

Discovery Radiomics via Evolutionary Deep Radiomic Sequencer Discovery for Pathologically-Proven Lung Cancer Detection

Mohammad Javad Shafiee, Audrey G. Chung, Farzad Khalvati, Masoom A. Haider, and Alexander Wong

Abstract— While lung cancer is the second most diagnosed form of cancer in men and women, a sufficiently early diagnosis can be pivotal in patient survival rates. Imaging-based, or radiomics-driven, detection methods have been developed to aid diagnosticians, but largely rely on hand-crafted features which may not fully encapsulate the differences between cancerous and healthy tissue. Recently, the concept of discovery radiomics was introduced, where custom abstract features are discovered from readily available imaging data. We propose a novel evolutionary deep radiomic sequencer discovery approach based on evolutionary deep intelligence. Motivated by patient privacy concerns and the idea of operational artificial intelligence, the evolutionary deep radiomic sequencer discovery approach organically evolves increasingly more efficient deep radiomic sequencers that produce significantly more compact yet similarly descriptive radiomic sequences over multiple generations. As a result, this framework improves operational efficiency and enables diagnosis to be run locally at the radiologist’s computer while maintaining detection accuracy. We evaluated the evolved deep radiomic sequencer (EDRS) discovered via the proposed evolutionary deep radiomic sequencer discovery framework against state-of-the-art radiomics-driven and discovery radiomics methods using clinical lung CT data with pathologically-proven diagnostic data. The evolved deep radiomic sequencer shows state-of-the-art diagnostic accuracy (88.78%) relative to previous radiomics approaches.

Index Terms—Discovery Radiomics, Radiomic Sequencing, Lung Cancer, Evolutionary Deep Intelligence, Evolved Deep Radiomic Sequencer.

I. INTRODUCTION

Lung cancer is the second most diagnosed form of cancer in men and women after prostate cancer and breast cancer, respectively. In 2016, lung cancer accounted for an estimated 158,080 deaths (approximately 27% of cancer deaths) and 224,390 new cases in Americans [1]. Similarly, lung cancer accounted for an estimated 20,800 deaths (approximately 26% of cancer deaths) and 28,400 new cases in Canadians [2]. Early detection of lung cancer can significantly impact the patient survival rate, making efficient and reliable lung cancer screening methods crucial.

Imaging-based cancer detection or radiomics-driven methods have recently grown in popularity to help streamline the cancer screening process and increase diagnostic consistency. Referring to the extraction and analysis of large amounts of quantitative features from medical imaging data, radiomics [3]

allows for the creation of a high-dimensional abstract feature space that can be utilized for cancer detection via the detailed characterization of cancer phenotypes. The prognostic potential of radiomics has previously been demonstrated in studies on lung and head-and-neck cancer patients [4], [5]. Aerts et al. [4] introduced a comprehensive study spanning over 1000 patients across seven datasets to demonstrate the application of radiomics towards differentiating between tumour phenotypes, indicating clinical and prognostic implications. In addition, radiomics has shown promise in combination with multi-parametric magnetic resonance imaging for breast cancer detection [6] and prostate cancer detection [7].

Radiomics-driven methods have previously been developed for malignant lung nodule detection using computed tomography (CT) images [8], [9], [10], [11]. Anirudh et al. [8] used weakly labelled lung data from the SPIE-LUNGx dataset to train a 3D convolutional neural network (CNN) and generate radiomic sequences for lung nodule detection. In contrast, Orozco et al. [9] generated wavelet-based radiomic sequences and demonstrated the effectiveness of wavelet-based features using a subset of images from the early lung cancer action project (ELCAP) and lung image database consortium (LIDC) datasets.

Shen et al. [10] proposed multi-scale convolutional neural networks (MCNN), a hierarchical framework for extracting discriminative features from lung nodules. Specifically, the framework comprises of alternating, stacked layers, and uses multi-scale nodule patches to learn class-specific features. More recently, Shen et al. extended their previous work to malignancy suspiciousness classification [11]. In addition, the extension simplified the training process via a multi-crop pooling architecture. An important aspect of these aforementioned radiomics-driven methods is that they leverage radiologist-driven nodule annotations for predicting the malignancy of lung nodules, rather than using pathology-proven data.

