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# An image-based deep learning framework for individualizing radiotherapy dose

Bin Lou, PhD<sup>1</sup>, Semihcan Doken, BA<sup>2</sup>, Tingliang Zhuang, PhD<sup>3</sup>, Danielle Wingerter, BE<sup>2</sup>, Mishka Gidwani, BS<sup>2</sup>, Nilesh Mistry, PhD<sup>3</sup>, Lance Ladic, PhD<sup>1</sup>, Ali Kamen, PhD<sup>1</sup>, Mohamed E. Abazeed, MD<sup>\*,2,4</sup>

<sup>1</sup>755 College Road East, Digital Technology and Innovation Division, Siemens Healthineers, Princeton, NJ, 08540;

<sup>2</sup>2111 East 96th St/NE-6, Department of Translational Hematology Oncology Research, Cleveland Clinic, Cleveland, OH, 44195;

<sup>3</sup>40 Liberty Blvd, Diagnostic Imaging Computed Tomography, Siemens Healthineers, Malvern, PA 19355.

<sup>4</sup>10201 Carnegie Ave/CA-5, Department of Radiation Oncology, Cleveland Clinic, Cleveland, OH, 44195.

# Abstract

**Background:** Radiotherapy continues to be delivered uniformly without consideration of individual tumor characteristics. To advance toward more precise treatments in radiotherapy, we queried the lung computed tomography (CT)-derived feature space to identify radiation sensitivity parameters that can predict treatment failure and hence guide the individualization of radiotherapy dose.

**Methods:** We used a cohort-based registry of 849 patients with cancer in the lung treated with high dose radiotherapy using stereotactic body radiotherapy. We input pre-therapy lung CT images into a multi-task deep neural network, Deep Profiler, to generate an image fingerprint that primarily predicts time to event treatment outcomes and secondarily approximates classical radiomic features. We validated our findings in an independent study population (n = 95). Deep

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#### DATA AVAILABILITY

<sup>&</sup>lt;sup>\*</sup>To whom correspondence should be addressed: Mohamed E. Abazeed, Cleveland Clinic, Phone: 216-445-0061, 2111 East 96th St, Fax: 216-636-2498, NE6-315, abazeem@ccf.org, Cleveland, OH 44195.

CONTRIBUTORS

D.W., M.G., T.Z. and S.D. assisted with data generation and analysis. M.G. and S.D. assisted with the writing of the Research in Context section and edited the manuscript. B.L. conducted the training and optimization the neural network, analyzed and interpreted the data and contributed to the writing of the Methods and Results. N.M. and L.L. assisted with interpretation and edited the manuscript. A.K. supervised the training and optimization of the neural network, assisted with interpretation and edited the manuscript. M.E.A. conceived, designed, analyzed, interpreted, and supervised the overall work and wrote the manuscript.

**Publisher's Disclaimer:** Deep Profiler and *i*Gray are based on research and are not currently commercially available. Due to regulatory reasons, their future availability cannot be guaranteed.

The datasets analyzed during the current study will be available from the corresponding author (abazeem@ccf.org) at the time of publication. Per institutional policy, the datasets are designated limited access. Upon receiving access, the investigator may only use them for the purposes outlined in the request to the data provider and redistribution of the data is prohibited.

Profiler was combined with clinical variables to derive *i*Gray, an individualized dose that estimates treatment failure probability to be <5%.

**Findings:** Radiation treatments in patients with high Deep Profiler scores fail at a significantly higher rate than in those with low scores. The 3-year cumulative incidences of local failure were 20.3% (95% CI: 16.0–24.9) and 5.7% (95% CI: 3.5–8.8), respectively. Deep Profiler independently predicted local failure (hazard ratio 1.65, 95% 1.02–2.66, p = 0.04). Models that included Deep Profiler and clinical variables predicted treatment failures with a concordance index of 0.72 (95% CI: 0.67–0.77), a significant improvement compared to classical radiomics or clinical variables alone (p = <0.001 and <0.001, respectively). Deep Profiler performed well in an external study population (n = 95), accurately predicting treatment failures across diverse clinical settings and CT scanner types (concordance index = 0.77 [95% CI: 0.69–0.92]). *i*Gray had a wide dose range (21.1–277 Gy, BED), suggested dose reductions in 23.3% of patients and can be safely delivered in the majority of cases.

**Interpretation:** Our results indicate that there are image-distinct subpopulations that have differential sensitivity to radiotherapy. The image-based deep learning framework proposed herein is the first opportunity to use medical images to individualize radiotherapy dose.

#### Keywords

artificial intelligence; personalized medicine; precision oncology; tumor heterogeneity

# INTRODUCTION

Medical imaging is integral to the management of patients with cancer, with significant roles extending from diagnosis to treatment response monitoring.<sup>1</sup> Its ubiquity in clinical practices notwithstanding, its current use remains largely subjective, exemplified by annotations of dimensions delimited by a range of human exactness. Computed tomography (CT) is the most frequently used modality across all cancers and comprises information beyond tumor geometry.<sup>2</sup> Information acquired by the scanner is conveyed by a matrix of voxels across thin sections of the body composed of X-ray attenuation values proportional to the density of the incident matter. These values can have a total range of >4,096 intensities. The human eye, on the other hand, resolves a minor proportion of these intensities.<sup>3,4</sup> Such limited discriminatory capacity clamors for 'machine-like' methods of information extraction and knowledge optimization.

