment (stability)
 - Chemist (reactions / impurities)

 - Scripting capability
 - Automated reporting

 - Further enhancements constantly delivered
 - ACD respond to new feature requests
-

Thank you