Comparative Analysis of Peak Detection Methods for Comprehensive Two-Dimensional Chromatography

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Objective: Evaluate the performance two-dimensional peak detection algorithms

- Peak detection aggregates data points of analyte peaks based on retention times and intensities.
- Two most common two-dimensional (2D) peak detection algorithms: Two-Step algorithm and Watershed algorithm.
- Vivó-Truyols and Janssen [J. Chromatography A, 1217:1375-1385, 2010] showed that undesirable shifting of second-column retention times can degrade the performance of 2D peak detection algorithms. They accounted for shift in the Two-Step algorithm but not with the Watershed algorithm.
 This research conducted experiments to compare performance of these 2D peak detection algorithms with shift correction for both algorithms.

Results: Watershed algorithm outperforms Two-Step algorithm for 2D peak detection

- Watershed algorithm is consistently more accurate for 2D peak detection with various levels of noise, peak widths, and retention-time shifts.

2D Peak Detection Algorithms

Two-Step algorithm: One-dimensional (1D) peak detection on each secondary chromatogram followed by merging detected 1D peaks.
 Watershed algorithm: Peak detection on 2D neighborhoods in both retention-time dimensions simultaneously.

Two-Step Algorithm

Watershed Algorithm

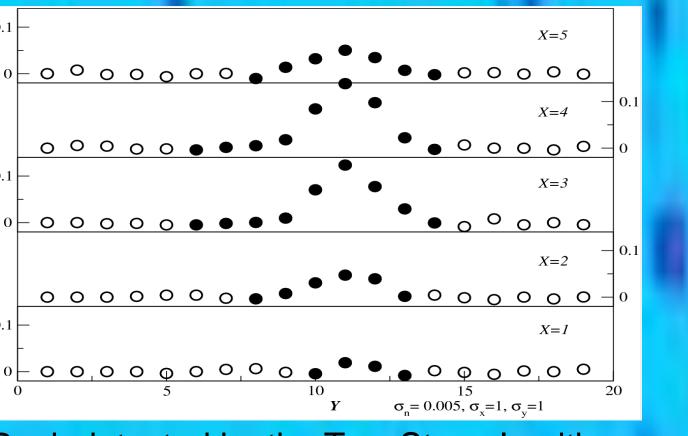
- 1. Perform 1D peak detection on each secondary chromatogram.
- 2. Merge detected 1D peaks subject to overlap and unimodality constraints.

 Overlap constraint parameterizes allowable shifts of the secondcolumn retention times for merging1D peaks.

– Unimodality constraint ensures that each 2D peak has a single apex.

1^{st} Points		4	2^{nd} Points			3^{rd} Points				4^{th} Points				5^{th}]	Poin	nts	Re	esult	t	
-37	74	6		-37	74	6	-37	74	6		-37	74	6		-37	74	6	-37	74	
145	200	136		145	200	136	145	200	136		145	200	136		145	200	136	145	200	13
243	213	264		243	213	264	243	213	264		243	213	264		243	213	264	243	213	26
332	236	(290)		332	236	290	332	236	290		332	236	290		332	236	290	332	236	29
324	451	277		324	451	277	324	451	277		324	451	277		324	451	277	 324	451	27
264	450	329		264	450	329	264	450	329		264	450	329		264	450	329	264	450	32
162	168	161		162	168	161	162	168	161		162	168	161		162	168	161	162	168	16
31	103	81		31	103	81	31	103	81		31	103	81		31	103	81	31	103	8
(62)	38	68		62	38	68	62	38	68		62	38	68		62	38	68	62	38	6

Progressive operations of the Two-Step algorithm: Each column of data is a secondary chromatogram. Points included in the main peak are shown in dark gray and other points are shown in light gray.



Peak detected by the Two-Step algorithm shown with filled circles.