There are relatively few radiomics-driven methods that perform lung cancer detection using pathology-proven diagnostic data [12], [13]. Kumar et al. [12] introduced an unsupervised deep autoencoder for feature extraction with a binary decision tree classifier for lung nodule classification. Shen et al. [13] proposed a domain-adaptation framework for lung nodule malignancy prediction; more specifically, Shen et al. propose CNN-MIL for learning transferable patient-level malignancy knowledge, which combines a convolutional neural network (CNN) model with a multiple instance learning model (MIL).

Recently, the concept of *discovery radiomics* was introduced

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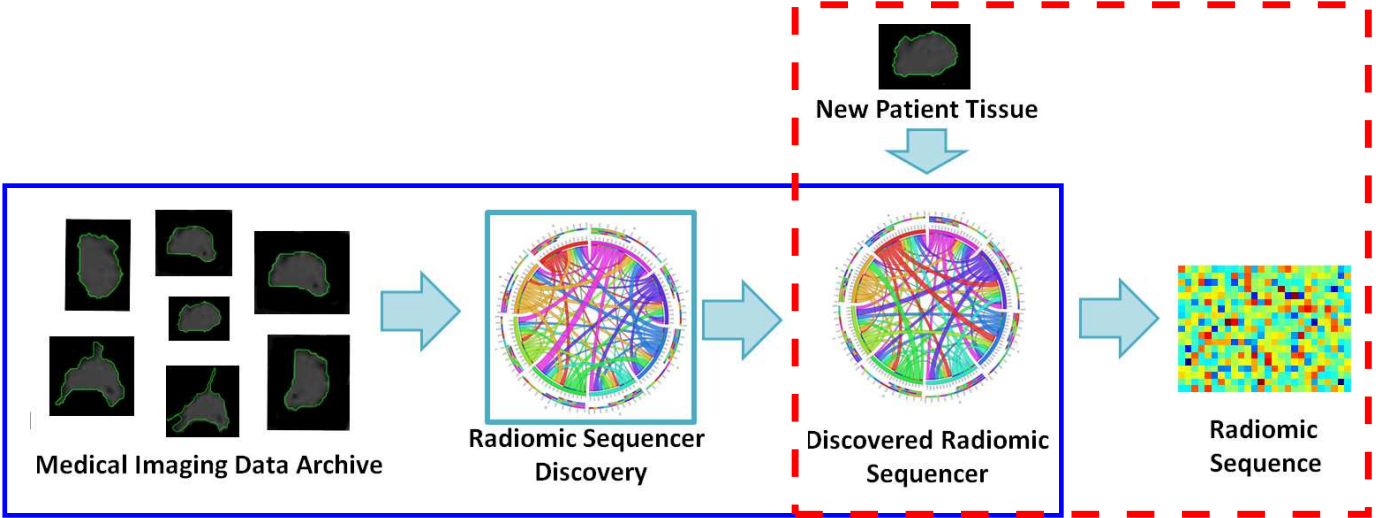


Fig. 1: Overview of the discovery radiomics framework for cancer detection. A custom radiomic sequencer is discovered via past medical imaging data; for new patients, radiomic sequences of abstract imaging-based features are generated for quantification and analysis.

where notions of using pre-defined, hand-crafted features for cancer detection are bypassed in favour of radiomic sequencers that produce abstract imaging-based features that are discovered directly from the wealth of readily-available medical imaging data. This allows for custom-tailored features to be discovered that can better characterize cancerous tissue and distinguish cancer phenotypes relative to conventional features. Discovery radiomics has shown promising results for both prostate cancer [14] and lung cancer [12], [15], [16] detection.

A number of different radiomic sequencers have been proposed within the discovery radiomics framework for the purpose of lung cancer detection. Kumar et al. [12] introduced the notion of deep autoencoding radiomics sequencers (DARS), which comprises of a deep autoencoder architecture. Shafiee et al. [15] proposed deep radiomics sequencers based on a deep convolutional StochasticNet [17] architecture, referred to as StochasticNet sequencers. More recently, Kumar et al. [16] leveraged deep radiomic sequencers built upon a deep convolutional neural network architecture.

While diagnostically powerful, the discovered radiomic sequencers were both computationally expensive and memory intensive, which could make it difficult for on-site clinical deployment and would require the transfer of patient information to more powerful cloud computing leading to patient privacy concerns. To mitigate computational requirements and increase operating efficiency, we propose a novel evolutionary deep radiomic sequencer discovery framework for discovering more efficient yet powerful deep radiomic sequencers. Using the concept of *evolutionary deep intelligence* [18], [19] to mimic biological evolution mechanisms, the proposed *evolutionary deep sequencer discovery* process discovers progressively more efficient yet diagnostically powerful deep radiomic sequencers over multiple generations. The resulting evolved deep radiomic sequencers (EDRS) that are not only significantly more efficient, thus making them more suitable for on-site clinical deployment, but can provide improved

diagnostic performance compared to existing deep radiomic sequencers.