Recent advances in image analysis have allowed for precisely this task. Radiomics permits the extraction of quantitative imaging descriptors or features that could characterize more objective tumor characteristics beyond human detection. This approach converts image data into a high dimensional feature space using a large number of data characterization algorithms.<sup>5,6</sup> Some of these features have been shown to capture distinct tumor characteristics and exhibit prognostic power, indicating some value to this approach.<sup>7</sup> Limitations to the utility of handcrafted image features, however, are their manual labeling and their inability to conform to a specific task. Manual labeling confines the feature space to elements that humans can learn and lack of deformability is a characteristic of the *a priori* design of the features, which cannot be modified based on the classification task at hand.

The process of feeding a machine raw data, like CT pixels, and allowing it to discover vectors for classification through the use of multiple layers of features is known as deep learning.<sup>8</sup> Compared to natural images, medical images have regulated quality that can reduce noise and therefore make them more useful for deep learning-based approaches.<sup>9</sup> However, while medical images can be an ideal source for deep learning, it remains difficult to secure a large quantity of clinically annotated datasets.<sup>10</sup> Since classification accuracy is dependent on the size of the initial training datasets, computational methods that seek to optimize model performance are critical.

Cancers are characterized by substantial diversity and the optimal therapeutic approach has been shown to vary on the basis of the genetic features of individual cancers.<sup>11,12</sup> Similarly, image-based profiling of tumors may reveal subpopulations that are more or less likely to be sensitive to a particular therapy and therefore guide its delivery. Classifications made by deep learning algorithms have begun to stratify patients on the basis of the type of cancer and genetic alterations.<sup>13,14</sup> However, very little progress has been made in the use of deep learning to predict tumor responses to individual anti-cancer therapies.

High dose radiation delivery to the lung via stereotactic body radiotherapy (SBRT) was developed with the intent to effect local tumor control while potentially obviating perioperative or long-term surgical morbidity in patients with early-stage lung cancer or oligometastatic disease to the lung. Despite several prospective clinical trials demonstrating excellent local tumor control rates in medically inoperable patients with lung cancer,<sup>15–17</sup> recent studies describe unacceptably high local failure rates in some patient subgroups.<sup>18–20</sup> Ongoing and future studies of lung SBRT are likely to be significantly informed by a more accurate and quantitative determination of treatment failure risk and the mitigation of that failure by adjusting radiotherapy dose.

Herein, we incorporated domain-specific information, namely radiomics, in the training signal of a deep neural network and then combined this data with clinical variables to predict the likelihood of treatment success after lung SBRT, a mainstay of treatment for patients with early-stage lung cancer and oligometastatic disease to the lung. Our results signify a new roadmap for deep learning-guided predictions and treatment guidance in the image-replete and highly standardized discipline of radiation oncology.

# METHODS

#### **Clinical Characteristics**

An institutional review board-approved study (IRB 14–562) was used to identify 1275 patients treated with lung stereotactic body radiotherapy (SBRT). Patients with primary (stage IA-IV) or recurrent lung cancer as well as patients with other cancer types with solitary or oligometastases to the lung were included. Patients without digitally accessible CT image or radiotherapy structure data were excluded from the study. A total of 944 patients met our eligibility criteria. 849 that were treated at the main campus in downtown Cleveland represented the internal study cohort. 95 patients that were treated at eight affiliate regional or national sites (Fairview, Ohio; Hillcrest, OH; Independence, OH; Mansfield, OH;

Sandusky, OH; Wooster, OH; Weston, Florida) represented the independent validation cohort.

Patients were treated based on either a pathological or radiographic diagnosis. All primary lung cancer patients were staged using CT of the chest. PET and imaging of the brain (magnetic resonance imaging [MRI] or CT) was employed when clinically indicated. In cases where imaging revealed mediastinal or hilar lymph nodes enlarged by accepted radiographic criteria or where the standardized uptake value (SUV) exceeded a value of 3.0 on PET, pathological mediastinal evaluation with endobronchial ultrasonography-guided sampling (EBUS) was requested.

Radiotherapy was conducted first by patient immobilization with abdominal compression to restrict breathing motion. In cases where motion could not be adequately restricted to less than 1 cm (11.3% of patients), Active Breathing Coordinator (ABC) (Elekta, Stockholm, Sweden) was used. Tumors within a 2-cm expansion of the tracheobronchial tree were categorized as central. A risk-adapted approach for radiation dose delivery was used. Most patients received 50 Gy in five fractions. When the RTOG 0236 trial commenced, eligible patients with peripheral tumors to 60 Gy in three fractions we treated as per protocol while patients with central tumors continued to receive 50 Gy in five fractions. Alternative fractionations were employed for patients enrolled in a clinical trial, if constraints for our standard fractionation schedules could not be met or at the discretion of the treating radiation oncologist. Local failure was defined as radiographic progression within 1 cm of the planning target volume (PTV) to maintain a consistent definition of local/marginal failure in clinical trials of SBRT. Failures within the same lobe of the lung but greater than 1 cm from the PTV of the initial treatment site were defined as lobar failure and were not considered in this analysis. 8.5% of patients received adjuvant chemotherapy. The main indication for adjuvant chemotherapy was a perceived high risk of treatment failure. The recommendation to deliver adjuvant treatments was also influenced by considerations of patient tolerance for additional therapy.

