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Graph-based Rate Control in Pathology Imaging with Lossless Region of Interest Coding

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Abstract—The increasing availability of digital pathology images has motivated the design of tools to foster multidisciplinary collaboration among researchers, pathologists, and computer scientists. Telepathology plays an important role in the development of collaborative tools, as it facilities the transmission and access of pathology images by multiple users. However, the huge ?le size associated with pathology images usually prevents full exploitation of the collaborative telepathology system potential. Within this context, rate control (RC) is an important tool that allows meeting storage and bandwidth requirements by controlling the bit rate of the coded image. In this paper, we propose a novel graph-based RC algorithm with lossless region of interest (RoI) coding for pathology images. The algorithm, which is designed for block-based predictive transform coding methods, compresses the non-RoI in a lossy manner according to a target bit rate and the RoI in a lossless manner. It employs a graph where each node represents a constituent block of the image to be coded. By incorporating information about the coding cost similarities of blocks into the graph, a graph kernel is used to distribute a target bit budget among the non-RoI blocks. In order to increase RC accuracy, the algorithm uses a rate-lambda $(\mathbf{R}-\lambda)$ model to approximate the slope of the rate-distortion curve of the non-RoI, and a graph-based approach to guarantee that the target bit rate is accurately attained. The algorithm is implemented in the HEVC standard and tested over a wide range of pathology images with multiple RoIs. Evaluation results show that it outperforms other state-of-the-art methods designed for single images by very accurately attaining the target bit rate of the non-RoI.

Index Terms—rate-control, HEVC, pathology images, graphbased signal processing, region of interest coding.

I. INTRODUCTION

THE introduction of high-throughput slide scanners has made possible the digitization of microscope specimens to produce multi-giga pixel color images, which are usually called *whole-slide images* (WSIs). This has fuelled the emerging area of digital pathology imaging [1], [2].

An important aspect of digital pathology imaging is the development of efficient tools to foster multidisciplinary collaboration among researchers, pathologists (e.g., for interobserver concordance studies), and computer scientists (e.g., for development and validation of computer-aided diagnosis (CAD) systems). Telepathology plays an important role in the development of collaborative tools, as it facilities the transmission and access of pathology images by multiple users. Specifically, through the use of telepathology, pathologists can access and annotate pathology images stored in a central database, consult with distant experts, and compare annotations made by other pathologists. Similarly, computer scientists can access the ground truth provided by pathologists to design and refine their CAD systems. Such collaborative telepathology systems have been actively developed in various pathology laboratories and clinics in Europe, North America and Australia [3], [4], [5].

A key challenge that prevents fully exploiting the potential of collaborative telepathology systems is the huge file size associated with pathology images, which poses heavy demands on transmission resources. To this end, such systems initially transmit the pathology images at a low resolution to account for low bandwidth connections. The users can then select the regions of interest (RoIs), e.g., a cell, groups of cells or multiple tissue subregions, on which they would like to concentrate [6]. The system then transmits the RoIs at full resolution, i.e., at a higher bit rate, so the users can 1) add annotations to them, or 2) access any existing annotations. An important concern here is providing a fast and reliable transmission of the RoIs especially in low bandwidth environments. It is also important to guarantee that the RoIs are transmitted in a lossless manner, so that their clinical usage is not affected. Lossy compression in conjunction with lossless RoI coding provide an attractive solution for such cases. For instance, users with low bandwidth connections may access the RoIs at full resolution in a lossless manner while obtaining a view of the remaining regions (i.e., the non-RoI) in a lossy manner [7], [8], [9]. In this context, transmitting the necessary data at the bit rate imposed by the connection is of high importance. In other words, it is important to achieve lossless RoI coding while reducing the quality of the non-RoI according to a target bit rate. To this end, rate control (RC) is an important tool that allows meeting any bandwidth requirements. Specifically, RC allows controlling the bit rate of the non-RoI while minimizing its overall distortion. An accurate RC mechanism helps to improve the fidelity of the non-RoI, because spending too few bytes is trivially not optimal, while spending too many bytes forces truncation of the transmitted non-RoI, which may yield suboptimal fidelity.

Block-based predictive transform coding (PTC) methods, such as the ones used in modern video codecs [10], [11], have been shown to provide an excellent performance for lossless and lossy coding of medical images and videos [12], [13], [14]. For the particular case of medical imaging data, a very limited number of block-based PTC methods that combine RC and lossless RoI coding have been proposed. Among the most

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recent ones, the work of Chen et al. in [13] proposes a twolayer system in the High-Efficiency Video Coding (HEVC) standard [11], where the enhancement layer is combined with a base layer to losslessly decode the RoI, while the base layer is used to decode the non-RoI at a lossy quality. In [15], we propose an RC algorithm in HEVC for pathology images with lossless RoI coding. This particular algorithm encodes the non-RoI by using RC and a model that approximates the corresponding rate-distortion (R-D) characteristics.

In the more general context of natural imaging data, important block-based PTC methods that combine RC and RoI coding may be found in the literature [16]-[17]. The work in [16] presents a scalable RoI coding method for H.264/SVC that employs a control mechanism that adjusts the quality of the RoI and non-RoI enhancement layers. In [18], Chen et al. exploit the properties of the Human Visual System to design a foveated just-noticeable-distortion model that helps adjusting the quantization levels of RoI blocks in H.264/AVC. The work in [19] proposes a framework for RoI coding that uses a preprocessing step to replace non-RoI areas by known pixels, thus relying on the R-D optimization process to optimally encode the data. The work in [20] presents a region-based RC method aimed at improving the objective quality of highdynamic range sequences. A similar idea is presented in [21] for intra-predicted frames. In [22], the authors present an RoI coding approach for videoconferencing that uses RC to assign more bits to blocks depicting facial features. The work in [23] proposes an RC scheme for RoI coding of screen-content videos in H.264/AVC by employing several R-D models. In [17], Meddeb et al. propose an RC algorithm for RoI coding in HEVC aimed at videoconferencing. Their algorithm assigns more bits to faces by employing two distinct R-D models.

Within the context of block-based PTC methods, the constituent blocks of a pathology image are usually correlated. It is then highly advisable to exploit this correlation during RC to determine the bit budget allocation that results in the set of QPs that most accurately attains a target bit rate at the highest reconstruction quality possible. The constituent blocks are then highly amenable to be represented as graphs, whose structure can be exploited during RC. Specifically, blocks can be represented as the nodes of an undirected graph and their similarities, in terms of their coding costs and region they depict, i.e., RoI vs. non-RoI, can be represented as the weight of edges that connect adjacent nodes. Based on such graph structure, we propose a graph-based RC algorithm with lossless RoI coding capabilities within the context of blockbased PTC of pathology images. Our algorithm losslessly encodes RoI blocks and allocates a target bit budget among non-RoI blocks by using a graph kernel, which allows for the distribution of this bit budget according to the weights assigned to the graph edges. Based on the bit budget allocation, the QP for each non-RoI block is then computed using a model that approximates the R-D characteristics of the non-RoI. Our proposed algorithm also employs the graph structure to guarantee that the target bit budget is respected as non-RoI blocks are sequentially encoded.

