

# Linear Support Vector Machine Model of an IR Spectral Library: Application to Skin Cancer

Rebecca C. Bradley, Justin D. Erwin, Tatiana Oberyszyn, Kathleen L. Tober, Charles L. Hitchcock, Heather C. Allen, and James V. Coe\*



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**ABSTRACT:** The primary result of this work is the derivation and measurement of the average “Decision Contribution Spectrum” using a mouse tumor sample data set and the linear support vector machine (SVM) method from a perspective of spectroscopy. The “Decision Contribution Spectrum” gives the average contribution to the decision (tumor/nontumor in this case) at each step along the spectrum. A library of more than four thousand infrared (IR) spectra was obtained with a Fourier Transform Infrared (FTIR) microscope imaging system on a frozen section of an SKH1 mouse tumor - an accepted murine model for studying squamous cell carcinoma in that it very closely recapitulates the human disease. A linear SVM model was trained and tested avoiding overtraining and offering simple feature selection. It was used to see how much data can be removed without affecting the quality of decisions. Then, two further efforts are described to move IR spectroscopy toward future use in human skin cancer detection: (i) the design of a reduced range and reduced sampling for a fast and hand-held, mid-infrared spectral probe, and (ii) the use of a fiber-loop sensor probe (with FTIR in this preliminary study) on live SKH1 mice that had tumors to detect cancer externally and show no ill effects on the mice. The combination of the latter efforts supports the feasibility of using a fiber-loop sensor with a fast and hand-held mid-infrared spectral probe for the detection of skin cancer on humans. This work does not demonstrate a working human skin cancer probe, rather it provides evidence for judging whether work on live human skin is justified.



## 1. INTRODUCTION

Spectral libraries and machine learning methods<sup>1</sup> offer opportunities to extract spectral knowledge and classify unknown samples. This work features binary tumor/nontumor decisions from spectra. The most important scientific contribution of this work is the development of a linear support vector machine method from the perspective of spectroscopy, i.e., the linear support vector machine (SVM) equations from Cortes and Vapnik<sup>2</sup> have been rewritten in terms of scaled spectra and used to derive the “decision contribution spectrum” giving the average contribution to the decision at each wavenumber step in the spectrum, i.e., each spectral step. This work also describes how the output of only three spectra and a constant allows the use of the decision equation without the training data, which is a great benefit when training is time-consuming or compared to methods requiring on-site training. Machine learning techniques and support vector machine methods are gaining wide attention for vibrational spectroscopy in physical chemistry<sup>3–7</sup> and biomedical applications.<sup>8–12</sup> Here we show the utility of linear SVM<sup>13–17</sup> decision equations for spectroscopic feature analysis while also avoiding overtraining.

This work starts by deriving the “decision contribution spectrum” and making the first measurement of it in the context of mouse tumors. Then, the results are used to make

progress toward the ultimate goal of a probe for human skin cancer. This work does not demonstrate the ultimate goal, rather we take the current positive results as a necessary but insufficient condition. We are judging whether work on live human skin is justified. There were three parts to this study: (1) Fourier transform infrared (FTIR) microscope imaging was recorded on a frozen section of an SKH1 mouse tumor yielding a library of 4064 IR spectra (2553 tumor spectra and 1511 nontumor). The efficacy of the linear SVM model was determined by training on half the data and testing with the other half. The “decision contribution spectrum” was then extracted to get the average contribution to the tumor/nontumor decision at each spectral step. (2) Data was removed (reduced ranges and tolerable increases in spectral step) to explore how much spectral data can be removed without adversely affecting decisions. The ranges studied started with H-stretching region vs the fingerprint region and ended with popular quantum cascade laser (QCL) ranges. (3) Finally, IR

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spectra were recorded on live SKH1 mice that had tumors induced by UV irradiation using an FTIR fiber optic adapter and a fiber-loop sensor probe. The results were examined for the ability to distinguish tumors on live skin with reduced spectral range and reduced sampling within the range.

The motivating question for this work is: Can direct infrared (IR) absorption spectra, as obtained by touching live human skin with a probe, detect skin cancer on a time scale useful during a visit to the doctor's office? Mid-IR vibrational spectroscopy has long been known to be able to detect cancer<sup>8,11,18–29</sup> without the need for labels such as fluorophores, radiolabels, and monoclonal antibodies,<sup>10,30</sup> and work on diagnostic methods provides a growing foundation.<sup>10,23,31–38</sup> Fourier Transform Infrared (FTIR) spectroscopy,<sup>36</sup> a traditional IR method, has been previously utilized for the detection of skin cancer,<sup>37,38</sup> but current designs are too slow for fast and inexpensive diagnostic work in a doctor's office. However, tunable IR lasers are increasingly available such as the quantum cascade laser (QCL),<sup>21,39–43</sup> yet of greatly reduced range of tunability (compared to FTIR) while multiple QCL systems are too expensive. Future devices might employ a QCL for skin cancer<sup>41</sup> as has been explored for glucose detection.<sup>44–46</sup> The work presented here uses FTIR data to design operational features of a fast QCL mid-IR spectral probe. The work is directed toward the design only, and the working probe is left for a future paper.