#### CT Image Dataset

Planning CT images with corresponding physician-designated gross tumor volumes (GTV) were used. Images with contrast were excluded. Four scanners were used in the internal study population, namely three Philips Brilliance CT Big Bore (annotated CT-1, CT-2 and CT-3) and a Philips AcQSim (CT-4). The number of cases scanned on each of the scanners were 499, 244, 40 and 61, respectively; the identity of the scanner could not be definitively determined for 5 cases. The independent validation cohort had CT scanners made by GE, Siemens or Philips and four distinct models were used: GE Medical Systems Discovery ST, Philips Brilliance CT Big Bore, Philips Gemini GXL and a Siemens SOMATOM Definition AS.

#### **Deep Profiler and Multi-task Learning**

The schema for deriving the Deep Profiler signature is shown in Figure 1a. For a step-bystep protocol for generating Deep Profiler scores and a detailed description of the multi-task learning framework, see Supplementary Methods.

#### **Classical Radiomics**

The 3D handcrafted radiomic features were extracted from GTV encompassing regions of interest (ROI). The handcrafted features can be divided into four groups: (1) intensity, (2) geometry, (3) texture, and (4) wavelet features. The intensity features quantified the first-order statistical distribution of the voxel intensities within the GTV. The geometry features quantified 3D shape characteristics of the tumor. The texture features described spatial distribution of the voxel intensities, thereby quantifying the intratumoral heterogeneity. The intensity and texture features were also computed after applying wavelet transformations to the original image. A total of 365 radiomic features were extracted. A list of all features can be found in Supplementary Table 1. All handcrafted features were extracted using Pyradiomics.<sup>21</sup>

We examined the performance of handcrafted radiomics to predict local failure. Five-fold cross-validation was also used for this analysis. Given that the number of radiomic features is much larger than the number of failures, either strong feature selection or model regularization was required to prevent overfitting. Feature selection was performed as previously described<sup>7</sup>. In the training set, we computed the performance of all individual features using C-index, and selected the one best feature from each of the four feature groups. These four features were then combined in a multivariate model for predicting local failure. Parameters estimated from the training were applied to the testing set for performance evaluation. To assess the performance of full handcrafted features, we also designed a multivariate model with Ridge  $L_2$  regularization on regression coefficients. Parameters were optimized using the training set and selected based on the performance in the validation set. Similar to the feature selection method, the final performance was evaluated using the testing set.

#### **Clinical Variable Integration and iGray**

We also assessed the complementary effect of the image score with other clinical risk factors such as biologically effective dose (BED) and histological subtypes. BED was calculated using an  $\alpha/\beta$  ratio of 10 Gy, modeled as a continuous variable. We assessed the effects of two main histological subtypes, adenocarcinoma and squamous cell carcinoma (SqCC) and modeled them as categorical data. In the presence of the competing risk (death), Fine and Gray regression modeling was used to examine the effect of all factors to the local failure. Univariate analysis was first used to confirm the significance level of each individual factor. All three variables were included in the multivariable model. For directly evaluating the effect of histological subtype between adenocarcinoma and SqCC variable, the model was fitted to a subset of the data (*i.e.* adenocarcinoma and SqCC patients only).

We used the multivariate regression model with Deep Profiler score and BED to both predict failure and calibrate the radiation dose to modulate the risk of local failure. *K*Gray was defined as the dose that results in a probability of failure of <5% at 24 months and is in units of BED. The calibration was achieved by estimating the cumulative incidence function (CIF) from the regression model. According to the assumptions in Fine and Gray's model, the predicted CIF can be computed for a subject with covariate vector **X** as follows

$$I(t|\mathbf{X}) = 1 - \left[1 - I_0(t)\right]^{\exp\left(\beta^{\mathrm{T}}\mathbf{X}\right)}$$

where  $I_0(t)$  is the estimated baseline CIF,  $\mathbf{X} = (x_{img}, x_{BED})^T$  is the covariate vector, and  $\boldsymbol{\beta} = (\beta_{img}, \beta_{BED})^T$  are the regression coefficients for image and BED covariates.

To estimate the feasibility of delivering *G*ray recommended doses, we permitted prescribed doses up to 180 Gy BED for GTVs that were outside of the central zone per RTOG  $0236^{15}$  and  $0618.^{22}$  For central tumors, we partitioned the central zone region, which is within a 2 cm radius of large airways or the proximal bronchial tree (PBT), into four equal segments. We assigned a gradient BED schema to tumors from the most proximal to the most distal segments: 108, 132, 149.5 and 168 Gy, respectively. 108 Gy BED (60 Gy in 8 fractions) has been previously shown to be safe for ultra-central tumors.<sup>23,24</sup> The use of 132 Gy BED in the next segment is per RTOG 0813, which indicated that the maximal tolerated dose in patients with centrally located tumors is 12 Gy in 5 fractions.<sup>25</sup> For tumors from 1-2 cm, minimal to no overlap between the treated volume and the PBT and central organs at risk is expected due to more limited respiratory motion in the central zone and PTV expansions of only ~5 mm. Nevertheless, we used a conservative linear gradient of risk to estimate putative safe doses in these regions. These latter estimates are theoretical as the relationships between dose escalation, a stratified central zone and toxicity have yet to be thoroughly investigated.

