

From classical to deep learning: review on cartilage and bon[e](http://crossmark.crossref.org/dialog/?doi=10.1007/s10462-020-09924-4&domain=pdf) segmentation techniques in knee osteoarthritis research

Hong‑Seng Gan1 · Muhammad Hanif Ramlee2 · Asnida Abdul Wahab³ [·](http://orcid.org/0000-0003-3222-1732) Yeng‑Seng Lee4 [·](http://orcid.org/0000-0003-3395-7338) Akinobu Shimizu[5](http://orcid.org/0000-0002-2719-5923)

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Abstract

Knee osteoarthritis is a major diarthrodial joint disorder with profound global socioeconomic impact. Diagnostic imaging using magnetic resonance image can produce morphometric biomarkers to investigate the epidemiology of knee osteoarthritis in clinical trials, which is critical to attain early detection and develop effective regenerative treatment/ therapy. With tremendous increase in image data size, manual segmentation as the standard practice becomes largely unsuitable. This review aims to provide an in-depth insight about a broad collection of classical and deep learning segmentation techniques used in knee osteoarthritis research. Specifcally, this is the frst review that covers both bone and cartilage segmentation models in recognition that knee osteoarthritis is a "whole joint" disease, as well as highlights on diagnostic values of deep learning in emerging knee osteoarthritis research. Besides, we have collected useful deep learning reviews to serve as source of reference to ease future development of deep learning models in this feld. Lastly, we highlight on the diagnostic value of deep learning as key future computer-aided diagnosis applications to conclude this review.

Keywords Bone segmentation · Cartilage segmentation · Knee osteoarthritis · Magnetic resonance imaging · Deep learning

 \boxtimes Hong-Seng Gan hongseng@unikl.edu.my

⁵ Institute of Engineering, Tokyo University of Agriculture and Technology, 2-24-16, Naka-cho, Koganei, Tokyo 184-0012, Japan

¹ Medical Engineering Technology Section, British Malaysian Institute, Universiti Kuala Lumpur, 53100 Gombak, Selangor, Malaysia

² Department of Clinical Sciences, Medical Devices and Technology Group (MEDITEG), Faculty of Biosciences and Medical Engineering, Universiti Teknologi Malaysia, 81310 Skudai, Johor, Malaysia

³ Faculty of Biosciences and Medical Engineering, Universiti Teknologi Malaysia, 81310 Skudai, Johor, Malaysia

⁴ Bioelectromagnetics Research Group (BioEM), Department of Electronic Engineering Technology, Faculty of Engineering Technology, Universiti Malaysia Perlis, 02600 Arau, Perlis, Malaysia

1 Introduction

Knee Osteoarthritis (OA) is a whole joint disease (Loeser et al. [2012\)](#page-45-0) caused by a multifactorial combination of biomechanical (Englund [2010\)](#page-42-0), biochemical (Sokolove and Lepus [2013\)](#page-48-0), systemic and intrinsic (Warner and Valdes [2016](#page-48-1)) risk factors. Often, the disease is associated with joint pain and progressive structural destruction of articular cartilage; and causes permanent physical impairment to the patients. In a recent literature update on OA epidemiology, knee OA has shown high prevalence rate across the globe (Vina and Kwoh [2018\)](#page-48-2). Besides, various studies have highlighted the harmful effect of knee OA on our economies in terms of countries' GDP losses (Hiligsmann et al. [2013\)](#page-44-0), direct healthcare cost burden (Palazzo et al. [2016\)](#page-46-0) and annual productivity cost of work loss (Gan et al. [2016;](#page-43-0) Sharif et al. [2017](#page-47-0)).

To date, the pathophysiology of knee OA is still not fully comprehended and there is a lack of efective cure to treat or halt the progression of knee OA (Favero et al. [2015\)](#page-43-1). Given that cartilage degradation is reversible at early stage, morphological alterations in articular cartilage and subchondral bone are identifed as two cardinal characteristics at the onset of knee OA development cycle. Studies have focused on biomarkers such as changes of cartilage volume, thickness and surface curvature (Collins et al. [2016](#page-42-1)) to quantify underlying morphological alternations. Ultimately, the goals are to capture the knee OA progression pattern, to develop effective disease modifying OA drug (DMOAD) and to design effective regenerative-based therapy/treatment (Zhang et al. [2016](#page-49-0)).

