

Assessment of Two-Dimensional Separative Systems Using Nearest Neighbor Distances Approach. Part I: Orthogonality Aspects.

Witold Nowik,^{*,†,‡} Sylvie Héron,[†] Myriam Bonose,[†] Mateusz Nowik,[§] and Alain Tchapla[†]

[†] Univ. Paris-Sud, Groupe de Chimie Analytique de Paris-Sud EA 4041, LETIAM, IUT d'Orsay, Plateau de Moulon, 91400 Orsay, France.

[‡] Laboratoire de Recherche des Monuments Historiques, 29 rue de Paris, 77420 Champs-sur-Marne, France.

[§] AGH University of Science and Technology, Faculty of Electrical Engineering, Automatics, Computer Science and Biomedical Engineering, Department of Measurement and Electronics, Al. A. Mickiewicza 30, 30-059 Kraków, Poland.

* Corresponding author: Tel: +33(0)140205651. Fax: +33(0)147033246. E-mail: witold.nowik@culture.gouv.fr. Present address: Centre de Recherche et de Restauration des Musées de France (C2RMF), 14 quai François Mitterrand, 75001 Paris, France.

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Table S-1. Standards of anthraquinoids.

Abbr.	Name	Supplier
<i>I4Cl</i>	1,4-dichloroanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>I5Br</i>	1,5-dibromoanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>I5Cl</i>	1,5-dichloroanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>I8Cl</i>	1,8-dichloroanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Aba</i>	1-bromoanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Aca</i>	1-chloroanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Afv</i>	Anthraflavic acid	Maybridge (Trevillet, Great Britain)
<i>Agl</i>	Anthragallol	H. Schweppe (Frankenthal, Germany)
<i>Aha</i>	1-hydroxyanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Ale</i>	Aloe-emodin	Extrasynthese (Genay, France)
<i>Ali</i>	Alizarin	Acros Organics (Geel, Belgium)
<i>Ang</i>	Anthraquinone	Sigma Aldrich (Saint Louis, MO, USA)
<i>Arf</i>	Anthrarufin	Sigma Aldrich (Saint Louis, MO, USA)
<i>Bba</i>	2-bromoanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Bca</i>	2-chloroanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Bha</i>	2-hydroxyanthraquinone	TCI Europe (Zwijndrecht, Belgium)
<i>Bua</i>	2- <i>tert</i> -butylanthraquinone	Sigma Aldrich (Saint Louis, MO, USA)
<i>Can</i>	2-anthraquinonecarboxylic acid	Sigma Aldrich (Saint Louis, MO, USA)
<i>Chr</i>	Chrysophanol (Chrysophanic acid)	Extrasynthese (Genay, France)
<i>Dan</i>	Danthrone (Chrysazin)	Sigma Aldrich (Saint Louis, MO, USA)
<i>Dma</i>	1,4-dimethylantraquinone	Extrasynthese (Genay, France)
<i>Emo</i>	Emodine	Acros Organics (Geel, Belgium)
<i>Eta</i>	2-ethylanthraquinone	Sigma Aldrich (Saint Louis, MO, USA)
<i>Flk</i>	Flavokermesic acid (Laccaic acid D)	H. Schweppe (Frankenthal, Germany)
<i>FraA</i>	Frangulin A	H. Schweppe (Frankenthal, Germany)
<i>FraB</i>	Frangulin B	H. Schweppe (Frankenthal, Germany)
<i>Hma</i>	2-hydroxymethylantraquinone	Acros Organics (Geel, Belgium)
<i>Hys</i>	Hystazarin	H. Schweppe (Frankenthal, Germany)
<i>Ker</i>	Kermesic acid	H. Schweppe (Frankenthal, Germany)
<i>Moh</i>	Methoxyhystazarin	H. Schweppe (Frankenthal, Germany)
<i>Oma</i>	2,3-dimethylantraquinone	Extrasynthese (Genay, France)
<i>Phy</i>	Physcion (Parietin)	Extrasynthese (Genay, France)
<i>Pur</i>	Purpurin	Sigma Aldrich (Saint Louis, MO, USA)
<i>Qlz</i>	Quinalizarin	H. Schweppe (Frankenthal, Germany)
<i>Qza</i>	Quinizarin	Sigma Aldrich (Saint Louis, MO, USA)
<i>Rba</i>	Ruberythric acid	H. Schweppe (Frankenthal, Germany)
<i>Rgl</i>	Rufigallol	H. Schweppe (Frankenthal, Germany)
<i>Rhe</i>	Rhein	Extrasynthese (Genay, France)
<i>Tec</i>	Tectoquinone	Sigma Aldrich (Saint Louis, MO, USA)
<i>Xpu</i>	Xanthopurpurin	H. Schweppe (Frankenthal, Germany)

Table S-2. Stationary phases.