#### Saliency Map

To find the voxels of an input volume that contribute the most toward the prediction of treatment failures, we took the derivative of the final partial likelihood loss with respect to

the input CT volume and evaluated each volume  $\mathbf{X}_i$  as  $\frac{\partial \mathcal{L}_s}{\partial \mathbf{X}} \Big|_{\mathbf{X}_i}$ . This derivative provides a

scalar quantity for each of the voxels in the input volume, indicating the influence of the variation of voxel to the output of the model. The magnitude of these values was projected on the CT image to create a saliency map.

#### **Statistical Analysis**

To quantify the predictive performance, the concordance index (C-index) was measured between network output and actual event (local failure) time. The concordance index is a measurement between 0 and 1 that indicates how well the prediction model can order the actual event times - 1 indicates perfect concordance while 0.5 indicates no better concordance than chance. The averaged C-index across all five folds was calculated. The confidence interval was calculated using a bootstrap approach. We calculated cross-validated C-indices based on bootstrap resampling of the testing set and repeated 1000 times. The 2.5th and 97.5th percentile of the bootstrapped C-index distribution was used as an estimation of the 95% confidence interval.

We compared the predictive performance of handcrafted radiomics and our imaging fingerprint using the C-index. The performance of tumor 2D CT size, the maximum 3D diameter and volume were used as comparators. We applied a bootstrap method to compare

the significance between different models. For each model, we randomly resampled the testing set and calculated the C-index. This was repeated 100 times for all five folds. Wilcoxon test was used to assess the significance between the C-index distributions of different models.

To further explore the association between the imaging index and failure time, competing risk analysis was performed to estimate the cumulative incidences of local failure. The Kaplan-Meier method is inappropriate for estimating the incidence rate of therapy failure in the presence of death because patient death leads to the censoring of the primary outcome. As mortality is not completely independent from therapy failure, death without evidence of local failure was treated as a competing event. The median score in the training set was computed and then applied as a threshold to stratify patients in the testing set into high and low risk groups. After the cross-validation was complete, each patient was classified into one of the risk groups. Cumulative incidence curves (CICs) were estimated for each group, and Gray's test was used to determine the significance of difference between two curves.<sup>26</sup> Statistical analysis was performed using R 3.2.5.<sup>27</sup>

#### Role of the funding source

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# RESULTS

#### **Deep Profiler Accurately Predicts Radiation Treatment Failures**

A total of 849 patients met our eligibility criteria. 86.9% of the patients enrolled received definitive treatment for early stage non-small cell lung cancer (Table 1). The cumulative incidence of local failure at 3 years was 13.5% (95% CI: 10.8–16.2). Patients were stratified into high and low risk groups based on a median score cutoff of a neural network derived imaging signature from the training set. This process was repeated for each partition and the results of all five folds were concatenated for statistical analysis. A total of 469 patients were stratified into the high-risk group and 380 patients were in the low risk group. Estimated CICs of local failure for overall population and each risk group are shown in (Figure 2a & b). Gray's test for equality across Deep Profiler risk groups was significant (p = <0.001). Patients in the low risk group failed radiotherapy at a significantly lower rate than do those in the high-risk group, with 3-year cumulative incidences of local failure of 5.7% (95% CI: 3.5–8.8) and 20.3% (95% CI: 16.0–24.9), respectively.

To determine the clinical setting(s) in which Deep Profiler can be most predictive of local failure, we examined the impact of tumor stage on Deep Profiler and its prediction accuracy. Scores varied based on tumor stage, with IA tumors having the lowest mean score (Figure 2c). Despite differences in the mean scores of Deep Profiler across some stages of disease, there was significant variation within and across individual stages. These results suggested that information beyond tumor stage was learned by Deep Profiler. Consistent with this

observation, Deep Profiler predicted local failure in patients with early- or late-stage cancers (Figure 2d & e).

To assess the influence of possible variation in the types of treatments delivered or CT image acquisition, we assessed the impact of motion management, the use of adjuvant chemotherapy and CT scanner type on Deep Profiler. Scores were not significantly different based on the type of motion management used for treatment (ABC versus abdominal compression, p = 0.353) (Supplementary Figure 1). Scores were, however, significantly higher in patients that received adjuvant chemotherapy (p = <0.001), although there was significant overlap across the two groups (Supplementary Figure 2). This data is consistent with the physician-directed recommendation of adjuvant chemotherapy on the basis of variables that are perceived to lead to a higher risk of treatment failure<sup>28</sup> and suggests that Deep Profiler could potentially inform these recommendations. Lastly, scores obtained from the two most frequently used CT scanners (both of which are Philips Big Bore had similar accuracy in predicting local failures (Supplementary Figure 3).

#### **Deep Learning Outperforms Classical Radiomics**

We compared the performance of our neural network-derived imaging index to twodimensional (2D) CT size, maximum 3D CT size, 3D tumor volume and classical radiomic features. Our learning-based framework is superior to classical radiomics features, which were in turn superior to tumor volume followed by 2D size values (Table 2). The superiority of Deep Profiler indicated that features beyond tumor size, which has been previously shown to be associated with local failure after high-dose radiotherapy to the lung,<sup>29</sup> can be identified using our deep learning algorithm.

On univariate analysis, a higher image-based risk score (Deep Profiler), lower radiation dose and histological subtype were associated with an increased risk of local failure (Supplementary Table 2). On multivariate analyses, all three factors remained significantly associated with local failure (Table 3). The multivariable models that included Deep Profiler and clinical variables predicted treatment failures with a C-index of 0.72 (95% CI: 0.67– 0.77), which was a significant improvement when compared to classical radiomics (p =<0.001) or 3D volume (p = <0.001). These results indicated that an image-based score can provide complementary information to the clinical established variables of histological subtype and radiation dose<sup>18</sup>.