Our proposed graph-based RC algorithm updates the R-D model's parameters after encoding each non-RoI block [15],

and includes two important novel contributions:

- Our algorithm distributes a target bit budget across the non-RoI blocks using a diffusion process on the graph representing the blocks. The advantage of this graphbased approach is that the bit budget is allocated more precisely according to the coding costs of blocks. This results in increasing the bit budget of difficult-to-code regions, while reducing the bit budget of easy-to-code regions.
- 2) Our algorithm also uses a graph-based approach for bit budget re-allocation; i.e., to compensate for any inaccuracies in attaining the target bit budget of each block. This is particularly useful for very large images comprising several blocks, such as pathology images, since these inaccuracies tend to amount to a large value after encoding several blocks.

It is important to mention that important methods have been recently proposed for bit budget allocation [24], [25] and re-allocation [26] in RC. Although many of these methods perform very well, they are based on R-D models and optimization schemes designed for video sequences, and not single images. To the best of our knowledge, our algorithm is the first one to employ graph-based approaches in RC for bit budget allocation and to guarantee that an overall target bit budget is respected even when the target bit rate of each block is not accurately attained.

Our graph-based RC algorithm is implemented in HEVC for the coding of several pathology images using intra-prediction [27]. Results show that it outperforms other state-of-the-art approaches for single images by very accurately attaining the target bit rate of the non-RoI, while reducing blocky artifacts.

The rest of the paper is organized as follows. Section II briefly reviews the R-D model used to determine the QP of each block within the context of block-based PTC. Section III details our proposed graph-based RC algorithm. Section IV presents the results on several pathology images coded at a wide range of bit rates. Section V concludes this paper.

II. RATE-DISTORTION MODEL FOR RC

Most modern video and image codecs employ R-D models to approximate the distortion incurred in the reconstructed signal when coded in a lossy manner at a particular bit rate. Based on this approximation, the appropriate QP is then determined for the transform coefficients representing the signal [24], [25], [28], [15], [29], [30], [31].

In this work, we employ an R- λ model to determine the QPs of the constituent blocks of the image within the context of block-based PTC. This particular model, which is also employed in HEVC [31], has been shown to provide a good performance with low computational complexity. It approximates the slope of the R-D curve, λ , of a block:

$$\lambda = -\frac{\partial D}{\partial R} = \alpha R^{\beta},\tag{1}$$

where R and D are the rate and distortion, respectively; ∂ denotes a partial derivative; and α and β are parameters related to the R-D characteristics of the whole image, the so-called



Fig. 1: Pipeline of the proposed graph-based RC algorithm.

model's parameters [31]. The values of these parameters are usually computed from training data.

Once λ is computed for a block, the corresponding QP can be determined using a linear relationship [32]:

$$QP = a\log\lambda + b,\tag{2}$$

where a and b are also parameters whose values are computed from training data.

It is important to note that if the approximation in Eq. 1 is accurate, the target bit rate is accurately attained for each block and thus for the whole image. However, if this approximation is inaccurate, the overall bit budget may be overspent or underspent. To improve the accuracy in attaining the target bit rate, RC methods based on an R- λ model usually employ a mechanism to fine tune the model's parameters as blocks are sequentially encoded. Specifically, the model's parameters are updated using the actual bit rate, R_{act} , and the actual λ value, $\lambda_{act} = \alpha R_{act}^{\beta}$, of each encoded block. After encoding of each block, α and β are updated as a weighted average of the model's parameters used in previously encoded blocks [28]:

$$\alpha_{updated} = \alpha + \delta_{\alpha} (\ln \lambda - \ln \lambda_{act}) \alpha, \qquad (3)$$

$$\beta_{updated} = \beta + \delta_{\beta} (\ln \lambda - \ln \lambda_{act}) \beta, \qquad (4)$$

where $\delta_{\alpha} = 0.1$ and $\delta_{\beta} = 0.05$ are constants that control the updating process [28].

III. PROPOSED GRAPH-BASED RC ALGORITHM

The proposed graph-based RC algorithm is depicted in Fig. 1. It comprises a lossless mode and a lossy mode with RC. Based on an RoI mask, it determines which blocks comprise the RoI and non-RoI. All blocks in the RoI are encoded losslessly, while those in the non-RoI are encoded in a lossy manner according to a target bit rate by using RC. The algorithm determines the QP of each non-RoI block using an R- λ model, whose parameters are updated after encoding each block. The lossy mode comprises two main parts: 1) graph-based bit budget allocation and QP estimation and 2) graph-based bit budget re-allocation.

A. Graph-based bit budget allocation and QP estimation

Representing signals as graph allows accommodating complicated data domains and exploiting their underlying structure, which is usually not possible following traditional digital signal processing methods designed for data on regular Euclidean spaces [33], [34]. Although images are 2D regular signals, they can be formulated as graphs by connecting every pixel (node) with its neighboring pixels (nodes), and by interpreting pixel values as the values of the graph signal at each node. This formulation allows defining non-local and semi-local graphs representing the connectivity of pixels based not only on their physical proximity but also on the similarity of their values. Processing imaging data as graphs has already attained promising results for segmentation [35], [36] noise removal [37], [38], classification [39], the design of graph-based transforms and wavelet-like filter banks [40], and for compression of dynamic 3D point cloud sequences [41], multiview images [42], and pathology images [43].

Let us consider a pathology image to be encoded using block-based PTC by using angular intra-prediction, which is a type of prediction commonly used in many modern video codecs, such as HEVC [27], [12], [44]. After angular intraprediction, both RoI and non-RoI blocks comprise residual values, i.e., the difference between the predicted blocks and the original blocks. The similarities of these residual blocks can be represented as an undirected graph, $G = (V, E, \mathbb{A})$, where each node in the finite set V, i.e., $v_n \in V$, represents a residual block, E is the set of weighted edges connecting nodes, and \mathbb{A} is a symmetric weighted adjacency matrix. Each node in G is connected to its four adjacent neighboring nodes, i.e., following a 4-connected pattern. If there is an edge e = (i, j)connecting nodes i and j, the entry $\mathbb{A}_{i,j}$ represents the weight of the edge, where $\mathbb{A}_{i,j} = \mathbb{A}_{j,i}$. If nodes i and j are not connected by an edge, $\mathbb{A}_{i,j} = 0$. A large $\mathbb{A}_{i,j}$ value represents a high similarity between the blocks represented by nodes iand j, according to a given criterion. Fig. 2 shows a sample pathology image divided into 576 blocks in a 24×24 grid and the corresponding 4-connected graph representing these blocks.

In this work, we employ the coding cost, $c_b \in [0, 1]$, of block b and its class, q_b , as the metrics to define the similarity between a pair of adjacent blocks, where $q_b = 1$ if block b is in the RoI and $q_b = 0$ if is in the non-RoI. The coding cost c_b is computed as follows:

$$c_b = \frac{HAD_b}{HAD_{max}},\tag{5}$$

where HAD_b is the value of the Hadamard Transform of block b, which is calculated as the sum of absolute differences between block b and its corresponding intra-predictions in the horizontal and vertical directions [45]; and HAD_{max} is the maximum HAD value of all blocks in the image. The Hadamard Transform is a fast and accurate way to estimate the coding cost of a block to be encoded using angular intraprediction and is currently employed in the HEVC standard [11]. Note that according to Eq. 5, those blocks with the smallest HAD values, i.e., those easy-to-code blocks, are assigned the lowest coding cost, while those with the largest HAD values, i.e., those hard-to-code blocks, are assigned the highest coding cost, $c_b = 1$.