## 2. SVM DECISION EQUATIONS WITH SPECTRAL LIBRARIES

The set of tissue spectra recorded for an experiment can be used as a library of predictors and the corresponding pathology assessments provide the response variables for training machine learning decision equations. The model used in this work is the supervised machine learning model called a Support Vector Machine (SVM) of Cortes and Vapnik,<sup>2</sup> which provides an optimal hypersurface for separating measurements of two classes (such as tumor and nontumor) by fitting the hypersurface to selected data called "support vectors" from the Predictor subset of spectra which lie between the two identified classes. Note that when using full IR spectra as the data set, support vectors have the form of full-range, digital IR spectra. A linear kernel function with spectral scaling minimizes overfitting and provides simplicity and feature selection, i.e., transfers best to future tests—at least for this skin cancer data set. The linear SVM decision equation value ( $d_k$ ) from the Cristianini and Shawe-Taylor text<sup>17</sup> can be re-expressed for a full IR test spectrum ( $\text{Test}_{k,j}$ ) as

$$d_k = b + \sum_i \alpha_i y_i \left\langle \frac{\text{SV}_{i,j} - \overline{\text{Train}}_j}{\sigma_{\text{Train}_j}} \middle| \frac{\text{Test}_{k,j} - \overline{\text{Train}}_j}{\sigma_{\text{Train}_j}} \right\rangle \quad (1)$$

where the index  $i$  is for support vectors,  $j$  for spectral steps (the dot product index), and  $k$  for the spectrum to be tested. Furthermore,  $b$  is the scalar bias constant,  $\alpha_i$  are the weights of the support vectors ( $\text{SV}_{i,j}$ ) chosen as spectra near the separating hypersurface, and  $y_i$  are the group membership [class 1 (tumor) and class 2 (nontumor) of the binary decision]. Since scaling is essential, the mean training spectrum ( $\overline{\text{Train}}_j$ ) is subtracted from spectra (both support vectors and the test spectra) with stepwise division of the result by the standard deviation of the training set ( $\sigma_{\text{Train}_j}$ ). The expression

within the dot product brackets is called the "kernel" which allows generalization to nonlinear models, but this work uses only the linear option. Mathematically,  $d_k$  is the perpendicular distance from the separating hyperplane to a test spectrum as a decision data point. To clarify,  $d_k$  has the form of distance, but there is a component for every step in the full IR spectrum, so it is a distance with 1626 components in this case, i.e., a hyper dimensional distance. Values of  $d_k > 0$  classify into one class (such as tumor), and  $d_k < 0$  classify into the other (such as nontumor). In order to use the decision equations in this form, the spectral data file of every support vector needs to be transmitted to the potential user and there can easily be hundreds or thousands of support vectors—each a full IR spectrum in this example.

Since many popular machine learning models produced overtrained spectral results on this data set (high training accuracy, low accuracy on new predictions or a failure to generalize), a linear SVM model<sup>13,17,47–49</sup> was chosen to represent these results (the "fitcsvm" function of the MATLAB programming environment from [MathWorks.com](https://www.mathworks.com)). A more useable SVM form for spectroscopists is attained by moving the support vector summation of eq 1 into the vector inner product bracket and commuting the row and column of the inner product. The decision equation is rewritten as

$$d_k = b + \left\langle \frac{\text{Test}_{k,j} - \overline{\text{Train}}_j}{\sigma_{\text{Train}_j}} \middle| \beta_j \right\rangle, \quad \text{where } \beta_j = \sum_i \alpha_i y_i \left( \frac{\text{SV}_{i,j} - \overline{\text{Train}}_j}{\sigma_{\text{Train}_j}} \right) \quad (2)$$

where  $\beta_j$  (the "fitcsvm.m" variable name) has the form of an IR spectrum when using the full set of spectral steps for training. The bracket at left indicates an inner dot product over spectral steps. The SVM program essentially determines optimized values for the bias offset  $b$  and  $\beta_j$ . In our opinion, the linear SVM result seems to be more closely related to a least-squares fit than popular machine learning models like deep neural networks. We call  $\beta_j$  the "SVM  $\beta$  spectrum". Once obtained, the decision equation itself can be extracted (by outputting three spectra and a constant, i.e.,  $\overline{\text{Train}}_j$ ,  $\sigma_{\text{Train}_j}$ ,  $\beta_j$ , and  $b$ ) and used independently of the programming environment to classify new spectra. Notice that the SVM  $\beta$  spectrum has contributions from all support vectors at each spectral step (see the right-side of eq 2), but such contributions have been separated-out of the left-side of eq 2. The multiplication of  $\beta_j$  by a scaled spectrum reveals the wavelengths that are most important in a specific decision regarding the chosen classes.

It is interesting to consider eq 2 in terms of the average class 1 ("T" for tumor) or class 2 ("NT" for nontumor) spectra, i.e.  $\overline{\text{T}}_j$  and  $\overline{\text{NT}}_j$ , respectively. The average decision equation value results can be written in terms of the individual spectral steps for tumor and nontumor as

$$\overline{\text{dNT}}_j = b + \sum_{j=1}^{j_{\max}} \left( \frac{\overline{\text{NT}}_j - \overline{\text{Train}}_j}{\sigma_{\text{Train}_j}} \right) \beta_j \quad \text{and } \overline{\text{dT}}_j = b + \sum_{j=1}^{j_{\max}} \left( \frac{\overline{\text{T}}_j - \overline{\text{Train}}_j}{\sigma_{\text{Train}_j}} \right) \beta_j \quad (3)$$

where  $j_{\max}$  is the number of spectral steps. Examination of the difference between  $\overline{dT}_j$  and  $\overline{dNT}_j$  at each spectral step gives the average “Decision Contribution Spectrum”

$$\overline{\Delta d}_j = \overline{dT}_j - \overline{dNT}_j = \left( \frac{\overline{T}_j - \overline{NT}_j - \overline{\text{Train}}_j}{\sigma_{\text{Train}}_j} \right) \beta_j \quad (4)$$