#### iGray and Personalized Radiation Dose Delivery

We posited that treatment failures can be mitigated by higher radiation doses and that we can model this relationship for the purpose of guiding dose individualization. First, we built a Fine and Gray's regression model using the imaging signature and dose of radiation. This enabled us to model the risk of local recurrence by tuning the dose of radiation accordingly. Importantly, the type of treatment delivered is the only mutable variable identified in the model; tumor size, CT image features and histology are fixed. Using this model, we calculated the probability of local failure at 24-months after treatment as a function of radiation dose. Our results indicated that local failure can be significantly reduced as a function of radiation dose (Figure 3a).

We then calculated the patient-specific dose that reduces the probability of treatment failure to <5%, *i*Gray, for each patient using a permuted holdout set design. The kernel densities of dose delivered compared to *i*Gray showed significant overlap (Figure 3b). The range of iGray was wider (21.15–277.1 Gy) with greater standard deviation (40.6 v. 30 Gy). The percent dose difference required to achieve iGray for each patient was calculated and its distributions were plotted for a function of each dose delivery interval (Figure 3c). These results indicated that *i*Gray is likely to be feasible in a majority of patients receiving high-dose radiotherapy to the lung.

To assess the feasibility of delivering *G* ray dose recommendations, we first estimated the impact of incremental dose increases on the probability of local failure in patients who received a BED of 100 Gy, the most frequent treatment dose in the cohort (n = 445). We used our model to estimate local failure probabilities at 24-months (Figure 3d) and showed that even incremental increases in the dose delivered to these patients can significantly reduce treatment failure probability. To generate an estimate of the extent of feasibility in all patients in our cohort, we used a gradient dose scheme that is extrapolated from previous dose escalation studies to avoid airway toxicity in based on the proximity of the tumor to the proximal bronchial tree (Figure 3e and Methods). Using this scheme, the cumulative relative frequency of safely achieving *i*Gray is 63.5% (Figure 3f).

#### Model Accuracy and Scalability

To examine the agreement between the observed outcomes and the multivariate model with the *i*Gray and BED, we calculated calibration curves. A calibration curve was obtained by plotting the average predicted probability at 1, 2, or 3 years after radiation treatment against CIC estimates of the actual outcome (Figure 4a). Our results indicated that our model accurately predicts treatment outcomes.

In addition, we sought to determine the impact of dataset size on prediction accuracy. To achieve this, we randomly selected 60% of the patients in the dataset and calculated the concordance indices using our deep learning platform and a classical clinical risk factor (i.e. volume) and compared it to our analyses using 100% of the patients. Our results indicated that whereas volume appears to reach a plateau in accuracy, our framework's performance is significantly higher with increases in sample size (Figure 4b). These results establish the scalability of deep learning in our dataset and suggest that improvements in accuracy are more likely using deep learning-based approaches compared to tumor volume measurements with dataset growth.

#### Voxel Saliency and Tumor Volume

To determine the significance of each voxel on treatment failure, we calculated a saliency map for each tumor. Saliency projects a weight in heatmap form to each voxel in the image and this weight reflects the importance of that voxel on the image risk score (Figure 5a). Critically, the majority of the most salient voxels were within the GTVs and PTVs across all tumors, indicating that the gross tumor and the peri-tumoral region are the most relevant voxels to the model (Figure 5b). This saliency detection method is also a critical examination of the spatial sampling methodology of cropping to a  $64 \times 64 \times 32$  sub-volume

encompassing the tumor, indicating that the volume is sufficiently large to encompass the most salient voxels but not too broad resulting in a classifier that fails to *understand* despite having high accuracy (*e.g.* spurious voxel associations).<sup>30</sup> Lastly, there were a number of salient voxels outside of the GTV (37.8%) and PTV (20.5%) across the dataset. The role of these outlying salient voxels in marginal treatment failures remains unclear.

#### **Deep Profiler Generalizes to Independent Populations**

We sought to measure the accuracy of Deep Profiler using a different but plausibly related independent population of patients who received SBRT to the lung. A total of 95 patients with 102 tumors (metachronous and/or synchronous treatments were included) from eight affiliate treatment centers met our eligibility criteria. Differences in baseline patient characteristic compared to our internal study population included a shorter median time to follow-up (p < 0.01), smaller tumors (p < 0.001) and lower radiation doses (p < 0.01) (Table 4). These results indicated sufficient differences between the internal and independent validation cohorts to allow for an assessment of both the reproducibility and transportability of the model.<sup>31</sup>

The cumulative incidence of local failure in this population at 2 years was 19.7% (95% CI: 10.9–30.4). Patients were stratified into high and low risk groups based on a median Deep Profiler score from a training dataset that included all 849 patients in our internal study population. Estimated CICs of local failure for overall population and each risk group are shown in (Figure 6). Gray's test for equality across Deep Profiler risk groups was significant (p = 0.002). Patients in the low risk group failed radiotherapy at a significantly lower rate than do those in the high-risk group, with 2-year cumulative incidences of local failure of 9.5% (95% CI: 2.8–21.3) and 39% (95% CI: 19.6–58.1), respectively. Deep Profiler predicted treatment failure with a C-index of 0.77 (95% CI: 0.66–0.92), which was calculated based on bootstrap resampling of the external dataset and repeated 1000x. These results indicate that Deep Profiler can predict treatment failures accurately across diverse clinical settings and distinct CT simulator scanners (Table 4).