We define the weight of an edge connecting nodes i and j



Fig. 2: (a) Pathology image divided into $24 \times 24 = 576$ blocks. The RoI is delimited by the red contour. (b) Corresponding 4-connected graph representing the RoI (red) and non-RoI (black) blocks. (c) Coding costs of blocks used to encode the G component, ranging from 0 (lowest cost - black) to 1 (highest cost - white). (d) 4-connected graph with edges proportional to the corresponding weight ranging from small weights (thin lines) to large weights (thick lines).

via a thresholded Gaussian weighting function:

$$W_{ij} = \begin{cases} \frac{1}{2} (e^{-(\frac{1-c_i}{\theta})^2} + e^{-(\frac{1-c_j}{\theta})^2}), & \text{if } i \text{ and } j \text{ adjacent} \\ & \text{and } q_i = 0, \, q_j = 0 \\ 0, & \text{otherwise}, \end{cases}$$
(6)

where θ is a parameter that determines the width of the Gaussian weighting function. Fig. 2c shows the coding costs of the $24 \times 24 = 576$ blocks used to encode the green color (G) component of the pathology image depicted in Fig. 2a. Fig. 2d shows the corresponding 4-connected graph after computing the weight of edges according to Eq. 6. Note that the weight assignment of Eq. 6 disconnects the nodes representing the RoI from those representing the non-RoI, as a weight = 0effectively represents no connectivity. It is worth noticing two important aspects about the weight assignment in Eq. 6. First, an edge connecting two nodes representing low coding-cost blocks is assigned a small weight, while one connecting two nodes representing high coding-cost blocks is assigned a large weight. Second, within a region comprising blocks of similar coding costs, the edges connecting the corresponding nodes are assigned similar values. This is illustrated in Fig. 2d, where the dark regions in Fig. 2c have edges with small weights (i.e., thin lines) due to the low coding costs of the corresponding blocks. Moreover, these weights have similar values within these easy-to-code regions.

Let us now define the combinatorial Laplacian of graph $G = (V, E, \mathbb{A})$:

$$\mathbb{L} = \mathbb{D} - \mathbb{A},\tag{7}$$

where the degree matrix, \mathbb{D} , is a diagonal matrix whose *i*th diagonal element, d_i , is equal to the sum of the weights of all the edges incident to node *i*. Since \mathbb{L} is a real, symmetric matrix, it has a complete set of orthonormal eigenvectors with associated real, non-negative eigenvalues [46], [34]. The spectral decomposition of the Laplacian is $\mathbb{L} = \Phi \Lambda \Phi^T$, where $\Lambda = diag(\lambda_1, \lambda_2, ..., \lambda_{|V|})$ is the diagonal matrix with the eigenvalues ordered according to increasing magnitude $(0 = \lambda_1 < \lambda_2 \le \lambda_3 \le ... \le \lambda_{|V|})$ as diagonal elements and $\Phi = (\phi_1 | \phi_2 | ... | \phi_{|V|})$ is the matrix with the correspondingly ordered eigenvectors as columns [46], [34]. We can then define

a heat kernel by exponentiating the Laplacian matrix, \mathbb{L} , with time *t*:

$$H_t = e^{-t\mathbb{L}} = I - t\mathbb{L} + \frac{t^2}{2!}\mathbb{L}^2 - \frac{t^3}{3!}\mathbb{L}^3 + \dots,$$
(8)

where I is the $|V| \times |V|$ identity matrix. By substituting the Laplacian in Eq. 8 by its eigenspectrum $\mathbb{L} = \Phi \Lambda \Phi^T$, the heat kernel is expressed as:

$$H_t = \Phi e^{-t\Lambda} \Phi^T. \tag{9}$$

Eq. 9 is a graph kernel represented as a $|V| \times |V|$ symmetric matrix [47], [48], in which the element for nodes *i* and *j* of graph *G* is:

$$H_t(i,j) = \sum_{k=1}^{|V|} e^{-\lambda_k t} \phi_k(i) \phi_k(j).$$
 (10)

Under the assumption that an amount of *heat* is *injected* at a node *i* of the graph and is allowed to diffuse through the edges, the heat kernel describes the flow of heat across the edges of the graph with time. In this work, we use such a heat kernel to *diffuse* a target bit budget across the edges of graph *G* so that each non-RoI node, or block, is assigned a portion of that bit budget by considering their coding cost similarities with adjacent blocks and the overall structure of the graph. To this end, we initially assign each non-RoI node *b* an amount of heat energy equal to $E_b^{t=0}$:

$$E_b^{t=0} = \begin{cases} \frac{HAD_b}{\sum_{|A|} HAD_b}, & \text{if } b \in A\\ 0, & \text{otherwise} \end{cases},$$
(11)

where A is the set of non-RoI nodes adjacent to the RoI. We then let the initial heat energy diffuse through the graph edges as time t progresses until convergence, i.e., until the largest difference between the heat energy accumulated by any non-RoI node at time t and t - 1 is $\leq d_{heat}$, where d_{heat} is a small constant. This results in a relatively smooth distribution of heat energy across the non-RoI nodes without incurring in large heat differences among adjacent non-RoI nodes.

After convergence of the diffusion process, we compute the bit budget, Ω_b , that is assigned to block b:

$$\Omega_b = \lfloor \Omega_{non-RoI} \times \sum_{v=1}^{|V|} H_t(v,b) \rceil, \qquad (12)$$



Fig. 3: (a)-(h) Heat energy accumulated by the blocks of the image in Fig. 2 as time progresses according to a diffusion process on the corresponding graph. The amount of heat energy ranges from small (*cold* blocks - blue) to large (*hot* blocks - yellow).

where $\lfloor x \rceil$ is the nearest integer function on x, $\Omega_{non-RoI}$ is the overall bit budget of the non-RoI, and $E_b^t = \sum_{v=1}^{|V|} H_t(v, b)$ is the amount of heat energy accumulated by node b at time t. The corresponding rate for block b is then calculated as:

$$R_b = \Omega_b / N_b, \tag{13}$$

where N_b is the number of pixels in the block. Based on R_b , the value of λ for block b can then be computed using the model in Eq. 1. The QP for block b is then computed using the linear relationship in Eq. 2.

It is worth noticing that assigning the initial heat energy based on Eq. 11 allows for the encoding of the non-RoI with peripherally increasing quality around the RoI [8], [9]. In other words, the non-RoI blocks spatially close to the RoI are expected to be assigned a higher bit budget than that assigned to the non-RoI blocks spatially far from the RoI, particularly for small values of t. Fig. 3 shows the heat energy accumulated for non-RoI blocks as time progresses according to a diffusion process on the graph depicted in Fig. 2d. At time t = 0, a unit of heat energy is distributed among those non-RoI nodes surrounding the RoI according to their coding costs, while the other non-RoI nodes are assigned zero heat. At t = 1, one can observe that non-RoI blocks with low coding costs tend to accumulate relatively small amounts of heat energy. This is due to the weight assignment in Eq. 6, which prevents the heat energy from flowing into easy-to-code regions. At t = 7, however, the distribution of heat energy is relatively smooth across all non-RoI blocks according their distance to the RoI and coding costs.