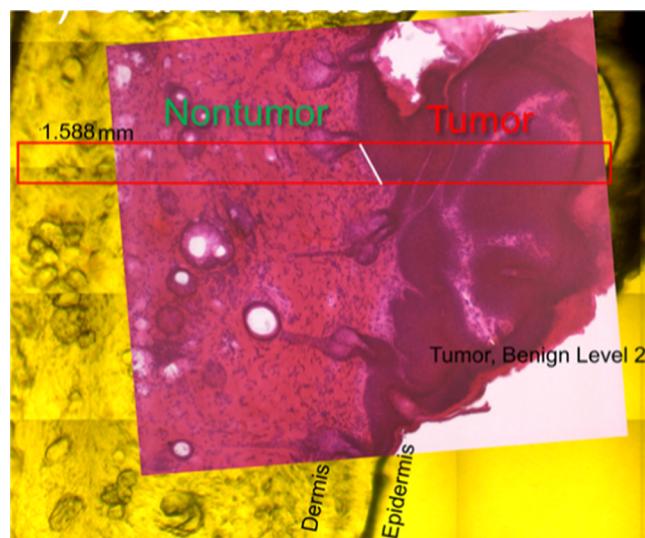
at each spectral step  $j$ . The quantity  $\overline{\Delta d}_j$  is determined by the average difference between tumor and nontumor spectra as scaled by the training set and multiplied by  $\beta_j$ , the “SVM beta” spectrum. Also note that each step of  $\beta_j$  corresponds to the summed contribution of all support vectors at that spectral step. An examination of  $\overline{\Delta d}_j$  across the spectrum identifies the importance of spectral steps (wavenumbers in this case) which is useful if one needs to reduce the number of wavelengths employed in measuring a spectrum. This can be used for feature selection in an average sense, i.e., the selection of the most important wavenumbers on average. Conversely, it indicates that measurements are not needed at all wavenumbers, so some measurements need not be made. It is useful to begin to learn about noise in the average “decision contribution spectrum”. How important are big changes in the IR spectral bands upon becoming cancerous vs contributions of the SVM beta spectrum itself? Which vibrational bands are most important to decisions? This formalism enables such questions to be investigated.

### 3. EXPERIMENTAL SECTION

Keratinocytic carcinoma (including basal cell and squamous cell carcinoma) is the most prevalent form of any cancer in humans.<sup>50</sup> The SKH1 mouse model of UV-induced cutaneous squamous cell carcinoma (SCC) is an accepted murine model for studying SCC development as it recapitulates the human disease,<sup>51–53</sup> so the detection of SKH1 mouse tumors serves as a good pretest for eventual use in humans for skin cancer. The animal protocol was designed to minimize pain or discomfort to the mice. All procedures were approved and performed in accordance with the University PHS Welfare Assurance number (A3261–01) and our Animal Care and Use Committee (IACUC protocol 2010A00000083, approved 2/4/16). An SKH-1 mouse developed tumors after exposure to UV, three-times daily, for 14 weeks. One tumor was obtained for a frozen section using FTIR microscope imaging and live mice with tumors were probed with a fiber-loop sensor and FTIR fiber optic adapter.

#### 3.1. FTIR Microscope Imaging of a Frozen Section.

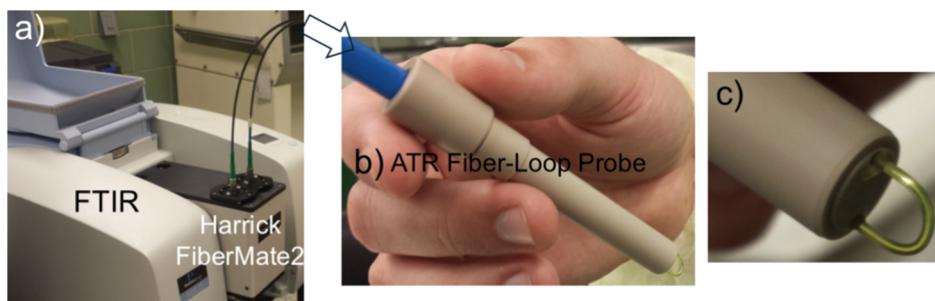
Full-range IR spectra were recorded on a frozen section of an SKH1 mouse tumor using hyperspectral microimaging with a PerkinElmer Spotlight 400 Fourier Transform Infrared (FTIR) instrument as shown in Figure 1. Details of acquiring a  $\sim 3 \mu\text{m}$  thick frozen section of an SKH1 mouse tumor are given in Supporting Information (see Figure S1). The red rectangle ( $1.588 \text{ mm} \times 0.100 \text{ mm}$  area) in Figure 1 of the frozen section was imaged with  $254 \times 16 = 4064$  square pixels each with  $6.25 \mu\text{m}$  square edges. An FTIR spectrum was recorded at each pixel ( $4000\text{--}750 \text{ cm}^{-1}$  spectral range,  $4 \text{ cm}^{-1}$  resolution,  $2 \text{ cm}^{-1}$  steps, 16 scans per pixel taking  $\sim 90 \text{ min}$ , with a liquid  $\text{N}_2$ -cooled MCT detector). Afterward, the exact same tissue in the same sample holder was stained with H&E<sup>54</sup> and imaged with a different optical microscope. The result has been overlaid in registry with the yellowish pre-IR imaging picture



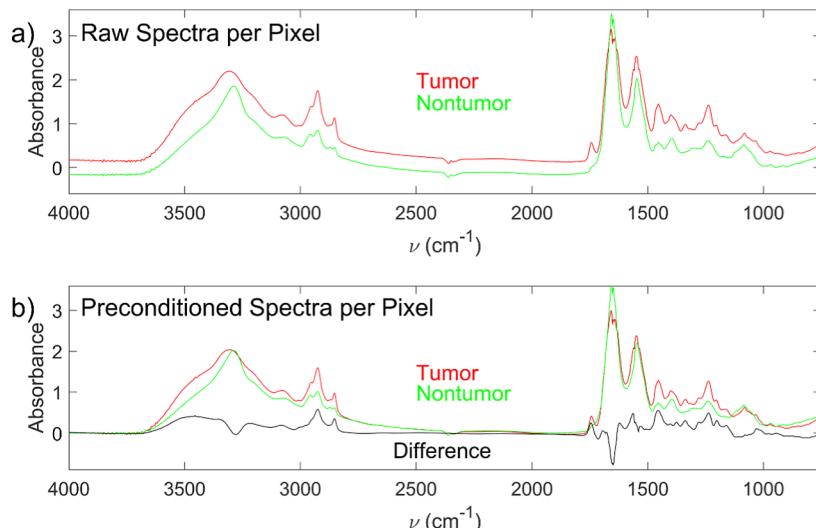
**Figure 1.** An unstained frozen section of  $\sim 3 \mu\text{m}$  of thickness was positioned on a ZnSe IR window (yellow underneath image) for examination under an IR microscope. The red rectangle indicates a region that was subjected to microscopic IR hyperspectral imaging. Afterward, an H&E stain (top reddish overlay) was obtained of the exact same tissue and imaged under an optical microscope. The two images were scaled, oriented, and overlaid in registry. Epidermis (skin exterior) is to the right, dermis (skin interior) is to the left. The tumor (right) stained dark red, while the nontumor (left) was much lighter. A white line shows the separation between tumor and nontumor to establish the response variables. Note that the dermis side of the dermis/epidermis interface was punctuated with hair follicles (vertically down the center).

