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Combining both quantum mechanics and Hierarchical Organisation of Spherical Environments for natural products 2D NMR spectra simulation

Sergio Ortiz ¹, Mustapha-Kamel Dali-Yahia ^{1,2}, Raphaël Grougnet ¹, Yannick Estevez ³, Sylvie Michel ¹, Sabrina Boutefnouchet ¹ and Grégory Genta-Jouve ^{1*}

Abstract

Structure elucidation of unknown compounds has been the task of natural products chemists for a long time and their approach seems to be the most efficient when it comes to identification. Very recently, Kokkotou *et al.* proposed a work-flow based on an integrative approach for new metabolite identification. This approach, including prediction of 2D NMR HSQC spectra, demonstrated the necessity for implementation of new algorithms leading to the prediction of 2D NMR spectra. Herein we present a method based on both quantum mechanics (QM) and Hierarchical Organisation of Spherical Environments (HOSE) of the prediction 2D NMR spectra.

Keywords

DFT GIAO — HOSE — NMR prediction — *seco*-tanaparthalide A — natural products

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Introduction

Identification of small molecules, such as metabolites, remains a difficult task [1, 2]. It is one of the largest challenges in chemistry today and has even been considered as the main bottleneck in metabolomics for the last decade [3, 4]. Structure elucidation of unknown compounds has been the task of natural products chemists for a long time and their approach seems to be the most efficient when it comes to identification [5, 6]. The main problem of the natural products approach is that it is time consuming. Indeed, the isolation and characterisation of a new compound is usually performed within months as it requires a sufficient amount of a pure compound to be successful. In the last decade, several hyphenated approaches have been proposed to overcome this issue, mainly using high performance liquid chromatography coupled to mass spectrometry (LC-MS) [7, 8, 9]. Very recently, Kokkotou *et al.* proposed a work-flow based on an integrative approach for new metabolite identification [10]. This approach, including prediction of 2D NMR HSQC spectra, demonstrated the necessity for implementation of new algorithms leading to the prediction of 2D NMR spectra.

Herein we present a method based on both quantum mechanics (QM) and Hierarchical Organisation of Spherical Environments (HOSE) of the prediction 2D NMR spectra. We don't intend to describe here the theory of NMR calculations (DFT or HOSE), for more information, the reader are encouraged to look over [11] for an overview of the DFT calculations

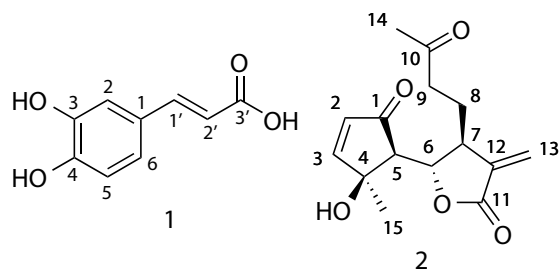
and [12] for an HOSE description. The main difference between the two approaches is time. While computation of hundreds of spectra can be done in less than a second using HOSE, several hours are required for the calculation using DFT. The main steps involved in NMR calculation using DFT have been well described by Willoughby *et al.* [13] and include a geometry optimization (of each conformer) followed by a frequency calculation. The NMR properties are then calculated (for each conformer) and the chemical shifts are computed using the Boltzmann equation.

In the current approach, the simulation of the 2D NMR spectra is based on the package Spinach [14]. The focus of the present work will be on 2D NMR spectra as several approaches already exist for the prediction of accurate 1D NMR spectra [15, 16]. The magnetic parameters are computed with Gaussian 09 [17] (coordinates, *g*-tensor, hyperfine coupling tensors, chemical shielding tensors, scalar couplings) and nmrshiftdb2 [18] (chemical shifts). To illustrate the methodology, the method has been tested on two compounds, caffeic acid (1) which is ubiquitous in plants and *seco*-tanaparthalide A (2), a sesquiterpene lactone isolated from the aerial parts of *Pentzia monodiana* Maire (1929) (Asteracea)[19]:

1. Experimental Section

1.1 General

¹H and ¹³C NMR experiments were performed in chloroform-*d*. Spectra were recorded on a Varian 400 MR spectrometer



equipped with a 5 mm inverse probe (Auto X PGF 1H/15N-13C) for compound **1** and on a Bruker AC a Bruker 400 MHz spectrometer (Wissembourg, France) for compound **2**. MS experiments were performed on a mass spectrometer ZQ 2000 Waters (Saint-Quentin, France). The ESI source conditions were capillary cone voltage 50 V in positive mode, spray voltage 3.4 kV. Column silica gel 60 0.025-0.04 mm (Macherey-Nagel GmbH & Co.) was used for column chromatography (CC). Analytical HPLC were performed on LaChrom Elite apparatus provided by VWR (Fontenay-sous-Bois, France) with a D-7000 interface, a L-7200 autosampler, a L-7100 pump, a L-7400 UV detector and running on EZChrom Elite 3.3 software. ODS reverse phase column (Phenomenex, 150 mm × 4.6 mm, 5 μm) was used for analysis. Preparative HPLC were performed on a AP-MOD-100 apparatus provided by Armen Instrument (Saint-Avé, France), injector Vanne Rheodyne 3725-038 inox, column Pursuit™ Varian with reverse phase (250 mm × 30 mm, 10 μm), detector Büchi UV/VIS Filter-photometer, integrator Merck D-2500, collector Büchi C-660. High pressure extractions were performed on a Speed Extractor E-914 apparatus provided by Büchi (Fawil, Switzerland) equipped with four cells (120 mL) and a collector with four flat bottom vials (220 mL). Maximum pressure and temperature can be adjusted from 50 to 150 bar and from 30 to 200 °C, respectively. CPC was performed on a SCPC-250+1000B apparatus provided by Armen Instrument (Saint-Avé, France) fitted with two rotors, containing respectively 1953 or 2016 twin-cells. Rotation speed can be adjusted from 0 to 3000 rpm for the 250 mL rotor and from 0 to 1500 rpm for the 1 L rotor. A valve incorporated in the CPC apparatus allowed operation in ascending or descending mode. Fractions were collected by a Büchi 684 collector (Flawil, Switzerland). The experiments were conducted at room temperature. All the reagents and solvents were purchased from Carlo Erba-SDS. Cyclohexane and EtOAc were distilled before use. Water was distilled from deionized water. TLC were performed on Merck silica-gel 60 F₂₅₄ aluminum sheets, using vanillin/H₂SO₄ as spray reagent.

1.2 NMR acquisition parameters

For compound **1**: The pulse conditions were as follows: spectrometer frequency (SF) 399.83 MHz (¹H) and 100.55 MHz (¹³C), acquisition time(AQ) 0.624 s, relaxation delay (RD) 2.0 s, spectral width 3205.1 (¹H) and 20105.6 (¹³C), a one-

bond coupling constant of 145.0 Hz, ns = 4. For compound **2**: (SF) 400.13 MHz (¹H) and 100.61 MHz (¹³C), acquisition time(AQ) 0.319 s, relaxation delay (RD) 1.5 s, spectral width 3205.1 (¹H) and 16103.1 (¹³C), a one-bond coupling constant of 145.0 Hz, ns = 2.

1.3 Plant material

Aerial parts of *Pentzia monodiana* were collected in National Park Hoggar (Algeria), in April 2011. A voucher specimen (voucher N° PM-tmp-002415) was deposited in the herbarium of the department of Pharmacognosy, University Paris Descartes, France.