II. METHODS

In this section, we will first discuss the concepts behind discovery radiomics and evolutionary deep intelligence. We will then present the proposed evolutionary deep sequencer discovery approach in detail.

A. Discovery Radiomics

The idea behind discovery radiomics can be described as follows (see Figure 1). Given past radiology data and corresponding pathology-verified radiologist tissue annotations from a medical imaging data archive, the radiomic sequencer discovery process learns a radiomic sequencer that can extract highly customized radiomic features (which we will refer to as a radiomic sequence) that are tailored for characterizing unique tissue phenotype that differentiate cancerous tissue from healthy tissue. The discovered radiomic sequencer can be applied to a new patient data to extract the corresponding radiomic sequence for cancer screening and diagnosis purposes.

As discussed earlier, one of the key limitation of previously proposed deep radiomic sequencers for the purpose of lung cancer detection is that, while diagnostically powerful, both computationally expensive and memory intensive, which could make it difficult for on-site clinical deployment and would require the transfer of patient information to more powerful cloud computing leading to patient privacy concerns. To mitigate computational requirements and increase operating efficiency to enable on-site clinical deployment, we will leverage the concept of *evolutionary deep intelligence* [18], [19] to discover highly efficient deep radiomic sequencers that still provide strong diagnostic performance. Besides being more compact, another key advantage of such evolved deep radiomic sequencers is that, by possessing smaller network architectures, they are particularly more appropriate in scenarios

characterized by a limited number of training data, which is an intrinsic aspect of medical applications such as lung cancer detection where annotated data is more limited.

B. Evolutionary Deep Intelligence

Prior to describing the proposed evolutionary deep sequencer discovery approach, it is first important to discuss the idea behind evolutionary deep intelligence. First introduced by Shafiee et al. [18], the general idea is to synthesize progressively more efficient deep neural networks over multiple generations. The evolution of deep neural networks is modeled in a probabilistic manner, where the architectural traits of ancestor networks are encoded by a probabilistic DNA. The probabilistic DNA is utilized to mimic biological heredity, and new offspring networks are synthesized stochastically based on this probabilistic model. To close the cycle of evolution, environmental factors are applied to the model to mimic random mutation and natural selection. At each generation, the offspring network (which is more efficient than its parent) is then trained to refine its modeling capabilities and maximize its modeling accuracy.

In an embodiment of the evolutionary deep intelligence framework, the evolution is initialized using a known network structure as the first generation. The network is trained based on the available training data and the weights associated with each synaptic strength are computed. The underlying heredity of the network (i.e., as the parent network) is encoded by the probabilistic DNA which is modeled based on the synaptic strengths. The environmental factors are then formulated into the model to account for the requirements needed to be satisfied by the offspring network. The offspring network is then synthesized by taking advantage of random mutation to diversify the offspring network from its ancestors. This process is repeated until all requirements are satisfied by the latest offspring network. Given its ability to produce progressively more efficient yet powerful deep neural networks, we are motivated to leverage the ideas behind evolutionary deep intelligence within the discovery radiomics framework to discover highly efficient yet diagnostically accurate deep radiomic sequencers for the purpose of lung cancer detection.

C. Evolutionary Deep Radiomic Sequencer Discovery

Motivated to leverage evolutionary deep intelligence within the discovery radiomics framework, we introduce an evolutionary deep radiomic sequencer discovery process for discovering deep radiomic sequencers. As seen in Figure 2, the evolutionary deep radiomic sequencer discovery framework discovers a more optimal deep radiomic sequencer generation by generation and, as a result, the generated radiomic sequence at each generation is more concise compared to radiomic sequences generated by previous deep radiomic sequencers in past generations.