by means of scaling and a slight counterclockwise rotation. Note that the H&E image had a ZnSe yellow color cast which was removed and then contrast-adjusted using Adobe Photoshop Elements 2.0 (“Enhance” tab, “Adjust Color” option, and “Color Cast”). The epidermis stained dark red with H&E, as did the tumor. Pixels to the right of the white line were indexed as tumor class, while pixels to the left were indexed as nontumor class for use as response variables for machine learning routines. The clear delineation between tumor and nontumor regions made for an ideal data set for fitting an SVM  $\beta$  spectrum, group decision equations, and feature selection.

**3.2. Live Mouse Spectra.** A fiber optic coupler (Harrick FiberMate 2) was placed in the sample region of a PerkinElmer Spectrum 100 FTIR (Figure 2a) and connected to an ATR fiber-loop probe sensor<sup>55,56</sup> (Art Photonics, Figure 2b). Mid-IR radiation flows through the fiber-loop sensor (zoom in Figure 2c) including a component that travels a few wavelengths outside of the loop as an evanescent wave before heading back to the spectrometer’s detector. After a background spectrum is recorded with the fiber-loop in air, then the fiber-loop is touched to skin (see Supporting Information and Figure S2) which absorbs IR from the evanescent wave due to the vibrational bands of tissue proteins, lipids, and other biomolecules yielding a sample spectrum. The negative log of the ratio of the spectrum signal (touching skin) to the background (air) gives an absorption spectrum of skin tissue. Fiber optics limited the useable range of the PerkinElmer Spectrum 100 FTIR to  $1800\text{--}700 \text{ cm}^{-1}$  (the FTIR instrument is typically  $4000\text{--}700 \text{ cm}^{-1}$ ) and spectra were recorded on and off tumors using 25 scan averages,  $1 \text{ cm}^{-1}$  steps,  $4 \text{ cm}^{-1}$



**Figure 2.** (a) Fiber optic coupler (Harrick FiberMate2) is placed in the sample compartment of a PerkinElmer Spectrum 100 FTIR. (b) An Art Photonics fiber-loop ATR probe sensor is coupled to the FTIR with mid-IR fiber optics. (c) Zoomed image of the fiber-loop sensor through which IR light travels from and back to the FTIR. The IR includes an evanescent component traveling a few wavelengths outside of the loop allowing spectra to be recorded of things that the probe touches.



**Figure 3.** (a) Raw average tumor (red) and nontumor (green) spectra of an SKH1 mouse frozen section. (b) Since the baselines were quite different, a baseline correction was applied before machine learning analysis. The tumor and nontumor difference (black trace) shows significant differences between the tumor and nontumor spectra.

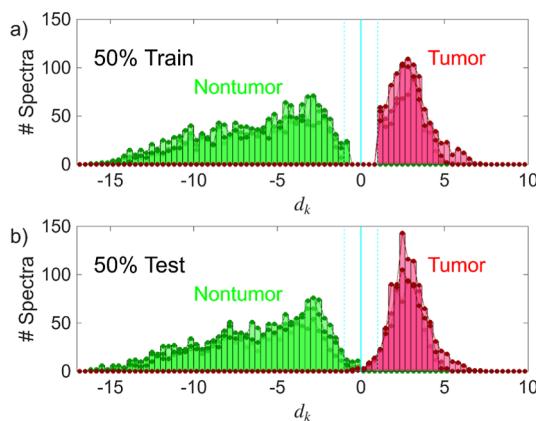
resolution, with a liquid N<sub>2</sub>-cooled MCT detector, requiring about 2.5 min each. The tumors had thick keratinized tops so that the probe could not push into the tumor as it could for normal skin, so these spectra had much less intensity because a smaller surface area of the fiber-loop probe touched sample. Note that tumors are often stiffer than normal tissue.<sup>57,58</sup> We obtained 16 nontumor and 12 tumor spectra for analysis.

## 4. RESULTS

**4.1. FTIR of SKH1 Tumor Frozen Section Results.** The tissue section had a clearly indicated transition from tumor to nontumor (white line in Figure 1) which was used to define the response variables. There were 2553 tumor spectra and 1511 nontumor spectra for a total of 4064 full-range spectra—each corresponding to a 6.25  $\mu\text{m} \times 6.25 \mu\text{m}$  pixel. Figure 3a shows the average raw IR spectra of the tumor (red) and nontumor (green) regions on a per pixel basis. The SKH1 mouse tumor shows an average increase in lipid CH<sub>2</sub> fat chains (2924  $\text{cm}^{-1}$  and 2852  $\text{cm}^{-1}$ , matching spectra of monoleate and lard) as has been seen in some other cancers.<sup>59,60</sup> It is interesting that the class baselines (probably due to scattering) were so different. Consequently, the spectra were preconditioned with a baseline correction as shown in Figure 3b. The absolute intensities are meaningful (as they are on a per pixel basis—unlike the live mouse spectra) and there are definitive

differences between the tumor and nontumor regions as highlighted by the black trace in Figure 3b which is the average difference spectrum. As a first test, the set of 4064 spectra were randomly divided into two groups with ~half for training and the remainder for testing. A linear SVM routine (MATLAB's "fitcsvm" function with scaling "Standardize" option) was trained on one-half and tested with the other. Histograms of the decision equation values [ $d_k$ , see eq 2] from three successive random partitions are overlaid for training in Figure 4a and for testing in Figure 4b. The nontumor results are plotted with green and the tumor results in red. Notice that there is no overlap between green and red for the trainings, so there are no errors in any of the trainings. Upon testing, notice a very small amount of overlap corresponding to small errors (0.34% in one run). A 10-fold cross validation was done using the 50% training results showing an error of  $0.35 \pm 0.41\%$ . The histograms provide visual evidence of an excellent model (of course it is only one tissue sample).