1.4 Seco-tanapartholide extraction and isolation

A sample of 557 g of aerial part of *P. monodiana* were mixed with sand (500 g). Extraction cells were filled with the mixture and charged in the apparatus. Extraction program consisted in two distinct cycles of 20 min with ethyl acetate. Each cycle comprised a pre-heat period of 5 min, pumping of ethyl acetate through the extraction cell unit with a final pressure of 100 bar, a hold-on time fixed at 5 min and a final flush of acetate extract into the corresponding vial. The extracts were concentrated under reduced pressure affording 42.72 g of ethyl acetate extract. A sample of 10 g of ethyl acetate extract was applied to a silica gel column with a gradient of cyclohexane/EtOAc (100:0, 80:20, 70:30, 60:40, 50:50, 40:60, 30:70, 20:80 and 10:90, v/v) to give 32 fractions. The fractions 17 to 22 (F17-22) were pooled on the basis of TLC profiles to perform a CPC procedure. The chosen tertiary and quaternary solvent systems containing cyclohexane/EtOAc/MeOH/H₂O (1/4/1/4, S1 v/v) and EtOAc/THF/H₂O (4/2/5, S2 v/v) were prepared by mixing the solvent. The resulting phases were separated just before use. The upper phases were used as the mobile phases, whereas the lower phases were employed as the stationary phases. A sample of 400 mg of F17-22 was dissolved in a 1:1 (v/v) mixture of the biphasic system of S1. The separation was performed in ascending mode on 250 mL rotor, flow rate of 5 mL min⁻¹ at 1600 rpm. A total volume of 1.5 L of mobile phase was collected in fractions of 10 mL. Then the extrusion step was initiated in ascending mode using the lower phase as the mobile phase to ensure that any residual extract was recovered. Compound **1** was isolated from fractions 16 to 20 (23 mg).

1.5 Magnetic properties calculations

All density functional theory (DFT) have been performed using the Gaussian 09W package [17] and the B3LYP functional at the 6-311+g(d,p) levels of theory. Structure optimisation was followed with frequency calculation in order to check the absence of imaginary modes. Calculations of the magnetic properties (coordinates, *g*-tensor, hyperfine coupling tensors, chemical shielding tensors, scalar couplings) have been performed on the optimized conformer. The resulting set of tensor values were converted to chemical shifts by subtracting the shielding tensor value of tetramethylsilane (TMS) at the same level of theory. HOSE chemical shifts prediction was

realised thanks to nmrshiftdb2[20, 21] using the DFT optimised tridimensional structure as input (.mol). NMR spectra were plotted using the Spinach 1.6 toolbox [14] running in the Matlab[®] environment.

2. Results and Discussion

In order to demonstrate the efficiency of the proposed methodology on a natural product, the whole work-flow was first applied to one of the most ubiquitous compound in plants: caffeic acid (**1**) and then to *seco*-tanapartholide A (**2**). While commercial caffeic acid (**1**) was used, the phytochemical investigation of the aerial parts of *P. monodiana* was undertaken to obtain compound **2**. After extraction of the plant material with ethyl acetate under pressure (100 bar), a first fractionation on silica gel was performed, this step was then followed by a CPC separation that yielded *seco*-tanapartholide A (**1**). After acquisition of ¹H-¹³C HSQC spectrum of **1**, the prediction of the different magnetic parameters was performed using both GIAO DFT (coordinates, *g*-tensor, hyperfine coupling tensors, chemical shielding tensors and scalar couplings) and the HOSE prediction (chemical shifts). In table 1 are summarized the experimental and predicted chemical shifts and couplings for compound **1** and **2**.

Case study 1: caffeic acid (1) In order to evaluate how close the chemical shifts predictions were to the experimental data, the mean absolute error (MAE) and the corrected mean average error (CMAE) were calculated. As expressed in table 1, both ¹H and ¹³C MAE values for the HOSE prediction were smaller from those obtained using DFT (MAE_{1H} = 0.08 and CMAE_{13C} = 1.94). Those results were also confirmed by the CMAE values (0.016 and 0.21 for ¹H and ¹³C respectively). A simulation of the HSQC spectrum was then performed to compare the both DFT and HOSE-DFT combined spectra. The current version of the Spinach toolbox[14] is able to read Gaussian 09 outputs file (.out or .log) in order to get the parameters values needed for the NMR spectrum computation. At this step it was then possible to introduce the full chemical shift tensors (in ppm) predicted using the HOSE prediction and imported as a .txt file. The overall work-flow is described below (Figure 1).