Stationary phase	Manufacturer	Column L x i.d. [mm]	Particle size [μm]	Bonding	Abbr.
<i>ChiraDex Gamma</i>	Merck	250 x 2.0	5	γ -cyclodextrin	<i>CDG</i>
<i>Cosmosil 5PYE</i>	Nacalai-Tesque	250 x 4.6	5	2-(1-pyrenyl)ethyl	<i>PYE</i>
<i>Discovery HS-PEG</i>	Supelco	250 x 4.6	5	Polyethyleneglycol	<i>PEG</i>
<i>Fluorosep-RP</i>	ES industries	250 x 4.6	5	Pentafluorophenyl	<i>FSP</i>
<i>Hypersil Gold</i>	Thermo Hypersil	150 x 2.1	5	C18 monolayer, endcapped	<i>Gold</i>
<i>Uptisphere NEC</i>	Interchim	150 x 2.0	5	C18 monolayer, non endcapped	<i>NEC</i>

Table S-3. Retention coefficients (χ).

Compound	Stationary phase					
	NEC	Gold	FSP	PYE	PEG	CDG
<i>14Cl</i>	0.727	0.735	0.911	0.877	0.788	0.139
<i>15Br</i>	0.817	0.813	0.988	0.971	0.940	0.122
<i>15Cl</i>	0.741	0.745	0.880	0.909	0.817	0.128
<i>18Cl</i>	0.752	0.720	0.923	0.851	0.799	0.107
<i>Aba</i>	0.716	0.713	0.800	0.744	0.780	0.139
<i>Aca</i>	0.675	0.673	0.726	0.708	0.703	0.133
<i>Afv</i>	0.168	0.181	0.323	0.109	0.717	0.154
<i>Agl</i>	0.247	0.280	0.381	0.270	0.623	0.181
<i>Aha</i>	0.674	0.667	0.692	0.700	0.656	0.156
<i>Ale</i>	0.398	0.402	0.512	0.641	0.486	0.124
<i>Ali</i>	0.373	0.386	0.503	0.385	0.609	0.165
<i>Anq</i>	0.590	0.579	0.765	0.497	0.584	0.102
<i>Arf</i>	0.765	0.757	0.855	0.943	0.740	0.167
<i>Bba</i>	0.848	0.838	0.966	0.884	0.853	0.183
<i>Bca</i>	0.792	0.801	0.929	0.850	0.781	0.169
<i>Bha</i>	0.360	0.383	0.516	0.291	0.676	0.122
<i>Bua</i>	1.000	1.000	1.000	0.708	1.000	0.172
<i>Can</i>	0.368	0.402	0.588	0.501	0.598	0.498
<i>Chr</i>	0.829	0.813	0.880	0.949	0.791	0.170
<i>Dan</i>	0.682	0.670	0.766	0.872	0.644	0.183
<i>Dma</i>	0.895	0.882	0.914	0.758	0.879	0.199
<i>Emo</i>	0.634	0.660	0.681	0.700	0.942	0.240
<i>Eta</i>	0.834	0.829	0.866	0.672	0.835	0.172
<i>Flk</i>	0.173	0.202	0.109	0.266	0.828	0.872
<i>Fra A</i>	0.412	0.477	0.500	0.701	0.572	0.201
<i>Fra B</i>	0.412	0.486	0.506	0.727	0.611	0.201
<i>Hma</i>	0.294	0.302	0.401	0.278	0.394	0.083
<i>Hys</i>	0.216	0.252	0.359	0.177	0.633	0.108
<i>Ker</i>	0.166	0.190	0.109	0.348	0.779	1.000
<i>Moh</i>	0.371	0.389	0.501	0.297	0.626	0.086
<i>Oma</i>	0.814	0.801	0.738	0.736	0.826	0.189
<i>Phy</i>	0.934	0.910	0.971	1.000	0.909	0.222
<i>Pur</i>	0.487	0.508	0.619	0.591	0.757	0.234
<i>Qlz</i>	0.482	0.495	0.500	0.772	0.705	0.236
<i>Qza</i>	0.753	0.741	0.833	0.929	0.724	0.194
<i>Rba</i>	0.013	0.078	0.075	0.121	0.000	0.000
<i>Rgl</i>	0.000	0.000	0.000	0.000	0.608	0.241
<i>Rhe</i>	0.430	0.458	0.632	0.914	0.639	0.567
<i>Tec</i>	0.716	0.707	0.776	0.615	0.718	0.154
<i>Xpu</i>	0.475	0.498	0.681	0.480	0.808	0.188