The methodology behind the proposed framework can be described as follows. Inspired by [20], [19], let the deep radiomic sequencer be modeled as $\mathcal{H}(N, \mathbb{S})$, denoting a network architecture with the set of neurons N and set of synaptic connectivities \mathbb{S} . In this study, we will utilize a deep

convolutional neural network (CNN) architecture for the deep radiomic sequencer (see Figure 3). The structural information of a deep radiomic sequencer at generation g can be encoded by \mathbb{S}_g . W_{g-1} is the set of weights that encode the strength associated with each synapse in the network at generation $g-1$ where a synaptic weight of zero indicates that the associated synapse is not connected. It should be noted that W_{g-1} can therefore encode the structural information, \mathbb{S}_{g-1} , of network at generation $g-1$. As a result, it is possible to reformulate $P(\mathcal{H}_g|\mathcal{H}_{g-1})$ as $P(\mathbb{S}_g|W_{g-1})$ without any loss on modeling accuracy. Thus, the probabilistic DNA of a deep radiomic sequencer at generation g is formulated as $P(\mathbb{S}_g|W_{g-1})$, such that at each generation g the structure of the sequencer \mathbb{S}_g is synthesized given the trained weights of the sequencer of the previous generation W_{g-1} .

The genetic encoding scheme (i.e., probabilistic DNA) can be formulated in different ways to favor special requirements needed to be applied when the new offspring deep radiomic sequencers are synthesized. For promoting computational efficiency and compactness, $P(\mathbb{S}_g|W_{g-1})$ is modeled such that it promotes the formation of a particular cluster of synapses while considering the synthesis of each individual synapse in the offspring deep radiomic sequencer as well [19]:

$$P(\mathbb{S}_g|W_{g-1}) = \prod_{c \in C} \left[P(S_g^c|W_{g-1}) \cdot \prod_{i \in c} P(s_g^i|w_{g-1}^i) \right] \quad (1)$$

where $P(S_g^c|W_{g-1})$ promotes the synthesis of a particular cluster of synapses, $S_g^c \subset \mathbb{S}_g$, given the weights of the network at generation $g-1$ and $P(s_g^i|w_{g-1}^i)$ is the probability that synapse $s_g^i \in S_g^c$ will be synthesized in the offspring deep radiomic sequencer at generation g .

A cluster of synapses can be defined and represented based on different factors, such as faster run-time of the offspring radiomic sequencer on a parallel computing device or decreased storage requirements relative to its ancestor sequencer. However, the main advantage of (1) is that the $P(S_g^c|W_{g-1})$ not only favors strong synapses which are more effective in maintaining a high modeling accuracy, it promotes the persistence of clusters of synapses in the offspring deep radiomic sequencer which can extract more discriminative features, resulting in a sequencer that can model the problem more accurately. Here we define a set of synapses constructing a filter in each convolutional layer as a cluster of synapses in the network structure of deep radiomic sequencer. As shown in Figure 3, each filter in a convolutional layer is responsible for producing one output channel of the layer. By extending this definition to all convolutional layers in the radiomic sequencer, the length of the radiomic sequence varies over the generations as the number of filters in the last layer determines the actual length of the radiomic sequence.

The probabilistic DNA, $P(\mathbb{S}_g|W_{g-1})$, is combined with the environmental factor model $\mathcal{F}(\mathcal{E})$ to mimic natural selection, such that the offspring deep radiomic sequencer for the next generation is comprised of stochastically selected synapses or clusters of synapses. The probabilistic model of the network structure, $P(\mathcal{H}_g)$, at generation g can be formulated as

$$P(\mathcal{H}_g) = \mathcal{F}(\mathcal{E}) \cdot P(\mathbb{S}_g|W_{g-1}) \quad (2)$$