B. Graph-based bit budget re-allocation

As explained in Section II, the actual number of bits used to encode each non-RoI block depends not only on the assigned bit budget but also on the accuracy of the R- λ model, i.e., on the accuracy of parameters α and β in representing the R-D characteristics of the non-RoI. To guarantee that the overall bit budget, $\Omega_{non-RoI}$, is respected and the target bit rate is attained, our algorithm fine tunes the model's parameters, α and β , after each non-RoI block is encoded, as detailed in Section II. However, despite this fine-tuning differences between the actual number of bits spent on each non-RoI block, b, and the corresponding target bit budget, Ω_b , may still arise. To further guarantee that the overall target bit rate is accurately attained, we employ a graph-based approach to re-allocate any underspent or overspent bit budget of non-RoI block b to those uncoded non-RoI blocks adjacent to b. To this end, we exploit the properties of the random walk matrix, \mathbb{P} , of the graph, $G = (V, E, \mathbb{A})$, representing the blocks:

$$\mathbb{P} = \mathbb{D}^{-1}\mathbb{A},\tag{14}$$

where entry $p_{i,j} = p_{j,i}$ describes the probability of going from node *i* to node *j* in one step of a Markov random walk on the graph.

Matrix \mathbb{P} provides information about how any underspent or overspent bit budget can be re-allocated to those uncoded non-RoI blocks adjacent to the current non-RoI block. Since matrix \mathbb{P} is calculated using matrices \mathbb{D} and \mathbb{A} , it inherently considers the coding costs similarities of blocks and the overall structure of graph G.

Let us consider an example 4-connected graph representing an image divided into $5 \times 5 = 25$ blocks, as depicted in Fig. 4, where blocks are sequentially encoded starting from non-RoI



Fig. 4: Sequential encoding of RoI and non-RoI blocks, represented as red and black nodes, respectively, of a graph. After encoding non-RoI block b, any underspent/overspent bit budget is re-allocated only to uncoded blocks adjacent to b, according to entries of the corresponding random walk matrix, \mathbb{P} , which is updated by sequentially removing from the graph nodes representing coded blocks.

block b = 1. Let us denote the actual number of bits used to encode non-RoI block b by $\widehat{\Omega}_b$ and the corresponding target bit budget by Ω_b . After encoding block b using $\widehat{\Omega}_b$ bits, the associated heat energy, \widehat{E}_b^t , can be expressed as:

$$\widehat{E}_b^t = \frac{\widehat{\Omega}_b}{\Omega_{non-RoI}}.$$
(15)

It then follows that if $\widehat{\Omega}_b \neq \Omega_b$, then $\widehat{E}_b^t \neq E_b^t$ due to the linear relationship in Eq. 15, where $\Omega_{non-RoI}$ is constant. In such a case, it is important to guarantee that the total heat energy, \widehat{E}_G^t , across all the nodes of the graph after encoding non-RoI block b is always equal to the initial amount of heat energy injected, $E_G^{t=0}$:

$$\widehat{E}_{G}^{t} = \sum_{v=1}^{|V|} \widehat{E}_{v}^{t} = E_{G}^{t=0} = 1.$$
(16)

Consequently, any overspending or underspending of Ω_b results in an apparent change of E_G^t [see Eq. 15]. In order to respect the overall bit budget, $\Omega_{non-RoI}$, Eq. 16 must be then satisfied after encoding each non-RoI block.

Let us assume that the first non-RoI block of the example in Fig. 4 is encoded using $\overline{\Omega}_1$ bits, where $\overline{\Omega}_1 < \Omega_1$. In other words, the target bit budget of block b = 1, Ω_1 , is underspent. To satisfy Eq. 16, the unused bits $\Omega_1 = \Omega_1 - \overline{\Omega}_1$ should be re-allocated among the uncoded (non-RoI) blocks adjacent to block b = 1 based on the entries of matrix \mathbb{P} . In this example, the uncoded (non-RoI) blocks adjacent to block b = 1 are blocks b = 2 and b = 6 (see Fig. 4). After re-allocating $\widetilde{\Omega}_1$, the new bit budget of block b = 2 is then $\overline{\Omega}_2 = \Omega_2 + (\widetilde{\Omega}_1 \times p_{1,2})$. Similarly, the new bit budget of block b = 6 is $\overline{\Omega}_6 = \Omega_6 +$ $(\Omega_1 \times p_{1,6})$, where $p_{1,2} + p_{1,6} = 1$ by definition of matrix \mathbb{P} . If block b = 2 is the next non-RoI block to be encoded, any bit budget difference, Ω_2 , should be then re-allocated only to its adjacent uncoded (non-RoI) blocks based on the entries of matrix \mathbb{P} , i.e., blocks b = 3 and b = 7, and not to block b = 31, which has already been coded (see Fig. 4). Consequently, matrix \mathbb{P} should be updated as blocks are sequentially encoded so that any nodes representing coded blocks be sequentially removed from G. This idea is illustrated in Fig. 4.

In general, any bit budget difference incurred after encoding non-RoI block b, $\tilde{\Omega}_b$, is re-allocated to the bit budget of its adjacent uncoded blocks, represented by set J, as follows:

$$\overline{\Omega}_{j} = \begin{cases} \max(\sigma \cdot \Omega_{j}, \Omega_{j} - (p_{b,j} \cdot |\widetilde{\Omega}_{b}|)), & \text{if overspending} \\ \forall j \in J \\ \min(\varsigma \cdot \Omega_{j}, \Omega_{j} + (p_{b,j} \cdot |\widetilde{\Omega}_{b}|)), & \text{if underspending} \end{cases}$$
(17)

where $\sigma = 0.95$, $\varsigma = 1.05$, $p_{b,j}$ is the $\{b, j\}$ entry of matrix \mathbb{P} , and $\sum_j p_{b,j} = 1$. Note that if non-RoI block *b* is adjacent to an uncoded RoI block *j*, probability $p_{b,j}$ is effectively 0 due to weight $W_{bj} = 0$, as defined by Eq. 6. Also note that $\sigma < 1$ and $\varsigma > 1$ guarantee that the bit budget Ω_j is not dramatically decreased if overspending or increased if underspending, respectively. In cases where $\tilde{\Omega}_b$ is not fully reallocated among blocks in set *J*, the bit budget re-allocation in Eq. 17 is iteratively applied to uncoded blocks adjacent to those in set *J* until Eq. 16 is satisfied.

After encoding non-RoI block b and re-allocating any bit budget difference, matrix \mathbb{P} is re-calculated by removing from G the node representing block b. In other words, after encoding block b, we compute the random walk matrix of graph $\tilde{G} =$ (\tilde{V}, \tilde{E}) , denoted by $\tilde{\mathbb{P}}$. The finite set of nodes, $\tilde{V} \subseteq V$, and the corresponding set of edges, $\tilde{E} \subseteq E$, are computed as follows:

$$V = V \setminus V_{encoded},\tag{18a}$$

$$\tilde{E} = E \setminus E_{encoded},\tag{18b}$$

where $V_{encoded}$ is the finite set of nodes of G representing coded blocks and $E_{encoded}$ is the corresponding set of edges incident on them.