The average contribution to the tumor/nontumor decision at each spectral step  $j$ ,  $\overline{\Delta d}_j$ , is given in Figure 5 (blue trace) using the full spectral library of baseline corrected spectra. Extended sections labeled "Noise" with blue arrows have little difference in the tumor and nontumor spectra due to the lack of fundamental vibrations in these regions. They contribute



**Figure 4.** (a) The linear SVM decision equation value histograms of three random training runs (random  $\sim 50\%$  of the spectra) are overlaid with true tumor (red) and true nontumor (green). The cyan line is the decision equation dividing line and the dotted cyan lines correspond to  $\pm 1$  standard deviation of the scaled support vectors. There are no training errors as illustrated by no overlap of the green and red distributions. (b) The corresponding testing for each of three runs shows a small amount of overlap which averages to an error of 0.35%, i.e. accuracy is 99.65%.

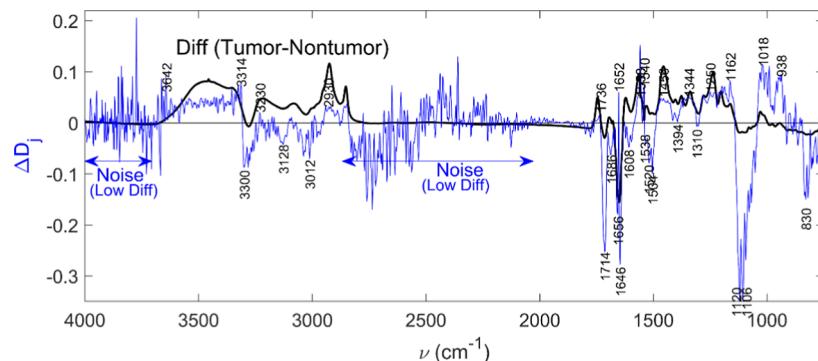
much noise to the tumor decision and might be profitably eliminated from the machine learning input. The important signals are in the H-stretch and fingerprint regions. Prominent peaks in the Decision Contribution Spectrum are labeled with vertical labels in  $\text{cm}^{-1}$  in Figure 5. In the fingerprint region, there are strong negative features at 1106, 1120, 1646, 1656, and  $1714\text{ cm}^{-1}$  and strong positive features at 938, 1018, 1162, 1344, 1456, 1540, and  $1736\text{ cm}^{-1}$ . In the H-stretch region, there are strong negative peaks at 3102, 3128, and  $3300\text{ cm}^{-1}$  and strong positive ones at 2930, 3314, and a broad positive range from 3314 to  $3642\text{ cm}^{-1}$ . These must be considered relative to the absorption bands in the FTIR spectra, but they often do not occur at the absorption band maxima. The largest integrated feature is the negative peak at  $1120\text{ cm}^{-1}$  extending from 1044 to  $1142\text{ cm}^{-1}$  which corresponds to a region with the  $\text{PO}_2$  symmetric stretch of many phosphorylated molecules ( $\sim 1083\text{ cm}^{-1}$ ) and C–O bands of carbohydrates like glycogen ( $1008\text{ cm}^{-1}$ ). The most intriguing feature is the sharp negative peak at  $1714\text{ cm}^{-1}$  extending from 1702 to  $1732\text{ cm}^{-1}$  which is in the region of ester-linked lipids ( $\sim 1741\text{ cm}^{-1}$ ). Finally, there

is much positive and negative structure in the amide I and II band regions suggesting protein band shape changes upon becoming cancerous. There does not seem to be one peak that dominates the decision; and all the bands in the H-stretch and fingerprint regions make contributions to the tumor decision, so in theory “the more, the better”. However, practical probe design considerations might favor one region over another. Which regions are best?

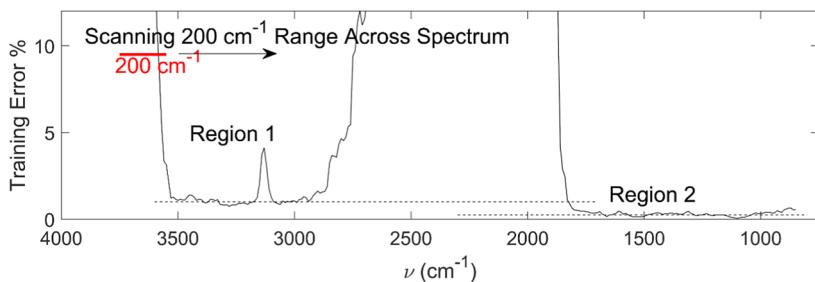
#### 4.2. Identifying Probe Ranges and Spectral Steps for Spectral Devices.