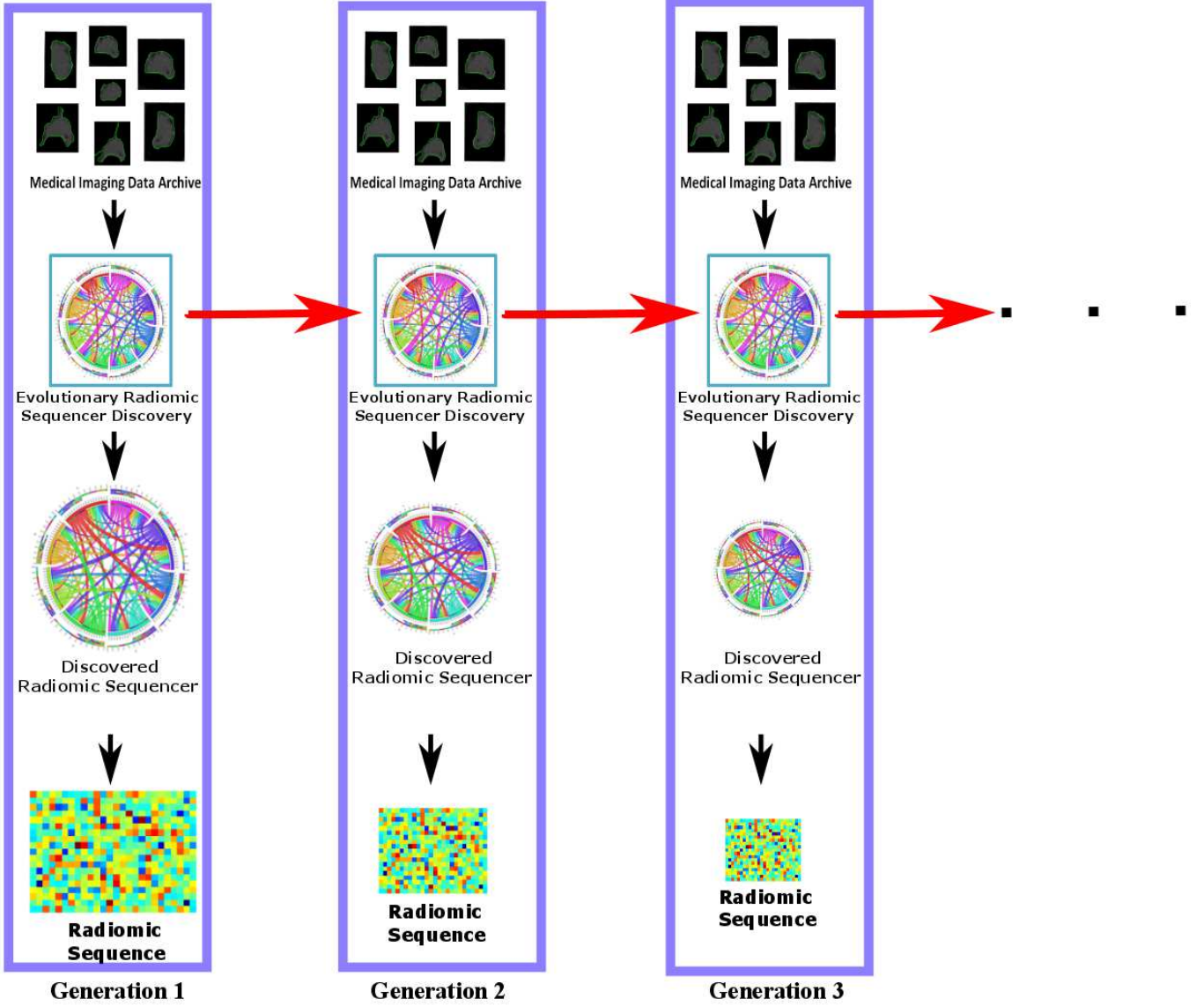


Fig. 2: Evolutionary deep radiomic sequencer discovery to synthesize optimized radiomic sequencer. As shown, the size of parameters of radiomic sequencer is decreased over generation resulting to a more concise radiomic sequence to describe the input radiology image.

where $\mathcal{F}(\mathcal{E})$ quantitatively encodes the environmental conditions, and the offspring deep radiomic sequencer structures must adapt to them to survive over generations. As mentioned before, the goal here is to synthesize a deep radiomic sequencer with fewer parameters while preserving the modeling accuracy; therefore, the environmental factor model, $\mathcal{F}(\mathcal{E})$, favors the formation of a deep radiomic sequencer with fewer parameters and increased efficiency over the generations. This property is applied via a cluster-based encoding scheme which decreases the number of filters of different layers over generations:

$$P(\mathcal{H}_g) = \prod_{c \in C} [\mathcal{F}_c(\mathcal{E}) \cdot P(S_g^c | W_{g-1})]. \quad (3)$$

More specifically, the environmental factor $\mathcal{F}_c(\mathcal{E})$ is formulated such that the offspring radiomic sequencer is limited to

80% of the total number of synapses in its direct ancestor sequencer.

III. RESULTS

A. Experimental Setup

The proposed evolutionary deep radiomic sequencer discovery framework was examined using the pathology-proven subset of the LIDC-IDRI [21], [22] dataset, and was compared to state-of-the-art methods. In this section, the configuration of dataset, the underlying network architecture of the discovered radiomic sequencers, and the competing methods are explained.