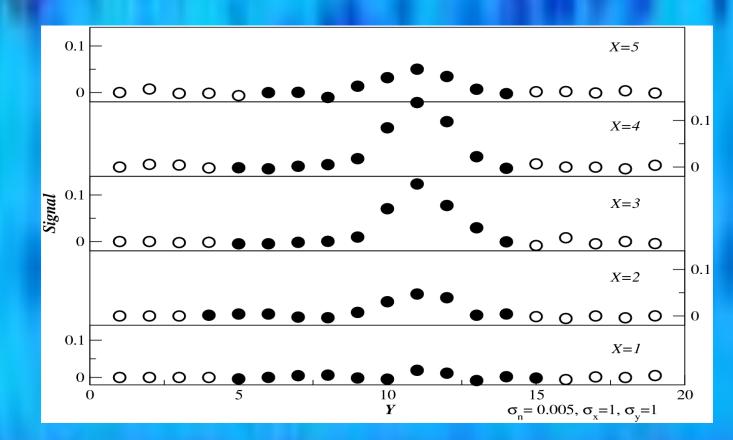
Traditional Watershed algorithm is inverted to find peaks rather than basins; Drain algorithm [Reichenbach *et al.*, *Chemo. Intell. Lab. Sys.*,**71**:107-120, 2004].

- 1. Data points that have the largest value in their neighborhood indicate a new peak.
- 2. Other data points belong to the same peak as the largest of their neighbors.

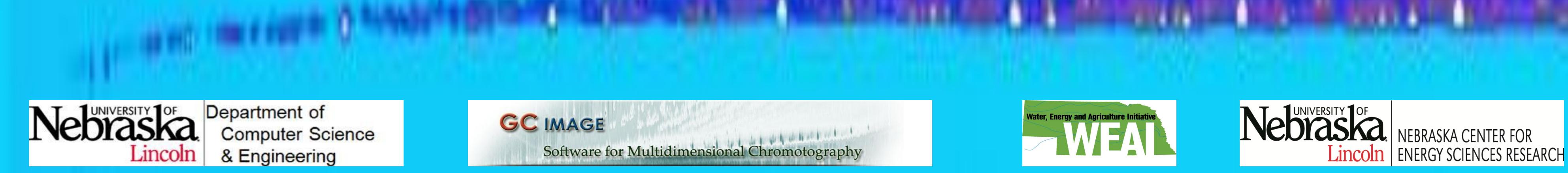
Retention-time shifts can be corrected for by shifting the data before peak detection or by adjusting the neighborhood.

1^{st} Point			2^{nd} Point			3^{rd} Point				6^{th} Point				9^{th}	Poir	ıt	Result			
-37	74	6	-37	74	6	 -37	74	6		-37	74	6		-37	74	6		-37	74	6
145	200	136	145	200	136	145	200	136		145	200	136		145	200	136		145	200	136
243	213	264	243	213	264	243	213	264		243	213	264		243	213	264		243	213	264
332	236	290	332	236	290	332	236	290		332	236	290		332	236	290		332	236	290
324	451	277	324	451	277	324	451	277	•••	324	451	277	•••	324	451	277		324	451	277
264	450	329	264	450	329	264	450	329		264	450	329		264	450	329		264	450	329
162	168	161	162	168	161	162	168	161		162	168	161		162	168	161		162	168	161
31	103	81	31	103	81	31	103	81		31	103	81		31	103	81		31	103	81
62	38	68	62	38	68	62	38	68		62	38	68		62	38	68		62	38	68

Progressive operations of the Watershed algorithm: Data points are labeled in intensity order in the 2D chromatogram.



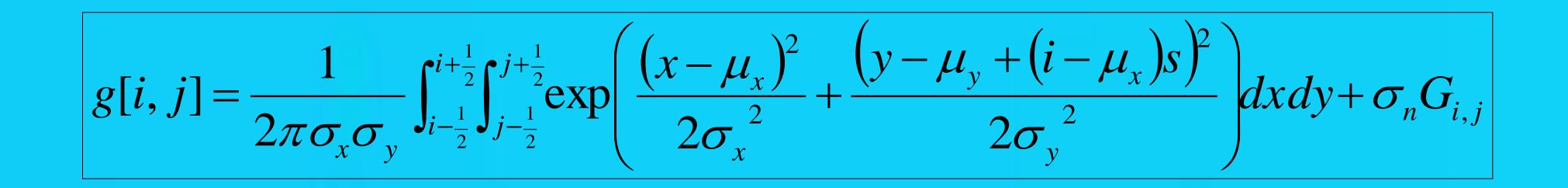
Peak detected by watershed algorithm shown with filled circles.