The regions  $3670\text{--}2790\text{ cm}^{-1}$  (Region 1) or  $1860\text{--}760\text{ cm}^{-1}$  (Region 2) of Figure 5 are good for decisions because they correspond to fundamental vibrational bands of biomolecules.<sup>10,61</sup> Region 1 is the H stretching region ( $\text{OH}$ ,  $\text{NH}$ , and  $\text{CH}$  stretches) with strong protein bands (amide A and B) and lipid bands ( $\text{C--H}$  stretches of  $\text{CH}_2$  chains and  $\text{CH}_3$ ), while Region 2 is sometimes called the “fingerprint” region which has lipid, amide I and II, phosphate, glycogen bands and many other biomolecules. If FTIR was too slow and complex (moving optical parts, liquid nitrogen detectors), then a QCL might be employed for a medical device with the disadvantage of a limited spectral range. So, which range is better for a limited range spectral device? Mittal and Bhargava<sup>62</sup> addressed this issue with breast tissues and found only small differences with “the fingerprint region-based classifiers consistently emerging as more accurate.” Region 2 seems to have strong and sharp changes in  $\overline{\Delta d}_j$  (see Figure 5) at the amide I and II bands and a big downward feature near phosphate and glycogen bands. Note that regions with some wavenumbers good for tumor decisions and others for nontumor are likely best for cancer decisions. The linear SVM calculations were repeated using only spectral data from each region, i.e. removing all data not in the specified range. Region 1 gave a training error of 0.27% (full data set was 0%) and had a 10-fold cross-validation error of  $0.54 \pm 0.34\%$ . Region 2 gave a training error of 0% (same as full range set) and a 10-fold cross-validation error of  $0.10 \pm 0.17\%$ . Again, like Mittal and Bhargava,<sup>62</sup> the fingerprint region is found to be more accurate.

QCLs are available in the fingerprint region (Region 2), but not the  $\text{OH}$ ,  $\text{NH}$ , and  $\text{CH}$  stretch region (Region 1). Consider that they frequently have only  $200\text{ cm}^{-1}$  tuning ranges, although larger ranges are possible.<sup>63</sup> So, a program using linear SVM was written to calculate the accuracy using only a  $200\text{ cm}^{-1}$  range of data and then that range was scanned across



**Figure 5.** Average contribution to the tumor/nontumor decision (blue trace) at each spectral step  $j$  for the SKH1 mouse frozen section. The black trace is the difference between the averaged and preconditioned spectra of tumor and nontumor. The regions label “Noise” are regions where there is little difference in spectra as there are no fundamental vibrations of biomolecules in these regions. The regions from  $1860$  to  $760\text{ cm}^{-1}$  and  $3670\text{--}2790\text{ cm}^{-1}$  show important positive and negative contributions to the tumor decision.



**Figure 6.** Training error using only a  $200\text{ cm}^{-1}$  range (red) of the full set as that range is tuned across the spectrum. The smallest errors are in Regions 1 and 2, but the errors in Region 2 (fingerprint region) are smaller than Region 1.

the spectrum. The training error results are shown in Figure 6. Again, like Mittal and Bhargava,<sup>62</sup> limited ranges in the fingerprint region are found to be more accurate—although both regions are useable.

Which of the four common single QCL ranges (that are often configured to work as one unit in IR microscopes<sup>42</sup>) is best for skin cancer work? The ranges  $1850\text{--}1644\text{ cm}^{-1}$ ,  $1642\text{--}1352\text{ cm}^{-1}$ ,  $1350\text{--}986\text{ cm}^{-1}$ , and  $984\text{--}780\text{ cm}^{-1}$  were investigated by using only data from each spectral step ( $2\text{ cm}^{-1}$  intervals) in these regions to obtain decisions. The Training errors and 10-fold cross-validation errors are given in Supporting Information (Table S1). The second (amide band region) and third region had the lowest errors, i.e., 10-fold cross-validation errors of  $0.30 \pm 0.30\%$  and  $0.05 \pm 0.16\%$ , respectively. More importantly, it is clear that one need not make measurements at each spectral step. Calculations were done using every other step ( $4\text{ cm}^{-1}$  intervals), every fifth step ( $10\text{ cm}^{-1}$  intervals), and every 10th step ( $20\text{ cm}^{-1}$  intervals). There is roughly a doubling of error when only every 10th step is used (90% of the data are dropped) vs use of all data. Details are in Supporting Information, Table S1. As an example, a QCL operating from  $1350$  to  $986\text{ cm}^{-1}$  could measure at 37 wavelengths in  $10\text{ cm}^{-1}$  steps obtaining a result as good as the full spectrum training. Therefore, in addition to reducing the range for a spectral cancer probe, one can also reduce the number of wavenumbers measured. In fact, 9 out of 10 measurements were dropped in analysis without significantly degrading decisions.

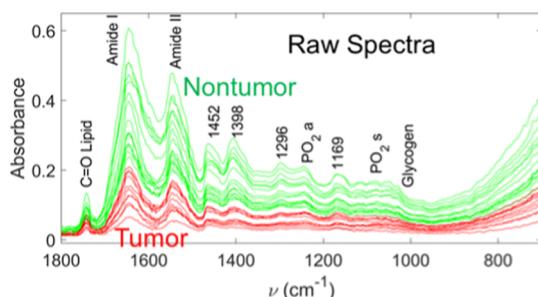
**4.3. Spectral Evaluation of Live Tissue.** The above results involved scanning tumor directly, now consider a situation closer to our desired application—namely probing the skin of a living entity. Raw spectra of living mice are shown in Figure 7 in which all the nontumor spectra were of higher absorbance intensity. Examination of the raw spectra in Figure 7 shows that there is perfect separation of tumor and

nontumor spectra based on the absolute intensity of the spectra. However, this is not useful as the probe can be pushed into tissue differently—by different investigators or on different occasions by the same investigator. Spectral preprocessing was guided by the previous imaging work and involved subtracting the baseline average in the region from  $1800$  to  $1770\text{ cm}^{-1}$  and normalizing the result to control for different probe pressure and tissue elasticity as shown in Figure 8a. The averages of the preconditioned spectra are given in Figure 8b showing significant differences (black trace) in spite of normalization. Finally, a linear SVM decision equation was trained with the 28 preconditioned spectra, and the corresponding histogram of the decision equation values is given in Figure 8c showing zero errors upon training. One can still discriminate tumor and nontumor on live skin even if the tumor elasticity hint is removed by normalization and the decision equations are different than that for frozen sections.