1) *Lung Dataset*: In this study, we used the subset of the LIDC-IDRI [21], [22] dataset that had corresponding pathology-proven diagnostic data. The CT images were captured using a broad range of scanner models from different

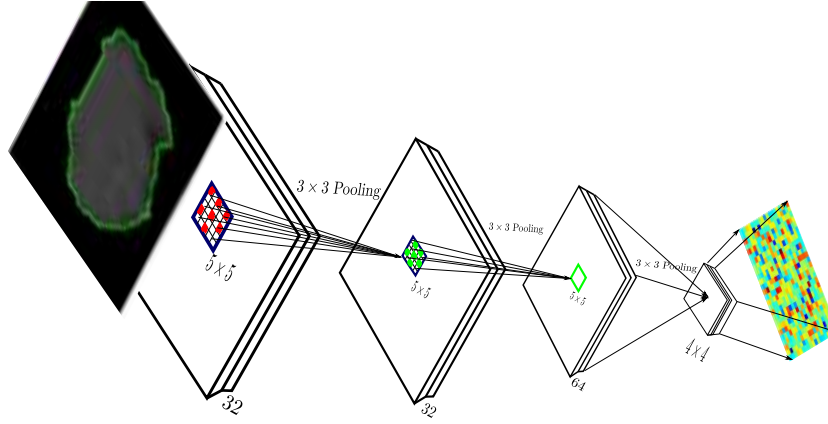


Fig. 3: Deep radiomic sequencer based on deep convolutional neural network architecture.

manufacturers by applying the following tube peak potential energies for acquiring the scans: $120kV$ ($n = 818$), $130kV$ ($n = 31$), $135kV$ ($n = 69$), and $140kV$ ($n = 100$). A subset of 93 patient cases which have definite diagnostic results was selected from the LIDC-IDRI. Using data augmentation, an enriched dataset of 42,340 lung lesions was obtained via the rotation of each malignant and benign lesion by 45° and 10° increments, respectively.

2) *Network Architecture*: The deep neural network architecture of the original, first generation radiomic sequencer used in this study builds upon the Lenet5 architecture [23]. The radiomic sequencer is comprised of three convolutional layers: $c_1 : 3 \times 3$, $c_2 : 5 \times 5$, and $c_3 : 3 \times 3$, where the first layer consists 32 filters, the second layer has 32 filters, and the last layer has 64 filters. The radiomic sequence generated by the original, first generation radiomic sequencer has a length of 16×64 , and is the input into two fully-connected layers ($f_1 : 64$ and $f_2 : 2$) to classify each input as cancerous or benign.

3) *Competing Frameworks*: The proposed evolutionary deep radiomic sequencer discovery was evaluated using the enriched dataset and quantitatively compared to four state-of-art radiomics-driven approaches [12], [13], [15], [16].

Kumar et al.'s deep autoencoding radiomic sequencer (DARS) [12] uses a five layer de-noising autoencoder trained by L-BFGS with 30 iterations and a batch size of 400, as suggested by past work [24]; a 200 dimension feature vector is extracted from the fourth layer and paired with a binary decision tree classifier. Shen et al.'s proposed convolutional neural network multiple instance learning (CNN-MIL) [13] is composed of three concatenated convolutional layers, each with 64 convolutional kernels of size 3×3 . Each convolutional layer is followed by a rectified linear unit and a max-pooling layer (4×4 pooling window in the first layer, and 2×2 in the subsequent layers), and two fully-connected layers are used as determine nodule malignancy. Shafiee et al.'s StochasticNet radiomic sequencer (SNRS) [15] is constructed using three stochastically-formed convolutional layers of 32, 32, and 64 receptive fields, respectively. Each receptive field is 5×5 in size, and is part of a random graph realization with a uniform neural connectivity probability of 0.5. Similarly, Kumar et al.'s

discovered radiomic sequencer (DRS) [16] comprises of three convolutional sequencing layers of 20, 50, and 500 receptive fields, respectively, each of size 3×3 .

B. Experimental Results

The proposed evolutionary deep radiomic sequencer discovery process was performed through 11 generations where in each generation, the environmental factor restricts the offspring radiomic sequencer to 80% of the total number of synapses in its direct previous network. By using this environmental factor, the number of parameters in the deep neural network of radiomic sequencer is decreased generation by generation, allowing for the generated radiomic sequences to more compact over generations. Decreasing the number of parameters in the sequencer is important as it affects the generalizability of the sequencer¹ such that a more generalized sequencer is less likely to be over-trained to the training data and can perform more accurately in the evaluation step.