Literally, MR imaging technology is the central modality to analyze the progression and incidence of knee OA due to its' ability to protrude soft tissue property of knee joint (Eckstein and Peterfy [2016](#page-42-2)). Based on the literature, MR imaging sequences such as dual energy steady state (DESS), fast low angle shot (FLASH), spoiled-gradient echo (SPGR), gradient recalled echo (GRE), turbo spin-echo (TSE), fast spin-echo (FSE), spin-echo spectral attenuated inversion recovery (SPAIR) and T1-weighted imaging sequence with fat suppression (FS) or water excitation (WE) are commonly used in cartilage imaging to produce high resolution knee images. Figure [1](#page-1-0) shows several MR imaging sequences used in knee OA research. Selection of MR imaging sequence is vital in consideration of a few factors such as signal-to-noise ratio, contrast-to-noise ratio and scanning time.

Knee segmentation (see Fig. [2](#page-2-0)) plays paramount role to extract biomarkers from MR image (Eckstein and Wirth [2011](#page-42-3)). The biomarkers contain valuable information to characterize, stimuli and predict the incidence and progression of knee OA. Two longitudinal multicenter knee image datasets i.e. the Osteoarthritis Initiative (OAI) (Peterfy et al.

Fig. 1 Diferent MR imaging sequences produce knee images with varied tissue contrast characteristic display. **a** Coronal view of FLASH, **b** coronal view of TSE, **c** sagittal view of T2 weighted image, **d** sagittal view of DESS

Fig. 2 Development of 3D models of knee is prerequisite to knee OA quantifcation. **a** Knee bone model consists of patella (PB), femur (FB) and tibia (TB), **b** posterior view of bone model. **c** Knee cartilage model consists of patellae cartilage (PC), femoral cartilage (FC) and tibial cartilage (TC). **d** A left knee cartilage model with subregion labels i.e. medial and lateral femoral cartilage, MFC and LFC; and medial and lateral tibial cartilage, MTC and LTC

[2008](#page-46-1)) and Multicenter Osteoarthritis Study (MOST) (Roemer et al. [2010\)](#page-47-1) distribute free image data to researchers upon request. A smaller knee image dataset known as Pfizer Longitudinal Study (PLS) also ofers up to 706 MR images from 155 subjects to support knee OA research. In addition, there are two reputable open competitions to promote joint evaluation on knee segmentation models: Segmentation of Knee Image 2010 (SKI10) by MICCAI (Heimann et al. [2010\)](#page-44-1) and MRNet by Stanford University (Bien et al. [2018\)](#page-41-0).

Below, we have compiled a list of existing reviews on segmentation techniques of musculoskeletal tissues (see Table [1](#page-3-0)). In summary, there are fve highlights about these reviews:

- 1. Majority of the reviews concentrated on cartilage segmentation, and covered a diverse semiautomatic and fully automatic segmentation models, properties of MR imaging sequence, as well as advantages and drawbacks of these imaging sequences;
- 2. Deep learning on cartilage segmentation was frst described by Ebrahimkhani et al. ([2020](#page-42-4)), but was limited to fve publications only;
- 3. Comparison of performance among deep learning, semiautomatic and fully automatic segmentation models was not available;
- 4. The last review on bone segmentation was performed by Aprovitola et al. (2016), which did not cover deep learning;
- 5. None of current reviews provided any insight about the diagnostic value of deep learning in knee OA studies.