We finish this section with some comments about the advantages of our graph-based RC algorithm to achieve quality consistency in the non-RoI. When computing QPs on a perblock basis based on coding costs, it is important to guarantee that adjacent blocks are reconstructed at similar qualities in order to reduce blocky artifacts, especially at very low target bit rates. These artifacts arise, for example, when a high-coding cost block is adjacent to a low-coding cost one and these two blocks are assigned bit budgets that result in very different QPs. To reduce these blocky artifacts, it is common to clip the QP of the current block in a narrow range determined by the QPs of previously coded adjacent blocks [28], [31]. This clipping process, however, may result in blocks encoded at bit rates that greatly differ from their target bit rates, which inevitably results in overspending or underspending the overall bit budget. Our graph-based RC algorithm avoids this problem by distributing the overall bit budget according to the structure of the graph representing the coding cost similarities of blocks. Specifically, our graph-based bit budget allocation results in a smooth bit budget distribution, as exemplified in Fig. 3h. This bit budget distribution helps to minimize blocky artifacts by smoothly transitioning from high coding-cost regions to low coding-cost ones. Moreover, our graph-based bit budget re-allocation allows to re-allocate any bit budget differences to uncoded non-RoI blocks according to the structure of the graph, which also helps to minimize blocky artifacts. Our graph-based RC algorithm, therefore, requires no clipping of QPs to attain quality consistency in the non-RoI.

IV. EXPERIMENTAL EVALUATION

We implement our graph-based RC algorithm in the HEVC standard using the reference software HM16.9 [49]. HEVC is a block-based PTC standard for video compression that allows for the compression of individual images by using the intraprediction coding mode, which can be employed in a lossless or a lossy fashion [27]. HEVC employs a tree structure to define the size of the constituent coding blocks (CBs) of the image. It employs the coding tree unit (CTU) as the basic unit, which consists of a luma coding tree block (CTB) and the corresponding chroma CTBs. For color images, one luma CB and two chroma CBs form a coding unit (CU) [11].

Current implementations of HEVC include an RC algorithm based on an R- λ model that takes into account the hierarchical coding structure of the standard to distribute a bit budget to each coding level, i.e., Groups-Of-Picture (GOPs), pictures and CUs; and to compute the best set of QPs to attain a target bit rate [31]. Specifically, a QP is computed for each largest CU (LCU). This RC algorithm also updates the model's parameters, α and β , as pictures and LCUs are encoded when using inter-prediction. Unfortunately, for the case of encoding of a single image using intra-prediction, the algorithm does not update the model's parameters after encoding each LCU, which usually results in large discrepancies between the target and actual bit rates if α and β do not accurately reflect the R-D characteristics of the image [15].

We evaluate four distinct approaches:

- 1) the current RC algorithm available in the HM reference software when α and β are computed *a priori* for each test image;
- the current RC algorithm available in the HM reference software when α and β are computed *a priori* for a large set of training images;
- 3) the RC algorithm proposed in [15] for HEVC, which is based on an R- λ model and updates the model's parameters after encoding each LCU; and
- 4) our proposed graph-based RC algorithm.

It is important to note that approaches 1 and 2 do not update the model's parameters, α and β , after encoding each LCU. However, approach 1 is expected to attain the target bit rate most accurately, as the model's parameters used by this approach for each image are computed using the same image as training data. For this reason, approach 1 is used as a baseline. It should also be noted that approach 1 requires compressing each test image, *a priori*, at a wide range of bit rates in order to determine their specific R-D characteristics and the corresponding model's parameters, which is not practical.

The accuracy of all evaluated approaches is computed in terms of the bit-rate error (BRE), which measures how accurately the target bit rate is attained; negative numbers indicate underspending $\Omega_{non-RoI}$, while positive numbers indicates overspending $\Omega_{non-RoI}$.

A wide range of pathology images with a single or multiple RoIs are evaluated, as tabulated in the first three columns of Tables I and II. These images are available through the Center for Biomedical Informatics and Information Technology of the US National Cancer Institute [50]. The test images are compressed using intra-prediction as a single RGB frame in 4:4:4 format with an LCU size of 64×64 samples. The HM reference software is modified in order to allow for lossless RoI coding in approaches 1 and 2. This is done by feeding residual blocks depicting the RoI directly to the entropy coder and by-passing any processing that affects the perfect reconstruction of these blocks. The LCUs representing the RoIs and the non-RoI are signalled to the encoder and decoder by a binary mask, which is computed a priori by manually delineating the RoIs. Any LCU that contains RoI pixels is considered as part of the RoI. A variety of target bit rates, expressed in terms of bits per pixel per component (bpppc), is used to compress the non-RoI of each of these test images, ranging from 0.067 bpppc to 2.0 bpppc. All images are 8 bpppc.

Fig. 5 depicts four of the test images and the corresponding heat energy accumulated by each of the constituent blocks after convergence of the diffusion process. It can be seen that our graph-based RC algorithm distributes the heat energy smoothly across all non-RoI blocks even when multiple RoIs are defined. Note that image LYMP3 includes sections depicting no tissue. In this case, the diffusion process prevents the corresponding blocks from accumulating a large amount of energy, since these smooth white sections are very easy to encode. This is evident in the lower left corner of Fig. 5g.

Average absolute BRE values of all evaluated approaches are tabulated in Tables I and II, along with the maximum and minimum absolute BRE values attained in each case, and the values attained per tissue type and for all tissue types. The last row of Table II also tabulates results for all the test images. Approach 1 attains the best performance, with average absolute BRE values very close to zero for all tissue types. Let us recall that approach 1 is the baseline approach and is evaluated only to show the accuracy of the current RC algorithm in HEVC when the appropriate model's parameters are used. Since this approach requires computing these parameters a priori, its applicability is very limited. Note however that for image KIRC4 (see Table II), approach 1 attains a maximum absolute BRE of 26.464%, which is attained at the very low target bit rate of 0.067 bppc. Since the model's parameters used by this approach are obtained for the

TABLE I: Characteristics of SKNF, END, LNGF, and ES images, and absolute BRE values (%) of all approaches