Simulation of Two-Dimensional Chromatograms to Compare Peak Detection Algorithms

Simulation allows controlled experimentation with varying levels of noise, peak widths, and retention-time shifts.

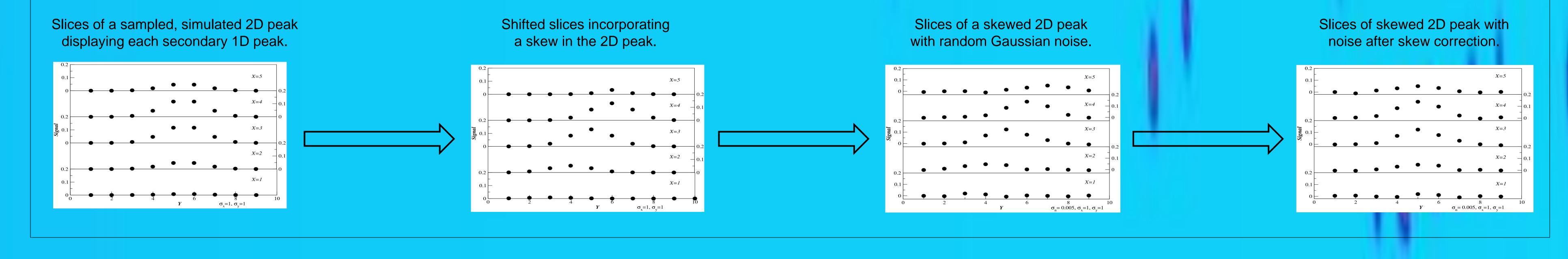
- Two-dimensional, standard Gaussian peak model, centered at (μ_x,μ_y), with unit-integral sampling, parameterized by:
 First-column peak width, σ_x.
 - Second-column peak width, σ_v .
- 2. Second-dimension retention-time shift, parameterized by:• Skew, s.
- 3. Zero-mean, Gaussian-distributed noise, *G*, parameterized by: • Standard deviation, σ_n .



Retention-Time Shift Correction

Retention-time shift correction is implemented for both algorithms as preprocessing for peak detection.

- 1. Estimate retention-time skew using cross correlation.
- 2. Shift simulated data to correct retention-time skew.