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“Orthogonality” MatLab script

```
% Clearing the workspace
clear all;
close all;
clc;

input_file_name = 'input.xls';
output_file_name = 'out.xls';

% Loading data from file 'input_file_name'
% Data format:
% - Row 1 contains names of systems
% - Column A contains names of chemicals
% - Columns B..n contain series of measured retention times of each chemical
%   for each system.
[Data, Labels] = xlsread (input_file_name);

NumericData = Data;

rows = size(NumericData,1);
cols = size(NumericData,2);

% % Normalization between the smallest and greatest values for each serie
% % - Subtract the smallest element of given column from all elemets in this
column:
NumericData = NumericData - (min(NumericData)' * ones(1,rows))';
% % - Divide each column element by maximum element in this collumn
NumericData = NumericData .* ((1./max(NumericData))' * ones(1,rows))';

dist_table = [];
idx = 0;
for A=1:(cols-1)
    for B = (A+1):cols

        idx = idx + 1;

        disp(sprintf('Mixing columns: ''%d'' and ''%d''',A, B));

        % Extracting 2 collumns
        data = [NumericData(:,A) , NumericData(:,B)];

        % Getting distances
        distances = linkage(pdist(data));
        distances = distances(:,3); % Taking only interesting data
        % Number of all distances
        N_d = size(distances,1);

        % Finding nonzero distances
        distances_nonzero = distances(logical(distances));
        %Number of nonzero distances
        N_nzd = size(distances_nonzero,1);
```

```

    % Arithmetic mean
    ArithmeticAverage = sum(distances_nonzero) / N_nzd;

    % Harmonic mean
    HarmonicAverage = N_nzd / sum(1./distances_nonzero);

    % Printing results
    fh = figure;
    plot(data(:,1), data(:,2), 'ro');
    title(sprintf('2D surface based on: '%s' and '%s' series.', ...
        Labels{1,A+1}, Labels{1,B+1}));
    xlabel(Labels{1,A+1});
    ylabel(Labels{1,B+1});
    print(fh, '-djpeg', sprintf('%d-%d.jpg',A,B));

    % Save distances
    dist_table = [ dist_table, distances];
    outcome{idx,1} = sprintf('%s-%s', Labels{1,A+1}, Labels{1,B+1});
    outcome{idx,2} = N_d;
    outcome{idx,3} = N_nzd;
    outcome{idx,4} = ArithmeticAverage;
    outcome{idx,5} = HarmonicAverage;
end
end

% Distances table
dist_table = [1:N_d]', dist_table];
dist_table_header = [{'di'}, {outcome{:,1}}];

% Sort values (by nonzero distances, then by Harmonic average)
outcome = sortrows(outcome,[-3 -5]);
% Insert header
outcome = [{'System', 'Total number of di', 'Number of nonzero di', ...
    'Arithmetic average', 'Harmonic average'};
    outcome];

% Print data to xls file
xls_row = 1;
xlswrite(output_file_name, dist_table_header, sprintf('A%d:%c%d', ...
    xls_row, 'A'+ idx, xls_row));
xls_row = xls_row + 1;
xlswrite(output_file_name, dist_table, sprintf('A%d:%c%d', ...
    xls_row, 'A'+ idx, xls_row + N_d -1 ));
xls_row = xls_row + N_d + 1 ;
xlswrite(output_file_name, outcome, sprintf('A%d:%c%d', ...
    xls_row, 'A'+ size(outcome,2) -1 , xls_row + idx));

disp 'Done!';

```