ID	Dimensions	р т	Approach 1 (baseline)			Approach 2			Approach 3			Proposed		
		KOI	avg	min	max	avg	min	max	avg	min	max	avg	min	max
Skin tissue. SKNF: skin fibroblast														
SKNF1	3200×2816	5	0.022	0.000	0.037	88.513	27.653	176.450	92.903	0.001	310.658	0.945	0.079	1.344
SKNF2	4096×3328	3	0.110	0.000	3.216	74.390	22.272	140.645	74.128	0.000	281.883	0.726	0.276	0.919
SKNF3	1600×2560	1	0.021	0.000	0.057	69.501	22.090	124.974	22.558	0.025	78.589	0.695	0.222	7.981
SKNF4	1280×4160	2	0.013	0.001	0.035	101.530	27.134	160.933	7.508	0.000	92.677	0.166	0.010	0.932
SKNF5	3328×3072	2	0.011	0.001	0.042	89.936	32.508	186.243	0.012	0.001	0.078	0.051	0.003	0.329
SKNF6	4160×1280	3	0.033	0.003	0.099	56.741	12.428	107.813	0.758	0.000	16.673	0.151	0.075	0.342
SKNF7	4096×3200	4	0.015	0.003	0.026	73.022	18.520	143.394	3.773	0.003	39.542	0.346	0.014	0.581
SKNF8	1920×2880	1	0.013	0.000	0.092	79.595	17.754	124.812	52.571	0.001	493.100	0.368	0.000	4.735
SKNF9	3392×2280	4	0.019	0.003	0.042	75.718	24.395	157.961	37.846	0.002	274.435	0.197	0.015	1.059
SKNF10	3520×2880	1	0.013	0.000	0.039	86.785	30.786	195.552	69.223	0.001	230.169	0.483	0.001	4.009
All SKN	F images		0.027	0.000	3.216	79.573	12.428	195.552	36.128	0.000	493.100	0.413	0.000	7.981
Endometrial tissue. END														
END1	2880×3200	4	0.016	0.001	0.050	58.477	7.397	130.567	25.418	0.025	190.371	0.411	0.022	-0.229
END2	3200×2816	3	0.015	0.001	0.042	63.827	5.810	166.758	26.910	0.003	211.514	0.532	0.062	1.920
END3	3072×2112	3	0.023	0.000	0.078	104.654	38.330	228.439	5.004	0.001	30.545	0.381	0.015	0.755
END4	3072×1920	2	0.010	0.000	0.037	102.863	40.558	218.528	125.714	0.006	1050.340	0.731	0.286	2.202
END5	4096×2368	1	0.036	0.002	0.084	100.585	33.183	234.546	149.344	0.002	1353.582	0.409	0.159	1.370
END6	2280×2112	2	0.016	0.003	0.032	36.723	5.582	72.883	48.888	0.003	294.768	0.289	0.059	1.370
END7	1280×4096	2	0.017	0.001	0.039	43.772	5.700	90.470	60.552	0.012	814.534	0.521	0.077	1.829
END8	2112×2816	4	0.014	0.000	0.046	67.466	8.905	112.454	9.307	0.001	133.010	0.327	0.007	1.211
END9	2816×3200	2	0.015	0.001	0.031	69.745	22.168	143.642	7.812	0.003	111.774	0.155	0.007	0.362
END10	3200×2880	1	0.017	0.000	0.050	92.653	37.843	191.037	1.971	0.000	28.569	0.279	0.087	0.754
All END	images		0.018	0.000	0.084	74.076	5.582	234.546	46.092	0.000	1353.582	0.403	0.007	2.202
Lung tiss	sue. LNGF: lun	g fibro	oblast											
LNGF1	3072×3840	2	0.006	0.001	0.017	59.009	17.330	118.868	4.453	0.001	13.384	0.112	0.042	0.378
LNGF2	3840×1920	5	0.017	0.000	0.054	72.731	14.143	154.644	39.825	0.031	193.198	0.834	0.351	1.720
LNGF3	3520×2880	1	0.010	0.000	0.027	98.892	33.136	204.011	27.781	0.000	151.635	0.291	0.020	0.645
LNGF4	2816×4800	5	0.007	0.000	0.014	57.582	7.736	144.040	0.186	0.000	4.840	0.063	0.006	0.221
LNGF5	$2816{\times}2560$	1	0.013	0.000	0.027	30.549	0.892	78.859	0.155	0.000	4.476	0.018	0.003	0.077
LNGF6	3392×2560	2	0.010	0.000	0.019	50.959	3.664	107.008	0.192	0.000	2.620	0.182	0.016	0.382
LNGF7	2816×2560	1	0.016	0.002	0.032	44.441	5.270	82.741	0.240	0.000	2.684	0.099	0.001	0.251
LNGF8	1600×3328	3	0.017	0.000	0.076	37.172	7.472	70.989	1.369	0.000	35.469	0.062	0.011	0.262
LNGF9	3200×3520	3	0.014	0.000	0.031	75.723	29.400	173.309	29.990	0.005	180.836	0.157	0.029	0.614
LNGF10	4096×1600	1	0.018	0.000	0.080	58.640	11.305	103.275	0.530	0.000	15.198	0.069	0.001	1.720
All LNG	F images		0.013	0.000	0.080	58.570	0.892	204.011	10.472	0.000	193.198	0.189	0.001	1.720
Embryon	nic tissue. ES: e	mbryc	onic stem	cells										
ES1	3200×2880	2	0.018	0.000	0.051	84.481	36.141	160.161	45.602	0.002	211.894	0.555	0.115	1.153
ES2	3328×4096	3	0.011	0.001	0.024	81.619	24.380	150.337	67.626	0.004	188.937	0.600	0.008	0.870
ES3	3328×3328	3	0.014	0.000	0.053	106.543	41.747	225.338	29.127	0.001	520.424	0.823	0.190	2.387
ES4	4480×3200	6	0.075	0.000	2.102	106.302	41.151	213.199	24.751	0.000	277.427	0.643	0.000	1.180
ES5	3200×3200	1	0.018	0.000	0.091	59.765	23.418	131.989	31.364	0.001	109.611	0.501	0.079	1.601
ES6	2560×2816	4	0.014	0.000	0.080	75.480	33.913	148.534	16.288	0.000	128.471	0.508	0.006	0.989
ES7	3520×4096	5	0.028	0.001	0.071	62.670	22.782	119.238	1.208	0.000	16.403	0.070	0.004	0.292
ES8	4480×4480	2	0.003	0.001	0.008	60.994	20.765	113.633	4.381	0.000	30.130	0.111	0.045	0.404
ES9	4160×4160	5	0.003	0.000	0.016	/5.899	29.067	131.535	2.007	0.000	22.876	0.104	0.005	0.355
ES10	5120×4480	3	0.006	0.000	0.028	66.311	23.558	132.134	2.651	0.000	42.384	0.054	0.010	0.222
All ES in	nages		0.020	0.000	0.271	78.287	29.223	153.063	23.191	0.001	157.787	0.385	0.051	0.941
All imag	es in Table I		0.019	0.000	3.216	72.627	0.892	234.546	28.971	0.000	1353.582	0.347	0.000	7.981
D		1.4												

Best results among approaches 2, 3 and the proposed algorithm are highlighted in bold for

whole image, i.e., non-RoI and RoIs, it is evident that when used to compress only the non-RoI, these parameters do not accurately represent the R-D characteristics of this region. As a consequence, approach 1 tends to perform poorly for this image at this very low target bit rate.

As expected, approach 2 attains the worst performance across all tissue types since this approach does not update the model's parameters after encoding each LCU. Consequently, if these parameters do not accurately reflect the R-D characteristics of the non-RoI, this approach fails to compute the appropriate set of QPs needed to attain the target bit rate.