The HSQC simulations are presented in the figure 2. Cross-peaks between ¹H and ¹³C for the HOSE values are not represented on figure 2 as no peak intensity and resolution were generated from this method. As expected from the values presented in table 1, a relatively good agreement was obtained between experimental HSQC spectrum and both simulated spectra. Only two protons were clearly separated from the experimental for the DFT prediction (H-2 and H-9 at δ_H 5.8 and 6.4 ppm instead of 6.22 and 6.78 ppm). On the other hand, only two signals corresponding to one proton (H-9 at δ_H 6.67 ppm) were clear separated from the experimental spectrum. This example clearly demonstrated the assets of the method. In order to test the validity of the method on another natural product, calculations were undertaken for a

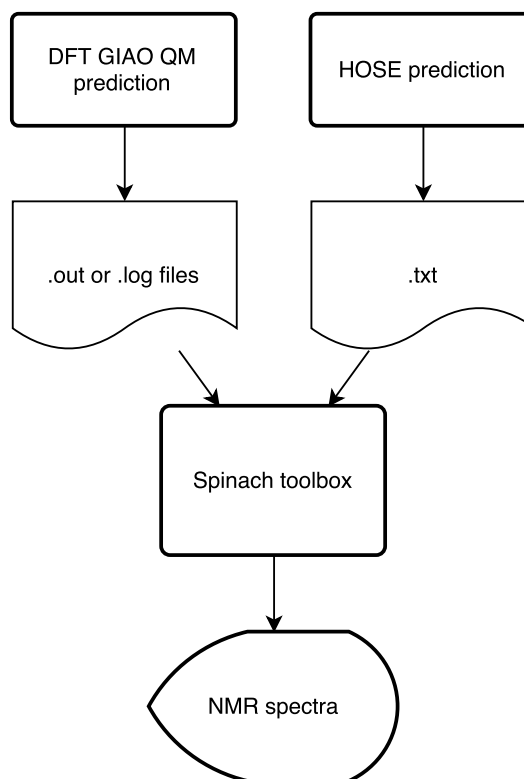


Figure 1. Global work-flow used for the NMR spectra prediction.

sesquiterpene lactone isolated from the aerial parts of *Pentzia monodiana*.

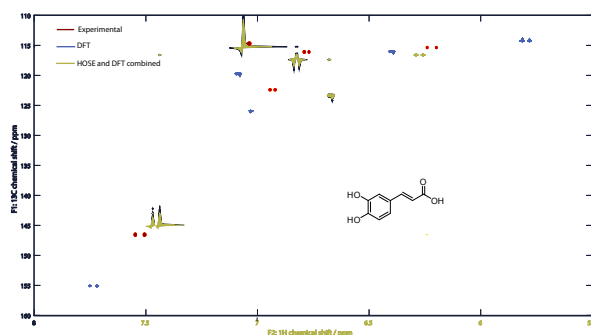


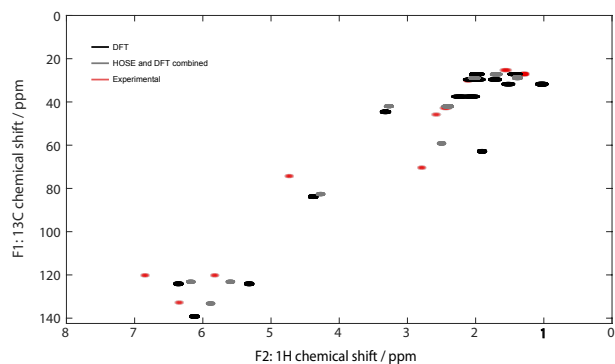
Figure 2. Overlapping of the experimental and predicted HSQC spectra of compound **1** (full scale available in SI).