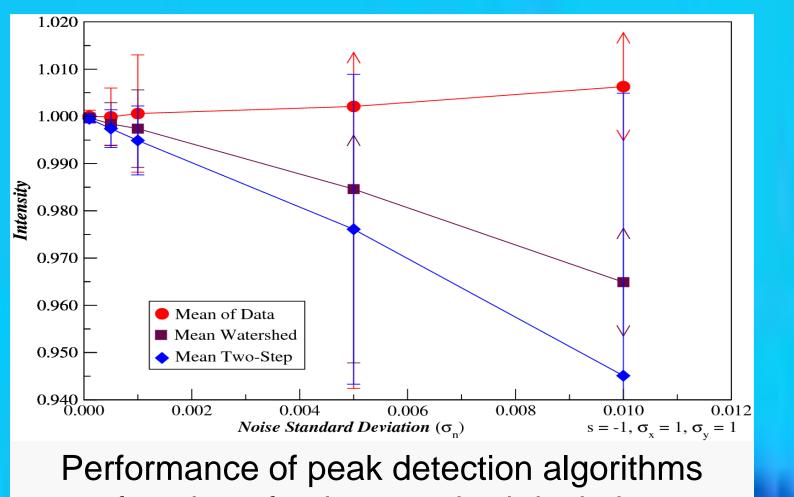


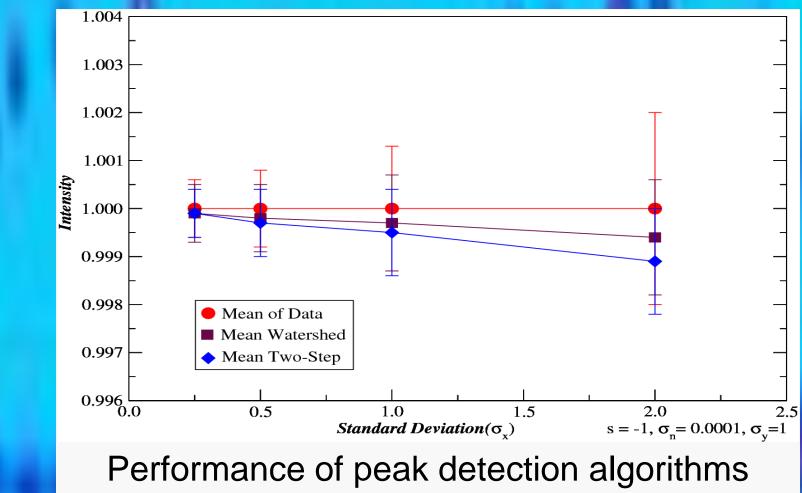
Experimental Results

- Four parameters are varied:
 - Noise standard deviation, σ_n , from 0.0001 to 0.01.
 - First-dimension peak-width standard deviation, σ_x , from 0.25 to 2.00.

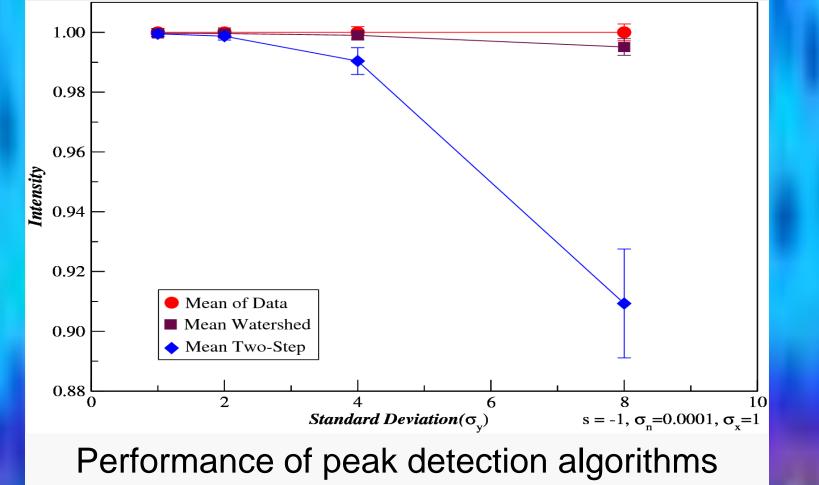
Skew	Peak	Peak	Noise	Array	\mathbf{Signal}	\mathbf{Signal}	\mathbf{WS}	\mathbf{WS}	\mathbf{WS}	\mathbf{WS}	2-Step	2-Step	$2\text{-}\mathrm{Step}$	$2\text{-}\mathrm{Step}$	Signif.
8	σ_x	σ_y	σ_n	\mathbf{Size}	Mean	\mathbf{Stdv}	Mean	\mathbf{Stdv}	Error	Failed	\mathbf{Mean}	\mathbf{Stdv}	Error	Failed	(1-p)
-1	1.00	1	0.0001	11×21	1.0000	0.0013	0.9997	0.0010	-0.0003	0	0.9995	0.0009	-0.0005	0	1.0000
-1	1.00	1	0.0005	11×21	0.9999	0.0061	0.9984	0.0045	-0.0015	0	0.9974	0.0040	-0.0024	0	1.0000
-1	1.00	1	0.0010	11×21	1.0006	0.0124	0.9974	0.0082	-0.0032	0	0.9949	0.0073	-0.0057	0	1.0000
-1	1.00	1	0.0050	$11{\times}21$	1.0021	0.0597	0.9846	0.0368	-0.0174	0	0.9761	0.0328	-0.0260	0	1.0000
-1	1.00	1	0.0100	11×21	1.0063	0.1227	0.9649	0.0706	-0.0415	0	0.9451	0.0598	-0.0612	0	1.0000
-1	0.25	1	0.0001	5×15	1.0000	0.0006	0.9999	0.0006	-0.0001	0	0.9999	0.0005	-0.0001	0	0.0000
-1	0.50	1	0.0001	7×17	1.0000	0.0008	0.9998	0.0007	-0.0001	0	0.9997	0.0007	-0.0003	0	0.9986
-1	1.00	1	0.0001	11×21	1.0000	0.0013	0.9997	0.0010	-0.0003	0	0.9995	0.0009	-0.0005	0	1.0000
-1	2.00	1	0.0001	20×30	1.0000	0.0020	0.9994	0.0012	-0.0006	0	0.9989	0.0011	-0.0011	0	1.0000
-1	1.00	1	0.0001	11×21	1.0000	0.0013	0.9997	0.0010	-0.0003	0	0.9995	0.0009	-0.0005	0	1.0000
-1	1.00	2	0.0001	11×30	1.0000	0.0015	0.9996	0.0012	-0.0003	0	0.9987	0.0013	-0.0013	0	1.0000
-1	1.00	4	0.0001	11×48	1.0000	0.0019	0.9990	0.0015	-0.0010	0	0.9904	0.0045	-0.0096	0	1.0000
-1	1.00	8	0.0001	11×84	1.0000	0.0028	0.9951	0.0028	-0.0048	39	0.9093	0.0182	-0.0906	341	1.0000
-1	1.00	1	0.0100	11×21	1.0063	0.1227	0.9649	0.0706	-0.0415	0	0.9451	0.0598	-0.0612	0	1.0000
-2	1.00	1	0.0100	11×31	0.9991	0.1503	0.9611	0.0671	-0.0380	0	0.9409	0.0598	-0.0581	0	1.0000
-4	1.00	1	0.0100	11×51	0.9977	0.1904	0.9595	0.0676	-0.0382	0	0.9419	0.0616	-0.0558	0	1.0000
-8	1.00	1	0.0100	11×91	0.9990	0.2589	0.9631	0.0696	-0.0359	0	0.9470	0.0603	-0.0520	1	1.0000