Approach 3 performs better than approach 2 since the model's parameters are updated after encoding each LCU. This approach can also attain minimum absolute BRE values very close to zero for some of the target bit rates, as tabulated in the

corresponding columns labeled *min*. However, it still attains very high average absolute BRE values for the majority of the test images. One reason for its poor performance is the fact that this approach has no mechanism to compensate for any bit budget differences incurred as blocks are sequentially encoded, which inevitable results in underspending or overspending the overall bit budget. This is an important disadvantage for pathology images, which are very large images comprising several blocks, since the individual inaccuracies of all the blocks tend to amount to a very large value. Moreover, approach 3 heavily relies on the accuracy of the R-D model and the bit budget allocation process, which is based on the coding cost of the current block, the coding costs of already compressed non-RoI blocks and the number of bits left in the bit budget without considering the coding cost similarities

TABLE II: Characteristics of KIRC, PANC, GBM, COAD, and LYMP images, and absolute BRE values (%) of all approaches

	D' '	D I	Approach 1 (baseline)			Approach 2			Approach 3			Proposed		
ID	Dimensions	ROI	avg	min	max	avg	min	max	avg	min	max	avg	min	max
Kidney tissue. KIRC: clear cell carcinoma														
KIRC1	4480×3200	3	0.008	0.000	0.045	110.100	30.893	220.927	42.256	0.001	390.622	0.241	0.056	1.299
KIRC2	4160×4480	2	0.018	0.002	0.036	86.347	26.181	175.229	5.312	0.003	88.297	0.198	0.012	0.403
KIRC3	1600×3328	3	0.014	0.001	0.038	48.807	3.195	124.374	89.602	0.088	568.023	6.613	1.443	39.125
KIRC4	3520×2880	1	0.891	0.001	26.464	97.763	33.758	218.182	32.788	0.005	291.756	0.821	0.123	3.081
KIRC5	1600×1920	3	0.023	0.000	0.103	52.562	1.984	138.571	90.502	0.019	257.921	0.341	0.012	1.712
KIRC6	2816×1920	2	0.022	0.000	0.068	49.205	7.808	105.949	9.651	0.002	108.634	0.680	0.217	2.668
KIRC7	3072×2880	1	0.017	0.000	0.040	57.522	0.975	140.611	11.817	0.000	96.679	0.722	0.060	2.527
KIRC8	2560×2816	4	0.022	0.001	0.085	60.108	0.089	159.384	0.847	0.000	15.097	0.238	0.028	1.008
KIRC9	2816×4096	3	0.010	0.000	0.023	85.706	20.490	191.507	5.678	0.008	67.909	0.615	0.021	1.108
KIRC10	1280×3200	1	0.036	0.002	0.077	59.377	14.684	122.057	7.629	0.008	194.585	0.570	0.244	0.987
All KIRO	C images		0.106	0.000	26.464	70.750	0.089	220.927	29.608	0.000	568.023	1.104	0.012	39.125
Pancreatic tissue. PANC														
PANC1	4800×3200	1	0.007	0.000	0.039	67.425	18.349	143.388	2.546	0.002	18.398	0.202	0.043	0.671
PANC2	1600×2560	2	0.011	0.001	0.052	45.144	9.217	91.600	0.985	0.061	17.828	1.336	0.044	4.217
PANC3	3328×3072	1	0.009	0.000	0.020	78.221	25.212	184.838	0.572	0.001	9.334	0.225	0.023	0.565
PANC4	2816×3200	3	0.026	0.005	0.039	46.819	0.650	107.293	1.269	0.001	15.001	0.086	0.001	0.479
PANC5	1920×2880	2	0.025	0.001	0.116	37.998	2.249	80.314	3.494	0.002	10.669	0.223	0.005	0.962
PANC6	2240×4096	4	0.007	0.000	0.039	78.399	22.327	166.724	11.408	0.000	64.197	0.221	0.036	0.968
PANC7	3328×3072	1	0.013	0.001	0.021	84.014	21.676	203.571	102.393	0.009	889.886	0.126	0.000	0.692
PANC8	3520×2560	3	0.010	0.000	0.024	27.679	0.045	79.809	0.535	0.000	6.980	0.056	0.001	0.439
PANC9	2112×2816	1	0.010	0.000	0.037	82.975	8.342	166.817	1.114	0.001	11.215	0.077	0.000	0.396
PANC10) 3072×2816	1	0.013	0.001	0.019	84.792	26.466	233.912	0.448	0.003	9.228	0.037	0.000	0.306
All PAN	C images		0.013	0.000	0.116	63.347	0.045	233.912	12.476	0.000	889.886	0.259	0.000	4.217
Brain tis	ssue. GBM: glio	blastor	na multif	orme										
GBM1	4480×3840	3	0.735	0.004	1.824	78.673	2.019	298.189	6.675	0.016	42.022	0.264	0.142	1.456
GBM2	3392×3072	1	0.006	0.000	0.033	46.117	0.186	144.933	19.984	0.000	137.293	0.015	0.000	0.074
GBM3	3520×2880	2	0.028	0.005	0.037	84.557	23.363	220.511	110.748	1.963	427.996	0.724	0.383	2.054
GBM4	2880×2816	4	0.017	0.002	0.035	123.321	33.411	319.569	0.390	0.000	5.800	0.129	0.010	0.647
All GBM	1 images		0.197	0.000	1.842	83.167	0.186	319.569	34.449	0.000	427.996	0.283	0.000	2.054
Colon ti	ssue. COAD: co	olon ad	enocarcir	юта		•								
COAD1	4096×3840	2	0.003	0.000	0.014	54.157	13.098	122.594	41.432	0.000	177.730	0.154	0.041	0.687
COAD2	2816×4480	3	0.010	0.004	0.019	52.397	0.077	134.907	1.936	0.001	9.374	1.611	0.089	4.712
COAD3	3840×3200	2	0.013	0.001	0.053	40.036	0.003	116.890	2.572	0.000	15.764	0.093	0.007	0.840
All COA	D images		0.009	0.000	0.053	48.863	0.003	134.907	15.313	0.000	177.730	0.619	0.007	4.712
Lymphatic tissue, LYMP: lymphoma														
LYMP1	1280×1280	1	0.042	0.001	0.097	36.771	1.627	78.672	9.374	0.004	87.621	0.673	0.281	5.630
LYMP2	1920×3840	2	0.047	0.002	0.084	27.684	0.045	139.748	0.128	0.001	1.322	0.166	0.009	0.571
LYMP3	4480×4480	3	0.064	0.000	0.364	40.198	0.256	131.634	19.990	0.000	162.425	0.361	0.020	2.293
All LYP	M images	-	0.051	0.000	0.364	34.884	0.045	139.748	9.831	0.000	162.425	0.400	0.020	5.630
All imag	es in Table II		0.080	0.000	26.464	61.960	0.003	319.569	21.881	0.000	889.886	0.533	0.000	39.125
A 11 inc	an in Tables I	und II	0.050	0.000	26 161	70 124	0.002	210 560	00 526	0.000	1252 502	0.450	0.000	20 125
All imag	es in Tables I a	па п	0.050	0.000	20.404	/0.124	0.003	519.309	22.336	0.000	1333.382	0.459	0.000	39.125

Best results among approaches 2, 3 and the proposed algorithm are highlighted in bold font

of adjacent blocks [15]. Consequently, approach 3 can easily fail if the model's parameters or the bit budget allocation is inaccurate. Note however that for some of the test images; i.e., SKNF5, LYMP2 and PANC2, approach 3 attains a very good performance. This indicates that the updating process results in a set of model's parameters that accurately represent the R-D characteristics of the non-RoI of these images.

Our proposed graph-based RC algorithm attains a consistent performance for all tissue types with the lowest average absolute BRE values. Specifically, the average absolute BRE value attained by our algorithm for all test images is 0.459%, which is much lower than that attained by Approach 3 (22.536 %) and Approach 2 (70.124 %). The minimum and maximum absolute BRE values attained by our algorithm are also very close to zero for all of the test images. Note that for image KIRK3, the maximum absolute BRE values attained by our algorithm and approach 3 are 39.13% and 568.02%, respectively, which are attained at very low bit rates (< 0.133 bpppc). These very high absolute BRE values can be explained by the fact that although both approaches update the model's parameters after encoding each LCU, the limited range of QP values available in HEVC makes it very challenging to accurately attain very low target bit rates for each LCU if the initial model's parameters are very different from those that accurately describe the R-D characteristics of the non-RoI. However, note that our algorithm still attains the lowest average absolute BRE for this image.