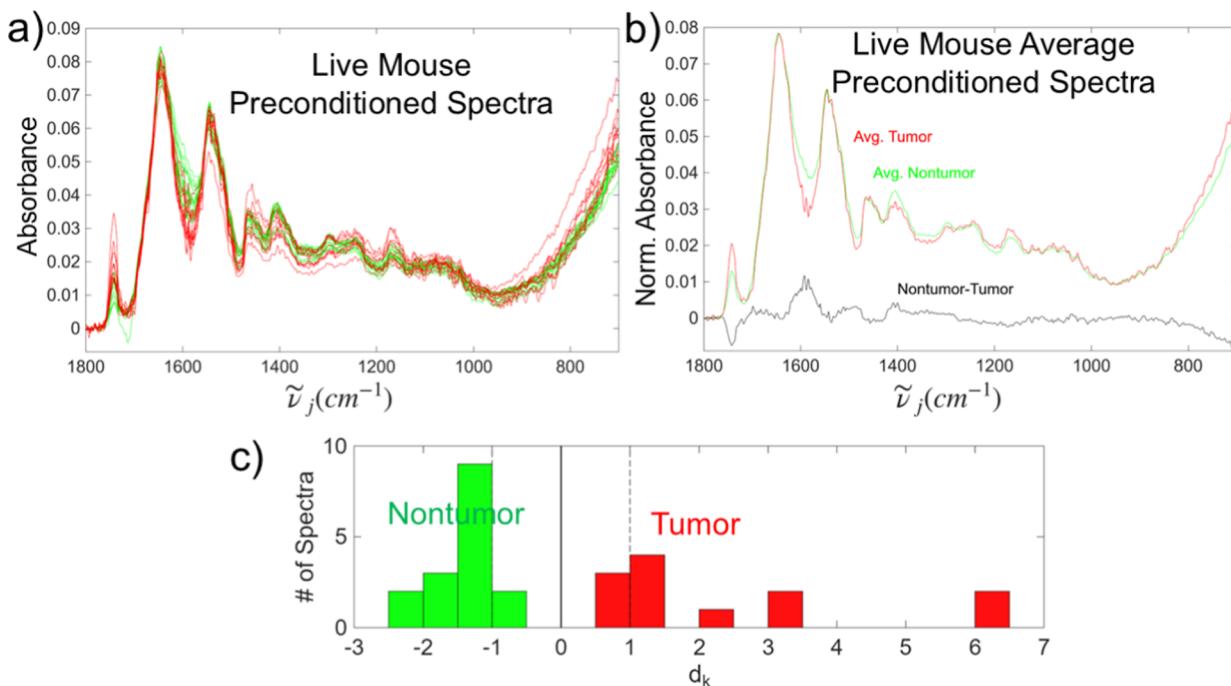
The average contribution to the tumor/nontumor decision at each spectral step [ $\overline{\Delta d}_j$  of eq 4] is plotted in Figure 9 with blue. The sharpness of the features was surprising with widths of  $\sim 4\text{ cm}^{-1}$  matching the FTIR resolution. The most intense features are in the amide I and II band regions although there is a concentration of smaller features in the  $1130\text{--}950\text{ cm}^{-1}$  region of glycogen and phosphorylated biomolecules. This type of feature analysis suggests that a probe for live skin might work best in the amide I and II band region. Also, one might not need to measure signals where  $\overline{\Delta d}_j$  is close to zero which means that spectra could be more quickly recorded by only measuring wavenumbers labeling the maxima and minima of  $\overline{\Delta d}_j$  or at large and equal steps across the region.

## 5. CONCLUSIONS

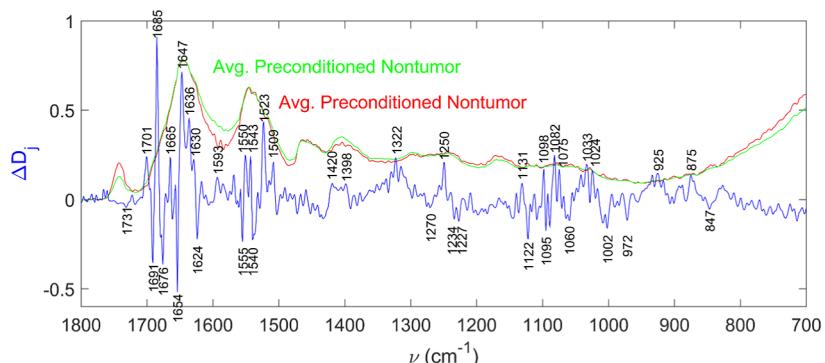
The large FTIR microscope imaging spectral data set (2553 full-range tumor spectra and 1511 full-range nontumor spectra) of the frozen section of the SKH1 hairless mouse tumor showed significant differences between the average tumor and nontumor spectra—even after baseline correction. The absolute intensities are meaningful as all spectra correspond to the same pixel area and tissue thickness, however the desire for use in more applications led to preconditioning with baseline correction and normalization. The data were analyzed with a linear SVM model which both avoids overtraining and offers simple feature selection of the “decision contribution spectrum”. Training randomly on  $\sim 50\%$  and testing on the remainder ( $\sim 50\%$ ) gave zero training errors and small testing errors (0.34% in one run). A 10-fold cross validation on the full library using the 50% training gave error of  $0.35 \pm 0.41\%$ . The errors of cross-validation and testing were small and similar, suggesting that linear SVM gave good



**Figure 7.** Raw probe FTIR spectra at the base of tumors (red) and off tumors (nontumor, green).



**Figure 8.** (a) The 12 tumor (red) and 16 nontumor (green) spectra after preconditioning with a baseline correction and normalization, i.e. no clear separation. (b) The average tumor (red) and nontumor (green) spectra after preconditioning in which the black trace is the difference between the average nontumor and tumor spectra showing significant changes. (c) Histogram of the linear SVM decision equation values showing zero mistakes in spite of preconditioning.