The performance of the proposed framework is examined in a 10-fold cross validation approach where 9 out of 10 subsets of the data are used in the training step while the 10th subset is used to evaluate the model. This training and testing process is repeated over all permutations of the training and testing subsets. The cross validation approach is combined with evolutionary deep intelligence, where in each validation step, the radiomic sequencers are synthesized generation by generation with the same training dataset and validated with the same testing data.

Table I shows the average performance of the proposed framework over 11 generations. As seen, by moving generation by generation, the number of filters used in the radiomic sequencer is decreased and the length of the radiomic sequence is correspondingly shortened. However, the performance of the radiomic sequencers improve over generations which demonstrates the increase in the generalizability of the models through generations. As seen, the performance of evolved radiomic sequencers (i.e., sensitivity, specificity and accuracy) increases after first generation and it reaches to a stable point

¹With limited training data, a model with fewer parameters and better or even same accuracy is more generalized.

(e.g., generation 7). However evolving the radiomic sequencer after 7th generation can improve the compactness of the radiomic sequences.

Table I demonstrates that the specificity of the radiomic sequencers increases when the sequencers are evolved over generations, which is a good indication of generalizability of the final mode. It is worth noting that in lung cancer classification, improving the specificity is challenging [25] and increasing the specificity while maintaining a reasonable sensitivity is highly desirable.

Table I also shows that the evolved radiomic sequencers can perform better in terms of sensitivity compared to the first generation original ancestor radiomic sequencer, resulting in a model with higher accuracy. As mentioned before, one of the important obstacles in using a deep neural network as the underlying architecture for a radiomic sequencer is the efficiency of the underlying deep neural network. As seen, the average number of filters constructing the radiomic sequencer is decreased over generations, indicating that the efficiency of the radiomic sequencer is increasing generation by generation. It is also worth noting that the number of filters of a deep neural network determines the number of parameters need to be computed in one forward pass of the network to compute the final prediction; therefore, decreasing this number can increase the efficiency of the radiomic sequencer.

Decreasing the number of filters in the model decreases the length of the radiomic sequence. As shown in Table I, the length of the radiomic sequence is shortened generation by generation and the length of radiomic sequence in the last generation is about half size of the radiomic sequence of the first generation, demonstrating that it is possible to increase the concision of the radiomic sequence while simultaneously increasing the modeling accuracy.

Figure 4 demonstrates the sensitivity of the evolved radiomic sequencers overlaid with the standard deviation across different folds of cross validation over multiple generations. By evolving the radiomic sequencers generation by generation, the sensitivity increases while the standard deviation decreases (notice that the purple margin narrows over generations). This is another indication of generalizability of the evolved radiomic sequencers as the variance of the models in different cross validation folds of evaluation decreases over generations. This effect is more obvious in Figure 5 as the standard deviation of the specificity measure is decreased generation by generation and as mentioned before, a more reliable specificity is highly desirable in lung cancer classification. Figure 6 shows the same behavior of the modeling accuracy over generations.

As the last experimental result, Table II shows the comparison of the proposed framework (EDRS) with other state-of-the-art approaches. It should be noted that the statistics and modeling performances of other state-of-the-art frameworks are reported directly from Kumar et al. [16] and Shafiee et al. [17]. As seen, the proposed radiomic sequencer in the discovery radiomics framework outperforms other state-of-the-art methods in sensitivity, specificity and accuracy.

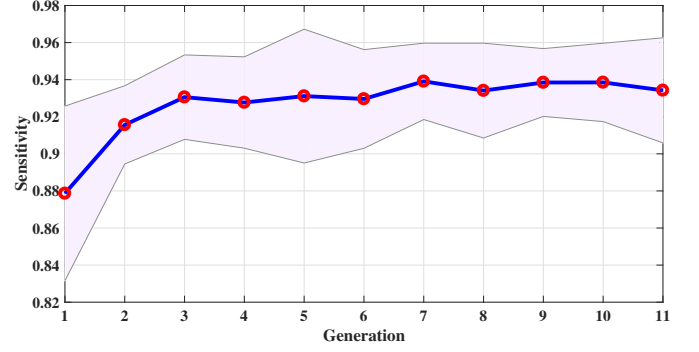


Fig. 4: Sensitivity of the evolved radiomic sequencers over generations. The standard deviation of the models based on 10-fold cross validation is overlaid with purple margin.

