

# Supporting Information

## A Colorimetric Sensor Array for Detection and Identification of Sugars

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### Methods.

All reagents were obtained from Sigma-Aldrich and used without further purification unless otherwise specified.

**Buffer:** 3-nitrophenylboronic acid and Na<sub>2</sub>HPO<sub>4</sub> were dissolved in nano-pure water to afford a 5 mM 3-nitrophenylboronic acid / 1 mM phosphate buffer (pH 6.33). The buffer was adjusted to pH 7.4 with 0.5 M NaOH in the aforementioned solution. A FisherScientific, Accumet<sup>®</sup> AP61 pH meter with a FisherScientific, Accumet<sup>®</sup> AP50 electrode was used for all pH measurements.

**Analytes:** The sugars and artificial sugars analyzed were used as delivered from Sigma-Aldrich. Analyte solutions were prepared by dissolving 25 mM of each analyte in pH 7.4 3-nitrophenylboronic acid / phosphate buffer.

**Scanner:** Data acquisition was performed using an Epson Perfection V200 flatbed photo scanner.

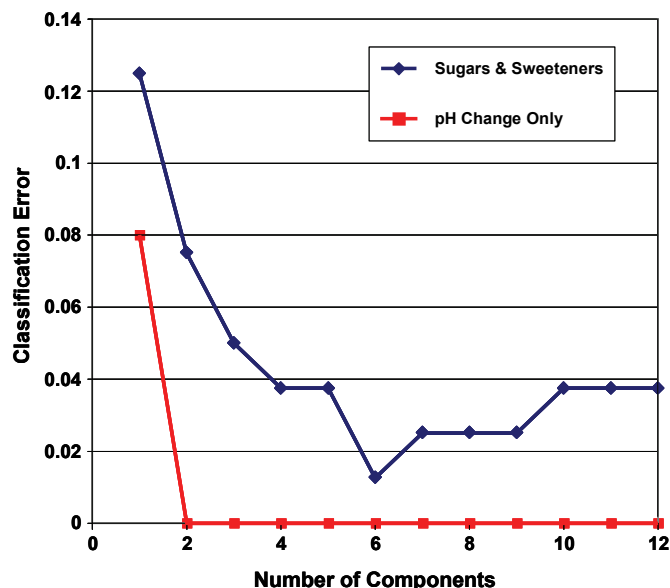
**Array Preparation:** Tetramethylorthosilicate (TMOS), Methyltrimethoxysilane (MTMS), methanol, and nano-pure water were combined in the molar ratio of 1:1:11:5. The mixture was stirred for 2 h at room temperature. The stirred formulation was added to the selected indicators (listed below in Table S1) and the solutions loaded into a block containing individual cylindrical wells (3/8" deep) for each pigment solution. A floating slotted pin printer capable of delivering approximately 100 nL was used to print the pigment-containing formulation onto the surface of a hydrophilic membrane (nitro-cellulose acetate, Millipore, Cat No. SSWP14250, 3.0 μm). Once printed, the arrays were placed in a nitrogen-flushed glove-bag for 24 hours and then cured in a 65°C oven for 24 hours. The arrays were once again placed in the glove-bag where there were stored until use (minimum of 12 hours).

**Experimental Procedure:** The prepared arrays were cut to size (approx. 1 in<sup>2</sup>) and submerged in a minimal amount of 5 mM 3-nitrophenylboronic acid / 1 mM phosphate buffer, adjusted to pH 7.4 (from this point forward referred to as "blank buffer solution"). The container holding the blank buffer solution and array was then placed in an ultrasonic cleaning bath for one min. to remove any excess indicators and to fully wet the array. The arrays were then placed into injection molded polycarbonate cartridges with two ports for injection/removal of aqueous solutions. Approximately 1.7 mL (cartridge volume) blank buffer solution was injected into the cartridge and the cartridge placed atop the flatbed scanner. A "before" image was obtained before the blank buffer solution was removed and replaced with analyte dissolved in the same solution. The array was scanned at 1 min. intervals for a total of 5 min. (equilibration usually occurred within 2 min.) and the 5 min. data acquisition denoted as the "after" image. The experiments were run in quintuplicate for each of fifteen analytes and a blank (control). RGB values were obtained in a difference map by subtracting the before image from the after image. To eliminate the possibility of subtraction artifacts caused by acquisitions near the spot edge, only the spot center is included in the calculation. Measurements can be performed using Photoshop<sup>™</sup> or with a customized software package, ChemEye<sup>™</sup> (ChemSensing, Inc., Champaign, IL 61821 <http://www.chemsensing.com>).