**Figure 9.** Average contribution to the tumor/nontumor decision (blue trace) at each spectral step  $j$  for the SKH1 mouse frozen section. Many maxima and minima are labeled in units of  $cm^{-1}$ . The average preadjusted spectra of tumor (red) and nontumor (green) are plotted for reference. The largest contributions to tumor decisions seem to come from the amide I and II band regions.

decision equations. The average Decision Contribution Spectrum regarding the tumor/nontumor decision [ $\overline{\Delta d}_j$ ] of eq 4 is given in Figure 5. There is noise in ranges devoid of vibrational bands. The largest integrated feature in the Decision Contribution Spectrum comes as a negative peak at  $1120\text{ cm}^{-1}$  corresponding to the  $\text{PO}_2$  symmetric stretch of many phosphorylated molecules, carbohydrates and/or polysaccharides. There is a sharp negative peak at  $1714\text{ cm}^{-1}$  with rapid changes in intensity which is in the region of ester-linked lipids ( $\sim 1741\text{ cm}^{-1}$ ). There is also much positive and negative structure in the amide I and II band regions suggesting protein band shape changes upon becoming cancerous. There does not seem to be one peak that dominates the decision; and all the bands in the H-stretch and fingerprint regions make contributions to the tumor decision.

Given good training and testing results, the effects of removing data were examined. Two spectral regions had sharp

positive and negative features with rapidly changing trends that indicate where fundamental vibrations in tissue change upon becoming cancerous. Region 1 was the H stretching region ( $3670\text{--}2790\text{ cm}^{-1}$ , amide A and B, lipid  $\text{CH}_2$  chains and  $\text{CH}_3$ ) and Region 2 was the “fingerprint” region ( $1860\text{--}760\text{ cm}^{-1}$ , lipid, amide I and II, phosphate, glycogen bands and many other biomolecules). Both regions can discriminate tumor from nontumor, but Region 2, the fingerprint region, does so with more accuracy (Figure 6). The fingerprint region was further divided into subregions commonly covered by popular commercial QCL systems. Such systems can be integrated, i.e. programming or tuning like one broadly tunable laser, but they are expensive. Considering that a device for medical practice might only be able to have one QCL, four subregions were tested, and each was found to do a decent job at discriminating tumor. The subregion from  $1350$  to  $986\text{ cm}^{-1}$  was most accurate. Then, each subregion was studied as spectral steps

were dropped revealing only a doubling of the error rate even after removing 90% of the data. This implies that practical mid-IR spectral probes can be designed with just one QCL (a very reduced range compared to FTIR) and that the device might measure with 10 or 20  $\text{cm}^{-1}$  steps or sampling intervals (at a higher resolution than FTIR) allowing fast and decisive spectra to be recorded on live human skin.

Finally, spectra were recorded on the outer skin of live mice. In this part of the study, 16 nontumor and 12 tumor spectra from live SKH1 hairless mice were recorded in the region from 1800 to 700  $\text{cm}^{-1}$  and there was excellent separation of tumor and nontumor spectra based on the absolute intensity. Preconditioned spectra were successfully trained with linear SVM which made no training errors in distinguishing tumor. The average Decision Contribution Spectrum of Figure 9 reveals the most critical wavenumbers in the protein and lipid region for live skin assay. It identifies critical wavenumbers that should and need not be measured. Since the mid-IR fiber optics filtered away the OH, NH, and CH stretching region, this work shows that a reduced range in the fingerprint region compared to that of traditional full-range FTIR can be viable in distinguishing cancer. Of course, the frozen section work already revealed greatly reduced ranges and increased sampling intervals that look promising. These results show that it is possible to detect skin cancer externally and with no ill effects on the living entities. The current positive results are necessary but insufficient conditions for demonstration of the ultimate goal of probing live human skin. We conclude that the combination of a fiber-loop sensor with a fast mid-infrared spectral probe (of reduced range and increased sampling interval relative to FTIR) is worthy of examination for live human skin. Clinical trials of this device are warranted on skin cancer in humans.

## ASSOCIATED CONTENT

### Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acsomega.Sc10854>.

A PDF file with figures and description are provided for the mouse frozen section, anesthesia and live mouse probing, and a table of errors upon removing spectral data ([PDF](#))

## AUTHOR INFORMATION

### Corresponding Author

**James V. Coe** – Department of Chemistry and Biochemistry, The Ohio State University, Columbus, Ohio 43210-1173, United States; Present Address: Emeritus Faculty at The Ohio State University; [orcid.org/0000-0001-5009-5472](#); Email: [coe.1@osu.edu](mailto:coe.1@osu.edu)

### Authors

**Rebecca C. Bradley** – Department of Chemistry and Biochemistry, The Ohio State University, Columbus, Ohio 43210-1173, United States; IR Medtek LLC, Gahanna, Ohio 43230, United States

**Justin D. Erwin** – Department of Chemistry and Biochemistry, The Ohio State University, Columbus, Ohio 43210-1173, United States

**Tatiana Oberyszyn** – Department of Pathology, The Ohio State University, Columbus, Ohio 43210, United States; Present Address: Vice Dean for Faculty Affairs and

Professor of Pathology, The Ohio State University College of Medicine

**Kathleen L. Tober** – Department of Pathology, The Ohio State University, Columbus, Ohio 43210, United States; Present Address: Director, Faculty Affairs Operations at The Ohio State University, College of Medicine.; [orcid.org/0000-0001-6201-6989](#)

**Charles L. Hitchcock** – Department of Pathology, The Ohio State University, Columbus, Ohio 43210, United States; Present Address: Emeritus Faculty at The Ohio State University.

**Heather C. Allen** – Department of Chemistry and Biochemistry, The Ohio State University, Columbus, Ohio 43210-1173, United States; [orcid.org/0000-0003-3120-6784](#)

Complete contact information is available at: <https://pubs.acs.org/10.1021/acsomega.Sc10854>

### Notes

The authors declare no competing financial interest.

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