Case study 2: *seco*-tanapartholide A (2) In the present example, DFT predictions for ¹³C shielding tensors were more accurate than the ones obtained using the HOSE algorithm, as MAE values were smaller, 2.91 and 4.11 ppm for DFT and HOSE respectively. Nonetheless, it is well known that quantum mechanical methods (QM) give quite frequently larger MAE's [22]. This last assumption was confirmed by looking at the ¹H shielding tensors predictions. Indeed, MAE's values were greater for the DFT (0.36) than for HOSE (0.26). To

Table 1. ^1H and ^{13}C NMR data for compound **1** and **2**

Experimental			Predicted				Experimental			Predicted			
position	^1H	^{13}C	DFT		HOSE		position	^1H	^{13}C	DFT		HOSE	
			^1H	^{13}C	^1H	^{13}C				^1H	^{13}C		
1	-	127.9	-	133.9	-	128.0	1	-	207.9	-	209.7	-	209.4
2	7.02	114.7	7.1	116.2	6.27	115.2	2	6.07	133.0	6.33	138.6	6.11	132.5
3	-	146.8	-	150.0	7.45	145.9	3	7.48	168.9	6.76	174.3	7.21	156.2
4	-	147.2	-	151.4	-	146.5	4	-	79.5	-	83.70	-	66.9
5	6.94	122.4	7.1	126.1	7.06	117.2	5	2.69	59.1	2.78	62.53	1.91	70.2
6	6.78	116.1	6.4	119.9	-	123.2	6	4.46	82.5	4.72	83.42	4.38	74.1
1'	7.53	146.5	7.8	155.2	-	144.9	7	3.46	41.9	2.57	44.31	3.32	45.7
2'	6.22	115.4	5.8	114.6	6.82	116.5	8	1.89	28.9	1.55	29.43	1.98	25.2
3'	-	171.2	-	166.6	6.67	171.5	9	2.60	42.0	2.43	37.29	2.25	42.7
		MAE	0.23	4.05	0.08	1.94	10	-	210.7	-	212.9	-	207.7
		CMAE	0.047	0.45	0.016	0.21	11	-	140.9	-	148.6	-	138.2
							12	-	168.9	-	172.9	-	170
							13a	6.36	123.0	5.81	123.6	6.35	119.9
							13b	5.78	-	6.83	-	5.31	-
							14	2.21	28.8	2.1	31.6	1.91	27
							15	1.58	27.2	1.28	27.0	1.19	28.9
								MAE	0.43	3.1	0.26	4.56	
								CMAE	0.03	0.19	0.02	0.29	

illustrate the values presented in table 1, the prediction of the HSQC spectra of compound **2** was conducted and was presented below. As illustrated on figure 3, an overall good agreement was observed between the predicted and the experimental spectra with a higher degree of similarity for the QM predicted spectrum as expected after calculation of the accuracy (see Table 1). However, a disparity was observed between the predicted and the experimental spectra for the equivalent protons (methyls or linear methylenes). For instance, the three H-14 protons (methyl) are represented as multiple signals at δ_H 2.08, 1.95 and 1.71 ppm while on the experimental, only one cross peak was observed at δ_H 2.10 ppm.


Figure 3. Overlapping of the experimental and predicted HSQC spectra of compound **2** (full scale available in SI).

To overcome this problem, the DFT GIAO full chemical shift tensors can be replaced by empirical calculated ones (obtained using the HOSE code) and then submitted to the Spinach toolbox. While the full chemical shift tensors (in ppm) were read from the Gaussian output files (.out or .log), Zeeman interactions may also be specified as scalars[14] and read from a .txt file using a short home made script. In the present case, hybridisation of both methods gave a slightly less accurate spectrum in terms of chemical shifts, especially

for the down-shielded signals at δ_H 6.11, 6.34 and 7.21 ppm. But one important improvement relied in the fact that the number of cross peaks observed on the HSQC spectrum fitted perfectly with the experimental spectrum (Figure 3). This last point was highlighted by Roussis' group in a recent paper in which they use HSQC spectra for dereplication purposes of the red alga *Laurencia*[10]. Using this method enabled the prediction of HSQC spectra but also any kind of 2D NMR spectra such as NOESY, HMQC or HMBC as it relies on the Spinach toolbox formalism[23]. Dereplication strategies using pattern recognition of NMR spectra have been thoroughly studied in the last decade[24, 25] and the proposed strategy is another tool available to the natural products chemists.