# DISCUSSION

Accurate estimates of the probability of treatment success for individual patients can significantly improve clinical outcomes. In this study, we show that the clinical responses of cancer to radiotherapy vary in a manner not fully explained by clinical and histopathological variables alone and that CT image-based features contribute to this variance. The most important message in our study is that predictive features can be learned from CT images and contribute to the individualization of radiation dose.

Quantitative image analyses to date have not been used to personalize cancer treatment delivery.<sup>32–34</sup> To address these limitations, we trained a machine to learn the multidimensional feature space in a large cohort of patients with cancer in the lung that was treated with a wide dose range of radiation. In unconstrained machine learning algorithms of imaging data, the machine predominantly seeks relationships between multi-dimensional inputs and outcomes data. However, most clinically available datasets have generally been smaller and more limited than the datasets other disciplines may use to tune their predictive

algorithms, and the quality and completeness of existing outcomes data could be key barrier to these approaches. To address these limitations, we used a multi-task approach that takes advantage of established image-based radiomic features to partially delimit and inform the neural network. We demonstrated that this approach, Deep Profiler, is superior to deep learning or classical radiomics alone. We also demonstrated that Deep Profiler can accurately predict treatment failures in varied clinical settings.

To limit spurious voxel associations with our predicted outcome, we incorporated prior knowledge by using the physician delimited tumor volume as part of the input into our network. Although manual annotation could bias the feature extractions, we showed that the voxels that are most deterministic for treatment failure localize within the physician contoured volumes (GTV or PTV). Conversely, some salient voxels localized to the peritumoral regions or tumor margin. Since classical radiomics approaches disregard image information outside of the GTV, the identification of these salient voxels is an additional advantage of this approach. The potential association of these voxels with marginal recurrences remains to be explored. To the extent that marginal salient voxels are predictive of local failures, automatic contouring of tumor saliency maps could represent a leap toward more accurate tumor volume delineation and informed inhomogeneous dose delivery.<sup>35,36</sup>

Our results have several additional clinical implications. First, there are image-distinct subpopulations that demonstrate differential sensitivity to radiotherapy. We showed that Deep Profiler has a wide range of values and is significantly associated with treatment failures across varied clinical settings, including plausibly related populations. These populations, in part, included distinct stages of disease, CT simulation scanners, motion management techniques, linear accelerators, radiation oncologists and therapists, geographies (local, regional and national) and longitudinal periods. Second, we provide an integrated method that uses image and, importantly, established clinical variables to individualize radiation dose. Moreover, *i*Gray uses the clinically validated linear quadratic model,<sup>37</sup> is empirically derived in that no assumptions are made regarding individual tumor radiosensitivity ( $\alpha$  and  $\beta$  in the tumor toxicity isoeffect remain constant) and its output is directly clinically actionable by recommending a dose that can be achieved using several treatment schedules. Third, our prediction accuracy is evolvable. A critical feature of neural network-based prediction is the potential for substantial improvements in accuracy with scale. As our dataset increases in sample size and/or is augmented by integration into large data sharing collaborations, the network is expected to substantially improve in prediction accuracy. This is in contrast with other computational methods like classical radiomics, whose accuracy appears to plateau in the early phases of dataset growth (see Figure 4). Another important element of the evolvability of our model is the eventual stratification of the dataset into more homogeneous populations based on variables such as cancer subtype, clinical stage, use of systemic adjuvant therapy, et cetera. This is particularly compelling considering the demonstrated preliminary efficacy of SBRT in patients with oligometastatic disease from distinct cancer types.<sup>38,39</sup> The use of SBRT in varied clinical settings will result in larger and more diverse datasets that are more amenable to data partitions, and therefore improved model accuracy.

An image-based framework for the personalization of radiotherapy dose can substantially alter the clinical radiotherapy paradigm. The radiation oncologist is advantaged because the dose of radiation delivered can be calibrated on the basis the risk of treatment failure, which itself is a continuum. This largely mitigates binary decisions of "to treat or not to treat" and instead permits the adjustment of radiation treatments to prevent treatment failures. *G*ray can assist in the design of image-stratified, radiotherapy-based trials. In this role, it can guide the evolution of radiotherapy toward dose delivery strategies that are calibrated on the basis of individual predictions of tumor control probability.

There are several characteristics of Deep Profiler and *i*Gray that suggest a lower implementation barrier. Due to the strict requirement for the acquisition of radiation planning CT images for radiotherapy, each radiation treatment center is likely to have an extensive CT dataset that could be utilized for model development and implementation. Combined with the automated feature algorithms of scalable deep learning-based prediction platforms, this represents an accessible opportunity to directly improve medical-decision support across broad cancer patient populations receiving radiotherapy.

The strengths of our study include the large number of patients evaluated, the completeness of the dataset, the use of a carefully annotated radiotherapy specific outcome (local failure) rather than surrogate of treatment failure (*e.g.* progression-free survival, cancer-specific mortality or overall survival) and the use of readily implementable and highly tractable image-based score as a backbone for our analyses. The limitations of our study include the following: we cannot fully account for all potential causes of bias, there is explicit population heterogeneity in our datasets (*e.g.* clinical stage, radiation dose, CT scanners, motion management, *et cetera*), the independent validation cohort is limited in size and we do not account for normal tissue toxicity. These limitations can, in part, be addressed with the incorporation of new datasets and emerging tools that predict lung toxicity,<sup>40</sup> respectively.