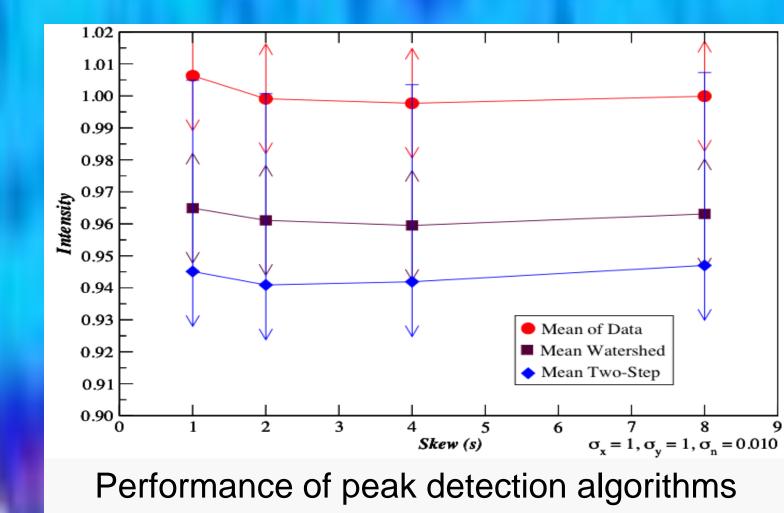
- Second-dimension peak-width standard deviation, σ_v , from 1 to 8.
- Skew, s, from -8 to -1.
- Each experiment is conducted 1000 times.
- Compare intensity mean and standard deviation of 2D peaks detected by the Two-Step and Watershed algorithms with the actual peak signal.
- The Watershed algorithm has better accuracy than the Two-Step algorithm when retention-time shift correction is used with both methods.
 Statistical significance indicates that the superiority of the Watershed algorithm is strongly supported and almost certainly would be observed in repeated experiments.





Results for 2D peak detection algorithms with various levels of noise (σ_n), peak widths (σ_x and σ_y), and retention-time skew (s). More comprehensive results are available by request.





as a function of noise standard deviation, σ_n .

as a function of first-column peak width, σ_x .

as a function of second-column peak width, σ_v .

as a function of skew, s.