Fig. 6 shows the BRE values attained by all evaluated approaches plotted against bpppc values for test images SKNF6, END1, LNGF1, PANC5, and KIRC8. Note that the baseline approach, i.e., approach 1, indeed attains the lowest BREs with values very close to zero. Approach 3 attains very low BRE values for high target bit rates; however, it usually performs poorly for low target bit rates. This is particularly evident for image END1. Let us recall that approach 3 attains quality consistency in the non-RoI by clipping the QP of the current block in a narrow range determined by the QPs of previously coded adjacent blocks. When multiple RoIs are



Fig. 5: Four test images and the corresponding heat energy accumulated by each of the constituent blocks after convergence of the diffusion process: (a),(e) GBM2; (b),(f) COAD3; (c),(g) LYMP3; and (d),(h) SKNF1. The amount of heat energy is depicted by a distinct color ranging from blue (*cold* blocks) to yellow (*hot* blocks). Blue blocks represent the RoI.

defined, like in the case of image END1, non-RoI blocks are likely to be surrounded by multiple RoI blocks, which may prevent the clipping process from having enough QPs to compute an accurate narrow range to clip the current QP. This inevitably results in inaccurately attaining the overall target bit rate. Our graph-based RC algorithm, on the other hand, assigns each non-RoI block a bit budget based on their coding costs similarities with adjacent blocks. These similarities are represented by the structure of the graph, G, representing the blocks. Therefore, when multiple RoIs are defined, the QP selection of a block only depends on the corresponding assigned bit budget. Moreover, any bit budget differences are re-allocated among uncoded blocks based on the structure of the same graph, G, which guarantees that the target bit rate is accurately attained.

Our graph-based RC algorithm consistently attains very low BRE values across all target bit rates and images plotted in Fig. 6. For image END1, which depicts four RoIs, our algorithm attains BRE values very close to zero, with a maximum absolute BRE value of only 1.375% (see Fig. 6d).

Fig. 7 shows a reconstructed section of the non-RoI of image LYMP2 encoded at the very low target bit rate of 0.133 bpppc, which is a low target bit rate at which the BRE values attained by our graph-based RC algorithm and those attained by approach 1 and approach 3 are the most similar. Note that our algorithm produces less blocky artifacts thanks to the graph-based bit budget allocation and re-allocation processes, both of which take into account the coding cost similarities of blocks. Blocky artifacts are more evident in the images reconstructed by approaches 1 (BRE = -0.005%) and 3 (BRE = -0.006%), despite the fact that their BRE values are closer

to zero than that of our algorithm (BRE = -0.439%). These evident blocky artifacts are mainly due to the bit budget assignment, which does not consider the coding cost similarities of adjacent blocks, therefore resulting in adjacent blocks being compressed at very different qualities despite the clipping process used to attain quality consistency. The Peak Signal-to-Noise Ratio (PSNR) values attained at this low target bit rate for the $\{R, G, B\}$ color components of the non-RoI of this image are $\{28.71, 27.62, 28.57\}$ dB, $\{28.44, 27.73, 28.50\}$ dB, and $\{28.55, 27.99, 28.60\}$ dB for approach 1, approach 3 and our algorithm, respectively.

A. Applicability to other medical images

The proposed graph-based RC algorithm is suitable for other medical images. However, it is particularly useful for coding very large medical images, such as pathology images. As previously discussed, when the number of blocks needed to encode an image is very large, RC tends to perform very poorly if there is no mechanism to compensate for the inaccuracies incurred after encoding each block, since the individual inaccuracies tend to amount to a large value.

We have tested our algorithm in other medical images. Specifically, 20 MRI and CT slices, with sizes ranging from 256×256 to 1024×1024 pixels and up to three RoIs. For these relatively small images, our algorithm attains very similar results to the average results reported in Tables I and II; i.e., average absolute BRE values of only 0.215 %. For these medical images, approach 3 attains accurate results (average absolute BRE values of 2.455 %), as the number of blocks needed to encode them is not very large, and therefore the



Fig. 6: BRE values (%) of the evaluated approaches for various bit rates (bpppc). (a),(b) SKNF6; (c),(d) END1; (e),(f) LNGF1; (g),(h) PANC5; and (i),(j) KIRC8. Plots in the right depict the same results as those in the left over a small range of BRE values centered at 0%.



Fig. 7: Reconstructed non-RoI section of test image LYMP2 encoded at 0.133 bpppc using (a) approach 1, (b) approach 3, and (c) the proposed graph-based RC algorithm.

inaccuracies in attaining the target bit rate of each block do not amount to a large value.

B. Implementation details

This section discusses the numerical implementation of our graph-based bit budget allocation. The heat kernel in Eq. 8 requires computing the complete eigenspectrum of the Laplacian matrix, L, which may be computationally expensive for very large graphs. For example, the graph for test image ES10 comprises $80 \times 70 = 5600$ nodes, when blocks of 64×64 samples are used. However, the Laplacian matrices of the graphs of all test images are symmetric, positive-definite, and very sparse. We take advantage of this fact to reduce the computational complexity by using the Krylov subspace projection technique [51], which is an iterative method for sparse matrix problems. This particular technique allows to approximate $e^{tA} = e^{-t\mathbb{L}}$ by an element of the Krylov subspace $\kappa_m \equiv span\{tA, (tA)^2, ..., (tA)^{m-1})\},$ where $m \ll |\mathbb{L}|$. The heat kernel in Eq. 8 is then computed using the following approximation:

$$e^{-t\mathbb{L}} \approx \mathcal{V}_m e^{t\mathcal{H}_m} \tau_1,$$
 (19)

where \mathcal{V}_m are the orthonormal basis of the Krylov subspace κ_m , \mathcal{H}_m is the upper Hessenberg matrix resulting from the Arnoldi process, and τ_1 is the first column of the identity matrix I_m .

V. CONCLUSION

This paper presented a new graph-based RC algorithm for RoI coding in pathology imaging within the context of blockbased PTC. The algorithm encodes the non-RoI in a lossy manner at a specific target bit rate and the RoI in a lossless manner. It employs a graph to represent the coding cost similarities of the constituent blocks of the image. Based on the structure of such graph, the algorithm distributes a target bit budget among the non-RoI blocks using a graph kernel. The target bit rate of the non-RoI is accurately attained by employing an R- λ model to sequentially approximate the R-D characteristics of the non-RoI as the constituent blocks are encoded. The structure of the graph is also exploited to guarantee that the target bit budget is respected by re-allocating any bit budget differences incurred after encoding each non-RoI block. The proposed algorithm is implemented in HEVC and compared to other RC algorithms designed to encode single images using block-based PTC with lossless RoI coding capabilities. Evaluations over a large variety of pathology images with multiple RoIs show that the proposed algorithm is capable of attaining the target bit rate very accurately while minimizing blocky artifacts in the reconstructed non-RoI.

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