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References

- [1] Nadja Bross-Walch, Till Kühn, Detlef Moskau, and Oliver Zerbe. Strategies and tools for structure determination of natural products using modern methods of nmr spectroscopy. *Chemistry & Biodiversity*, 2(2):147–177, 2005.
- [2] Thomas Hoffmann, Daniel Krug, Stephan Hüttel, and Rolf Müller. Improving natural products identification through targeted lc-ms/ms in an untargeted secondary metabolomics workflow. *Analytical Chemistry*, 86(21):10780–10788, 2014.
- [3] Steffen Neumann and Sebastian Böcker. Computational mass spectrometry for metabolomics: Identification of metabolites and small molecules. *Analytical and Bioanalytical Chemistry*, 398(7-8):2779–2788, 2010.
- [4] Reza Salek, Christoph Steinbeck, Mark Viant, Royston Goodacre, and Warwick Dunn. The role of reporting

- standards for metabolite annotation and identification in metabolomic studies. *GigaScience*, 2(1):13, 2013.
- [5] John W. Blunt, Brent R. Copp, Robert A. Keyzers, Murray H. G. Munro, and Michele R. Prinsep. Marine natural products. *Nat. Prod. Rep.*, 31:160–258, 2014.
- [6] Lloyd W. Sumner, Zhentian Lei, Basil J. Nikolau, and Kazuki Saito. Modern plant metabolomics: advanced natural product gene discoveries, improved technologies, and future prospects. *Nat. Prod. Rep.*, pages 212–229, 2015.
- [7] Cristiano S. Funari, Philippe J. Eugster, Sophie Martel, Pierre-Alain Carrupt, Jean-Luc Wolfender, and Dulce Helena S. Silva. High resolution ultra high pressure liquid chromatography-time-of-flight mass spectrometry dereplication strategy for the metabolite profiling of brazilian lippia species. *Journal of Chromatography A*, 1259(0):167 – 178, 2012.
- [8] Kerstin Scheubert, Franziska Hufsky, and Sebastian Bocker. Computational mass spectrometry for small molecules. *Journal of Cheminformatics*, 5(1):12, 2013.
- [9] Jean-Luc Wolfender, Guillaume Marti, Aurélien Thomas, and Samuel Bertrand. Current approaches and challenges for the metabolite profiling of complex natural extracts. *Journal of Chromatography A*, 0(0):136 –164, 2014.
- [10] Katerina Kokkotou, Efstathia Ioannou, Marianna Nomikou, Florian Pitterl, Ariadni Vonaparti, Eleni Siapi, Maria Zervou, and Vassilios Roussis. An integrated approach using uhplc-pda-hrms and 2d hsqc nmr for the metabolic profiling of the red alga *Laurencia*: Dereplication and tracing of natural products. *Phytochemistry*, 0(0):–, 2014.
- [11] Density functional calculations of nmr chemical shifts and esr g -tensors. *Theoretical Chemistry Accounts*, 99(2):71–82, 1998.
- [12] W. Bremser. Hose — a novel substructure code. *Analytica Chimica Acta*, 103(4):355 – 365, 1978.
- [13] Patrick H. Willoughby, Matthew J. Jansma, and Thomas R. Hoye. A guide to small-molecule structure assignment through computation of (^1h and ^{13}c) nmr chemical shifts. *Nat. Protocols*, 9(3):643–660, 2014.
- [14] H.J. Hogben, M. Krzystyniak, G.T.P. Charnock, P.J. Hore, and Ilya Kuprov. Spinach - a software library for simulation of spin dynamics in large spin systems. *Journal of Magnetic Resonance*, 208(2):179 – 194, 2011.
- [15] Yuri Binev and Joao Aires-de Sousa. Structure-based predictions of ^1h nmr chemical shifts using feed-forward neural networks. *Journal of Chemical Information and Computer Sciences*, 44(3):940–945, 2004.