**D-Glucose Concentration Study:** Concentration-dependence studies were performed by exposing several arrays to blank buffer solution (described previously) followed by subjecting the arrays to various concentrations of D-glucose dissolved in the same blank buffer solution. Concentration profiles were constructed by plotting the total Euclidean distance of the array color change vs. D-glucose

concentration using 1 mM, 5 mM, 10 mM, 25 mM, 50 mM, 100 mM, and 200 mM concentrations of D-glucose dissolved in blank buffer.

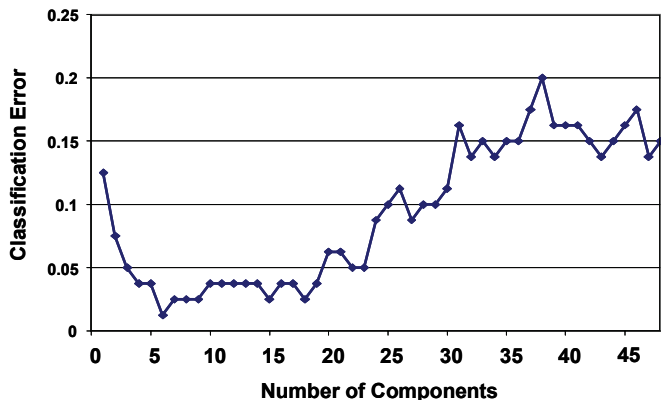
**D-Glucose Cycling Experiment:** An array was exposed to alternating solutions of blank buffer and 25 mM D-glucose dissolved in the same buffer. The experiments were carried out using a flow system (Masterflex<sup>®</sup> Console-Drive, Model No. 7520-60, peristaltic pump; set at 20 mL/min.). An array was prepared using the same procedure mentioned above. The cartridge was heat-sealed and a strip of silicone rubber was used to cover the inlet/outlet ports in order to construct a liquid-tight system. A three-way Teflon valve was added to the flow system to provide a quick and responsive method of switching among analytes. The array was exposed to the same pH 7.4 5 mM 3-nitrophenylboronic acid / 1 mM phosphate buffer system used throughout all the experiments for 10 min. to allow for equilibrium with data acquisition (scanning) performed every min. thereafter. The 0 min. time scan was used as the "before" image. Blank buffer was flowed through the array and scans taken every min. for 5 min. The analyte was switched to 0.05 M D-glucose and data acquired for 7 min., followed by 6 min. of blank buffer solution. This process was repeated for a total of three complete cycles with blank solutions at the beginning and end. The experiment was performed in triplicate.



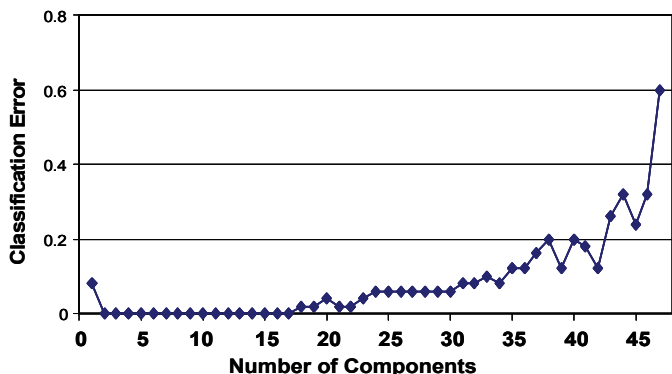
**Figure S1.** Classification error rate for Linear Discriminant Analysis (LDA) as a function of increasing numbers of components for both the control data in which only pH was changed compared to data for sugar and sweetener analytes. For each dimensionality, the LDA classification error was established using a leave-one-out cross validation.