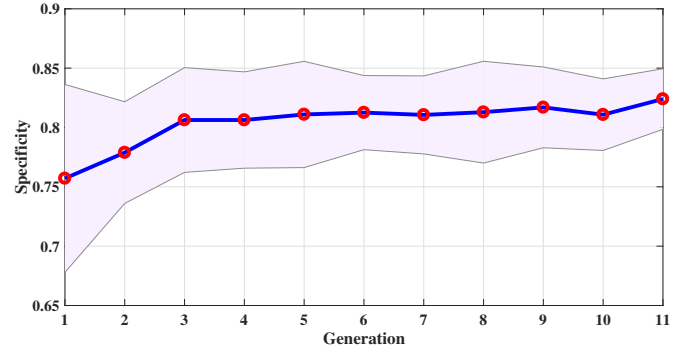


Fig. 5: Specificity of the radiomic sequencer overlaid by their modeling standard deviation over generations. As seen, the generalizability of radiomic sequencer increase generation by generation as the standard deviation of modeling decreases.

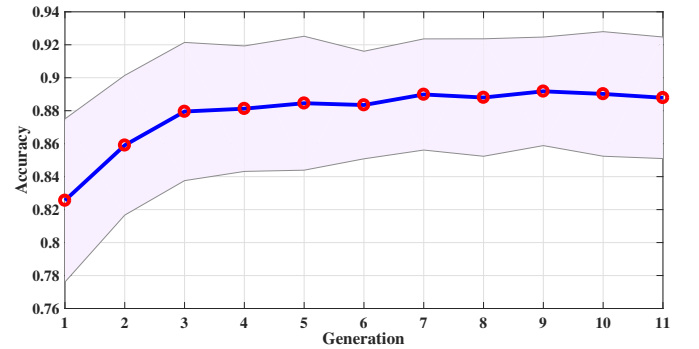


Fig. 6: Radiomic sequencers modeling accuracy over generations.

TABLE I: Radiomic sequence lengths and the modeling accuracies over generations. “A.N.F” stands for average number of filters in the sequencer and “R.S.L” column represents the average length of the radiomic sequence at each generation. Since the numbers are averaged over 10 folds of evaluation they are reported with one floating point precision. As seen while the radiomic sequences become more compact over generations, the modeling accuracy, sensitivity, and specificity are increasing.

	A.N.F.	R.S.L.	Sensitivity	Specificity	Accuracy
Gen.1	194.0	3104.0	0.8786	0.7570	0.8255
Gen.2	180.4	2886.4	0.9156	0.7788	0.8590
Gen.3	171.0	2736.0	0.9305	0.8063	0.8795
Gen.4	161.1	2577.6	0.9276	0.8062	0.8812
Gen.5	150.9	2414.4	0.9311	0.8109	0.8845
Gen.6	142.6	2281.6	0.9295	0.8125	0.8834
Gen.7	135.1	2161.6	0.9390	0.8105	0.8898
Gen.8	125.8	2012.8	0.9341	0.8129	0.8879
Gen.9	118.5	1896.0	0.9384	0.8169	0.8917
Gen.10	111.2	1779.2	0.9385	0.8107	0.8901
Gen.11	104.5	1672.0	0.9342	0.8239	0.8878

TABLE II: Comparison with state-of-the-art methods for lung cancer classification. As seen the proposed EDRS framework outperforms other methods in sensitivity, specificity, and accuracy.

	Sensitivity	Specificity	Accuracy
DARS [12]	0.8314	0.2018	0.7501
CNN-MIL [13]	–	–	0.7069
SNRS [15]	0.9107	0.7598	0.8449
DRS [16]	0.7906	0.7611	0.7752
EDRS	0.9342	0.8239	0.8878

IV. CONCLUSION

In this paper, we proposed a new evolutionary deep radiomic sequencer discovery framework to better uncover more efficient yet powerful radiomic sequencers for the purpose lung cancer classification. An evolutionary deep intelligence approach is incorporated within the discovery radiomics framework to evolve the underlying deep neural network architecture of the deep radiomic sequencer over multiple generations and discover a more efficient and generalized deep radiomic sequencer. The ultimate goal here is to synthesize a new deep neural network as the underlying core of radiomic sequencer with a fewer number of parameters which produce more concise radiomic sequences that can better capture the differences between healthy and cancerous lung tissue. Results show that by evolving and discovering more efficient radiomic sequencers, the diagnostic accuracy can be increased despite the limited number of training data. Experimental results demonstrate that the evolved deep radiomic sequencer discovered using the proposed evolutionary deep radiomic sequencer discovery approach can outperform other state-of-the-art radiomics-driven methods.

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