- [16] Yuri Binev, Maria M. B. Marques, and Joao Aires-de Sousa. Prediction of ^1h nmr coupling constants with associative neural networks trained for chemical shifts. *Journal of Chemical Information and Modeling*, 47(6):2089–2097, 2007.
- [17] M. J. Frisch, G. W. Trucks, H. B. Schlegel, G. E. Scuseria, M. A. Robb, J. R. Cheeseman, G. Scalmani, V. Barone, B. Mennucci, G. A. Petersson, H. Nakatsuji, M. Caricato, X. Li, H. P. Hratchian, A. F. Izmaylov, J. Bloino, G. Zheng, J. L. Sonnenberg, M. Hada, M. Ehara, K. Toyota, R. Fukuda, J. Hasegawa, M. Ishida, T. Nakajima, Y. Honda, O. Kitao, H. Nakai, T. Vreven, J. A. Montgomery, Jr., J. E. Peralta, F. Ogliaro, M. Bearpark, J. J. Heyd, E. Brothers, K. N. Kudin, V. N. Staroverov, R. Kobayashi, J. Normand, K. Raghavachari, A. Rendell, J. C. Burant, S. S. Iyengar, J. Tomasi, M. Cossi, N. Rega, J. M. Millam, M. Klene, J. E. Knox, J. B. Cross, V. Bakken, C. Adamo, J. Jaramillo, R. Gomperts, R. E. Stratmann, O. Yazyev, A. J. Austin, R. Cammi, C. Pomelli, J. W. Ochterski, R. L. Martin, K. Morokuma, V. G. Zakrzewski, G. A. Voth, P. Salvador, J. J. Dannenberg, S. Dapprich, A. D. Daniels, Ö. Farkas, J. B. Foresman, J. V. Ortiz, J. Cioslowski, and D. J. Fox. Gaussian 09 Revision D.01. Gaussian Inc. Wallingford CT 2009.
- [18] Stefan Kuhn, Nils Schlorer, Heinz Kolshorn, and Raphael Stoll. From chemical shift data through prediction to assignment and NMR LIMS - multiple functionalities of nmrshiftdb2. *Journal of Cheminformatics*, 4(Suppl 1):P52, 2012.
- [19] Paul Ozenda. *Flore et végétation du Sahara*. CNRS Editions, 2004.
- [20] Stefan Kuhn and Nils E. Schlörer. Facilitating quality control for spectra assignments of small organic molecules: nmrshiftdb2 – a free in-house nmr database with integrated lms for academic service laboratories. *Magnetic Resonance in Chemistry*, 53(8), 2015.
- [21] Christoph Steinbeck, Stefan Krause, and Stefan Kuhn. Nmrshiftdbconstructing a free chemical information system with open-source components. *Journal of Chemical Information and Computer Sciences*, 43(6):1733–1739, 2003.
- [22] Mikhail Elyashberg, Kirill Blinov, Yegor Smurnyy, Tatiana Churanova, and Antony Williams. Empirical and dft gao quantum-mechanical methods of ^{13}c chemical shifts prediction: competitors or collaborators? *Magnetic Resonance in Chemistry*, 48(3), 2010.
- [23] Luke J. Edwards, D.V. Savostyanov, Z.T. Welderufael, Donghan Lee, and Ilya Kuprov. Quantum mechanical nmr simulation algorithm for protein-size spin systems. *Journal of Magnetic Resonance*, 243:107 – 113, 2014.
- [24] Feng Qiu, James B. McAlpine, David C. Lankin, Ian Burton, Tobias Karakach, Shao-Nong Chen, and Guido F. Pauli. 2d nmr barcoding and differential analysis of complex mixtures for chemical identification: The ac-

taea triterpenes. *Analytical Chemistry*, 86(8):3964–3972, 2014.

- [25] Jane Hubert, Jean-Marc Nuzillard, Sylvain Purson, Mahmoud Hamzaoui, Nicolas Borie, Romain Reynaud, and Jean-Hugues Renault. Identification of natural metabolites in mixture: A pattern recognition strategy based on ^{13}C nmr. *Analytical Chemistry*, 86(6):2955–2962, 2014.