**Responses to pH Changes Alone:** Solutions comprised of blank buffer solution adjusted to known pH values via addition of 0.5 M HCl or 0.5 M NaOH dissolved in the same blank buffer solution were produced. The arrays were exposed in a similar fashion as previously discussed to blank buffer solution to obtain a before image. The blank buffer solution was then withdrawn from the cartridge and replaced with the buffer solutions adjusted to the following pH

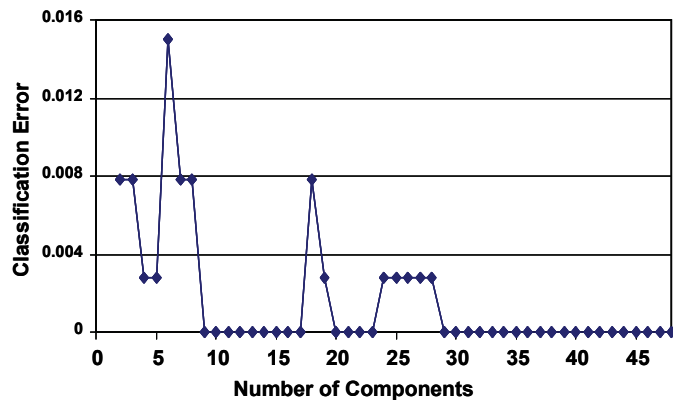
values: 2.0, 3.0, 4.0, 5.0, 6.0, 6.5, 7.0, 7.4, 8.0, and 8.5. Images were obtained at one min. intervals for a total of 5 min., with the last min. used in the production of difference maps. Tests of each pH solution were done in quintuplicate, and a principle component analysis was performed using the digital database. As shown in Figure S1 and S3, the pH change is 92% accurate with only one dimension and 100% accurate with only two dimensions. In contrast, six dimensions are required for optimal classification of the sugar and sweetener data, as discussed in the main text. Above 12 principle components, the inclusion of excess noise results of increasing errors in classification.



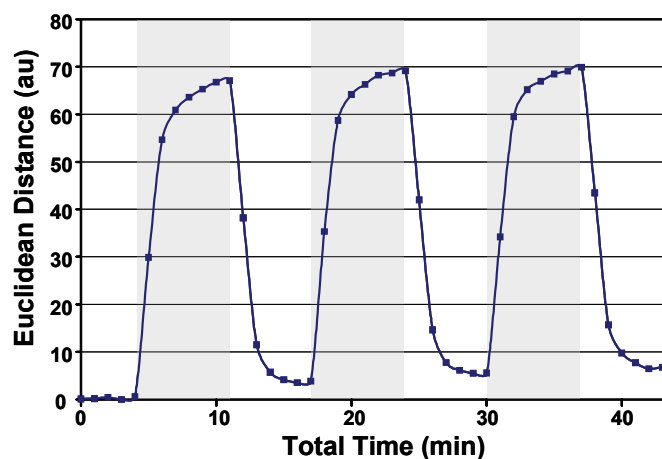
**Figure S2.** Classification error rate for Linear Discriminant Analysis (LDA) as a function of increasing numbers of components using 15 sugars and one control as the analytes. For each dimensionality, the LDA classification error was established using a leave-one-out cross validation. The error rate is a minimum with six dimensions.



**Figure S3.** Classification error rate for Linear Discriminant Analysis (LDA) as a function of increasing numbers of components. Data set includes blank buffer adjusted to varying pH values (measuring the array's response to changes in pH only). For each dimensionality, the LDA classification error was established using a leave-one-out cross validation. The error rate is zero with only two dimensions.