In summary, we combined clinical variables with deformable radiomic features through the deep learning of CT imaging-based features to *individualize* radiation dose delivery using a clinically meaningful unit, the Gray (*i*Gray). This framework could be readily implemented for pretreatment risk stratification and risk-adapted dose optimization in clinical trials and, ultimately, in everyday clinical practices that use radiotherapy.

#### **Supplementary Material**

Refer to Web version on PubMed Central for supplementary material.

#### Acknowledgments

DECLARATION OF INTERESTS

B.L., A.K., N.M., L.L. and M.E.A. are named inventors in a patent pending for the use of Deep Profiler and *i*Gray to personalize radiotherapy dose. M.E.A. receives grant support, travel support and honoraria from Bayer AG. M.E.A. receives grant support from Siemens Healthcare. M.E.A. is also supported by NIH KL2 TR0002547, NIH R37 CA222294, the American Lung Association and VeloSano.

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#### **RESEARCH IN CONTEXT**

#### Evidence before this study

CT images comprise voxel intensities that, to the extent that they are discernable by the treating physician, can guide the manual delineation of tumor volumes. They do not, however, currently contribute to the individualization of radiation dose prescriptions. Extraction and analysis of rigidly defined radiomic features has been used to transform medical imaging data into quantifiable variables used to predict survival, other failure modes and response to therapeutic agents.

#### Added value of this study

To our knowledge, this study is the first to implement a deep neural network using deformable multi-tasking with the ability to create new radiomic features to predict the risk of failure for patients treated with radiotherapy. This study also represents an innovation in personalized medicine by the projection of an optimized radiation dose, *i*Gray. The cohort of patients evaluated represents one of the largest datasets of chest CT images heretofore used in outcome prediction analysis.

#### Implications of all the available evidence

Accurate estimates of the likelihood of response to treatments coupled with optimized dose delivery can significantly improve clinical outcomes and limit toxicity for patients treated with radiotherapy. Our framework could provide readily implementable treatment strategy guidance for under-resourced medical facilities and populations. The ability of the neural network, Deep Profiler, to generate new predictive features represents a major advance in radiomics and artificial intelligence (AI). Augmenting this impact, Deep Profiler's prediction accuracy is scalable in that it will improve as our dataset increases in sample number via natural growth, federated datasets and data partitions into more homogenous populations.

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#### Figure 1.

Study design and neural network architecture. (a) Deep Profiler and *i*Gray are obtained using a 5-fold cross-validation with an 80:20 ratio for training and validation within each fold, respectively. *i*Gray is calculated by combining image and clinical data and using the cumulative incidence function of the regression model. (b) Neural network structure. The neural network consists of three main parts: an encoder for extracting imaging features and building a task-specific fingerprint, a decoder for estimating handcrafted radiomic features and a task-specific network for generating an image signature for therapy outcome prediction. A 3-D convolutional neural network (CNN) was used as an encoder for extracting imaging features. A fully-connected layer was adopted to link the latent fingerprint space with classical radiomics. Another neural network was used to predict the outcome based on latent fingerprint variables. Since therapeutic outcomes contain time-to-event information, we used a proportional hazards model to relate the time that passes before local failure occurs to classify failures.



#### Figure 2.

Deep Profiler predicts local failure. Estimated cumulative incidence curves for local failure in the overall population (a) or apportioned by the median Deep Profiler score based on each cross-validation step followed by concatenation (b). (c) Violin plot of Deep Profiler scores by tumor overall stage. The mean (point) and standard deviations (point range) are shown. (d) Estimated cumulative incidence curves for local failure apportioned by the median Deep Profiler score for early stage (IA-IIB) (e) or late stage tumors (III, IV and recurrent) (f). Gray's test was used to test for equality across Deep Profiler risk groups.

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#### Figure 3.

Ameliorating treatment failure by adjusting the radiation dose. (a) Heatmap demonstrating the relationship between Deep Profiler score (*x*-axis), *i*Gray in biologically effective dose (BED) units (*y*-axis) and the probability of local failure (*right* legend). As *i*Gray dose increases, the risk of failure decreases and vice versa. (b) The kernel density estimation of the actual dose of radiation delivered and *i*Gray. (c) Violin plots of the distribution for the percent change in dose delivered required to achieve iGray stratified by the four treatment categories (*y*-axis). (d) The probability of local failure was calculated for patients receiving the most common treatment regimen of 100 Gy BED after incremental increases in radiation dose. The overall rate of local failure is significantly diminished at the highest doses. (e) A depiction of the proximal bronchial tree (PBT). A proposed theoretical dose scheme to avoid proximal airway toxicity is shown in the bottom (see Methods). (f) The cumulative relative frequency of feasibly delivering *i*Gray per the scheme in (e). Some *i*Gray doses are shown (arrows) to highlight the range in which a substantial decrement in feasibility occurs.



#### Figure 4.

Model performance and the scalability of the deep neural network. (a) The calibration curves for the multivariable model that includes *i*Gray and BED demonstrated strong agreement between the estimated and observed 1-, 2-, and 3-year outcomes. Vertical bars represent 95% confidence intervals for observed local failure probabilities. (b) Comparison of model performance using the full data set and 60% of the dataset demonstrates the superiority and the potential scalability of the deep learning algorithm. Horizontal lines and error bars represent the mean C-indices and standard errors across five folds.