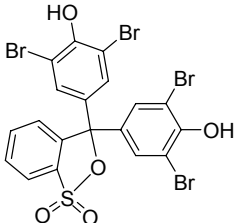
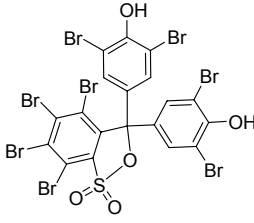
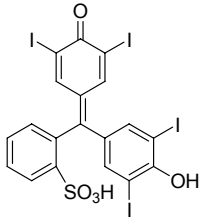
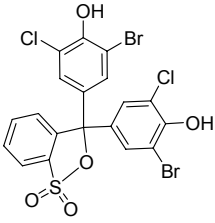
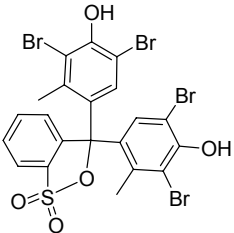
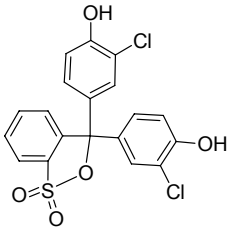
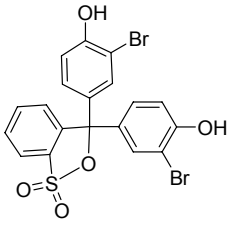
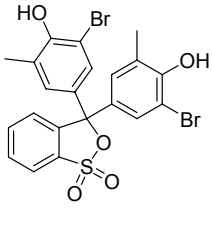
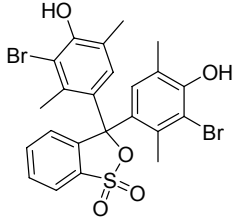
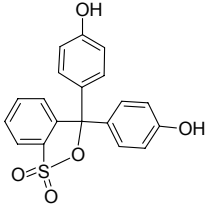
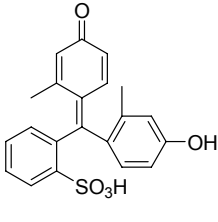
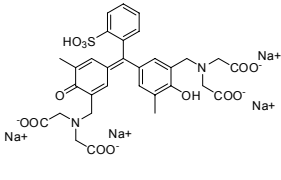
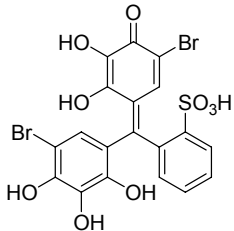
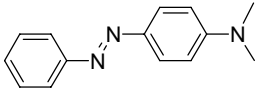
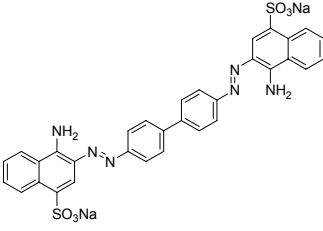
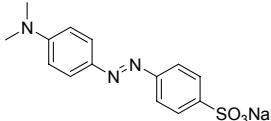


**Figure S4.** Classification error rate for Hierarchical Cluster Analysis as a function of increasing numbers of principal component dimensions. Nine dimensions are the minimum necessary for error-free clustering of 80 trials of 15 different sugars plus the control.



**Figure S5.** Repeated cycling of the array between 25 mM D-glucose exposure (gray) and buffer. The array was exposed to a flow of buffer solution (20 mL/min) and a “before” image obtained; the flow was then switched to the same buffer infused with glucose. Due to dead volume and mixing times in the flow apparatus, full equilibration required ~6 min; in the absence of such dead volumes, the intrinsic response time of the array is <30 sec.

**Table S1.** List of Indicators Used

<p><b>1. Bromophenol Blue</b></p> 	<p><b>2. Tetrabromophenol Blue</b></p> 	<p><b>3. 3',3'',5',5''-tetraiodo-phenolsulfonephthalein</b></p> 	<p><b>4. Bromochlorophenol Blue</b></p> 
<p><b>5. Bromocresol Green</b></p> 	<p><b>6. Chlorophenol Red</b></p> 	<p><b>7. Bromophenol Red</b></p> 	<p><b>8. Bromocresol Purple</b></p> 
<p><b>9. Bromoxylene Blue</b></p> 	<p><b>10. Phenol Red</b></p> 	<p><b>11. m-Cresol Purple</b></p> 	<p><b>12. Xylenol Orange tetrasodium salt</b></p> 
<p><b>13. Bromopyrogallol Red</b></p> 	<p><b>14. Methyl Yellow</b></p> 	<p><b>15. Congo Red</b></p> 	<p><b>16. Methyl Orange</b></p> 

**Table S2.** Structures of Natural and Artificial Sugars

Name	Structure
D-(-)-Fructose	
D-(+)-Galactose	
D-(+)-Glucose	
β-Lactose	
Maltitol	
D-Mannitol	
D-(+)-Mannose	
D-(+)-Melibiose	
L-Rhamnose	

Name	Structure
D-(-)-Ribose	
Saccharin	
Sorbitol	
Sucrose	
Xylitol	
D-(+)-Xylose	