# Figure 5.

Tumor saliency extends beyond the physician delimited tumor volume. (a) A saliency map represents an overlay of heatmap color (*red*=high saliency; *black*=low saliency) on voxels in the CT image region of interest. Blue contour lines represent the delineation of tumor volume. Two patient examples are shown. (b) The proportion of voxels with saliency >0.20 within the gross tumor volume (GTV) (*green*), the planning target volume (PTV) or beyond both volumes (*gray*) are shown.



#### Figure 6.

Deep Profiler accurately predicts local failure in an external study population. Estimated cumulative incidence curves for local failure apportioned by the median Deep Profiler score derived from the internal study population.

#### Table 1.

#### Baseline Characteristics of the Study Population

Characteristics	
No. patients	849
Follow-up, months	20.93 (11.03-37.97)
Age	74.1 (67.6–80.7)
Sex	
Female	440 (51.8%)
Male	409 (48.2%)
Treated tumor size, cm	2.3 (1.6–3.4)
Overall stage	
Ι	645 (76%)
II	81 (9.5%)
III	8 (0.9%)
IV	74 (8.7%)
Recurrent	41 (4.8%)
Histology	
Adeno	255 (30.0%)
SqCC	248 (29.2%)
NSCLC (NOS)	47 (5.5%)
Neuroendocrine	14 (1.7%)
Other	22 (2.6%)
Non-diagnostic biopsy	74 (8.7%)
No biopsy	189 (22.3%)
Indications for treatment	
Definitive	738 (86.9%)
Salvage	52 (6.0%)
Oligometastatic	50 (5.9%)
Other	9 (1.1%)
Total dose, Gy	50 (30-60)
No. fractions	5 (1–10)
BED, Gy	100 (39–180)

 $^{I}$ Continuous variables are represented as medians with inter-quartile ranges, with the exception of total dose, no. of fraction and BED, Gy, which are represented by median and range.

<sup>2</sup>Abbreviations: Adeno, adenocarcinoma; BED, biologically effective dose; CT, computed tomography; IQR, inter-quartile range; NOS, not otherwise specified; SqCC, squamous cell carcinoma; SUV, standardized uptake values.

#### Table 2.

# Prognostic performance of different models

Model	Concordance Index	Confidence Interval	v. Deep Profiler <i>p</i> -value
2D CT Size	0.610	[0.545, 0.672]	2.05×10 <sup>-32</sup>
Max 3D diameter	0.655	[0.600, 0.712]	$1.06 \times 10^{-20}$
3D Volume	0.669	[0.611, 0.726]	9.78×10 <sup>-14</sup>
Classical Radiomics (feature selection)	0.651	[0.600, 0.710]	4.23×10 <sup>-25</sup>
Classical Radiomics (regularization)	0.680	[0.625, 0.739]	$1.18 \times 10^{-10}$
Deep Profiler	0.711	[0.660, 0.767]	-

# Table 3.

# Predictors of Local Failure in Multivariable Analysis

	HR	95% L	90% U	<i>p</i> -value
Deep Profiler signature	1.645	1.016	2.663	0.042
BED (continuous)	0.978	0.969	0.987	0.026
Adeno vs. SqCC	0.494	0.281	0.868	0.029
Adeno vs. Others	0.515	0.286	0.927	0.027

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#### Table 4.

#### Baseline Characteristics of the External Validation Population

Characteristics		P value
No. patients / tumors	95 / 102	
Follow-up, months	16.4 (11.4–24.6)	<0.01
Treated tumor size, cm	1.8 (1.3–2.7)	<0.001
Overall stage		0.29
Ι	78 (76.5%)	
II	10 (9.8%)	
III	0 (0 %)	
IV	5 (4.9%)	
Recurrent	9 (8.8%)	
Histology		0.21
Adeno	43 (42.1%)	
SqCC	24 (23.5%)	
NSCLC (NOS)	8 (7.8%)	
Neuroendocrine	1 (0.9%)	
Other	1 (0.9%)	
Non-diagnostic biopsy	6 (5.9%)	
No biopsy	19 (18.6%)	
Indications for treatment		0.52
Definitive	88 (86.2%)	
Salvage	9 (8.8%)	
Oligometastatic	5 (4.9%)	
Other	0 (0%)	
Total dose, Gy	50 (34–60)	0.02
No. fractions	5 (1–5)	<0.01
BED, Gy	100 (72–180)	< 0.01
CT Simulator Type		NA
GE Medical Systems Discovery ST	14 (13.7%)	
Philips Brilliance CT Big Bore	22 (21.6%)	
Philips Gemini GXL	17 (16.7%)	
Siemens SOMATOM Definition AS	49 (48.0%)	

 $^{I}$  Continuous variables are represented as medians with inter-quartile ranges, with the exception of total dose, no. of fraction and BED, Gy, which are represented by median and range.

<sup>2</sup>Abbreviations: Adeno, adenocarcinoma; BED, biologically effective dose; CT, computed tomography; IQR, inter-quartile range; NOS, not otherwise specified; SqCC, squamous cell carcinoma; SUV, standardized uptake values.

 $\frac{3}{p}$  values were calculated using Pearson's Chi-squared test for categorical variables and by the non-parametric test of medians for continuous variables. \*p value of < 0.05 was considered statistically significant.