In recent years, deep learning (LeCun et al. [2015](#page-44-2)) becomes very popular in academia. Many reviews on deep learning has been published; covering various technical aspects such as architectures of deep learning variants (Dargan et al. [2019;](#page-42-5) Khan et al. [2020](#page-44-3); Shrestha and Mahmood [2019](#page-47-2)), useful data repositories for deep learning practitioners (Sengupta et al. [2020](#page-47-3)), deep learning libraries and resources (Raghu and Schmidt [2020](#page-46-2)), as well as advantages, disadvantages and limitations of deep neural network models (Serre [2019](#page-47-4)). We also compiled existing reviews on deep learning in medical image analysis: (Greenspan et al. [2016](#page-44-4); Hesamian et al. [2019;](#page-44-5) Litjens et al. [2017](#page-45-1); Lundervold and Lundervold [2019;](#page-45-2) Maier et al. [2019;](#page-45-3) Shen et al. [2017;](#page-47-5) Singh et al. [2020](#page-47-6); Zhou et al. [2019](#page-49-1))**.**

This review covers original research articles, book chapters, conference proceedings and symposium in knee cartilage and bone segmentation methods published from January 1st 1990 until now. The search was conducted via PubMed, IEEE Xplore, Science Direct, Google Scholar and arXiv. Keywords "Osteoarthritis", "Image", "Segmentation", "Deep Learning", "MRI", "Cartilage", and "Bone" were used during the review process. Figure [3](#page-4-0) illustrates the taxonomy of knee cartilage and bone segmentation method in this review.

The review aims to contribute in the following aspects:

- 1. This survey gathers existing reviews on musculoskeletal segmentation in Table [1](#page-3-0) to provide an overview about the recent development trend of knee segmentation
- 2. This survey collects existing reviews on technical aspects of deep learning and deep learning for medical image analysis. The objective is to promote bilateral knowledge transfer between deep learning and medical image analysis feld by providing suitable source of reference at the ease of readers;
- 3. Since knee OA was regarded as a "whole joint" disease, bone model plays an important role in successive cartilage segmentation. Thus, we performs an extensive survey on both knee cartilage and bone segmentation models;
- 4. This is the frst survey on deep learning-based knee bone segmentation used in knee OA research, and we put all related models under one special sub-section;
- 5. The survey provides an updated list of deep learning-based knee cartilage segmentation models under one special sub-section;
- 6. The survey compares the performance of classical and deep learning segmentation models in the perspective of statistical evaluation and quantifcation value of biomarkers;
- 7. The survey highlights on diagnostic values of deep learning in knee OA research by including related studies in prediction, detection and simulation.

The rest of this review is organized as follows: Sect. [2](#page-5-0) presents the pathogenesis of knee OA. Sections [3](#page-6-0) and [4](#page-18-0) reviews existing bone and cartilage segmentation models,

Fig. 3 Taxonomy of knee bone and cartilage segmentation methods

respectively. Section [5](#page-32-0) discusses performance of imaging biomarkers in quantitative morphometric analysis. Section [6](#page-38-0) discusses the diagnostic value of deep learning in knee OA research.

2 Pathogenesis of knee osteoarthritis

Destruction of cartilage is mainly due to the loss of chondrocytes (Charlier et al. [2016](#page-41-2)) and alteration in extracellular matrix (Maldonado and Nam [2013](#page-45-4)). When the damage worsens, a broad secondary changes such as development of osteophytes, remodeling of subchondral bone, meniscal degeneration and formation of bone marrow lesions (BMLs) are triggered. In the following sub-sections, we elaborate the involvement of articular cartilage and subchondral bone during the pathogenesis of knee OA.

2.1 Articular cartilage

Human articular cartilage comprises of dense layer of highly specialized chondrocyte, matrix macromolecules such as collagen and proteoglycans, and water. Since cartilage has low metabolic activities, it is extremely vulnerable to shear stress on its surface. Under normal circumstance, chondrocytes plays imperative role to synthesize the turnover and proliferation of these macromolecules whenever tissue damage is detected. The symbiosis relationship helps to maintain a healthy cartilage condition. In case of knee OA, the homeostasis between synthesis and breakdown of degraded extracellular matrix components is disrupted, which adversely afects the cell ability to maintain and restore cartilaginous tissues (Man and Mologhianu [2014](#page-45-5)).

Aggrecanases and collagenases are components of matrix metalloproteinase (MMP) which are responsible to degrade the aggrecan, a causal proteoglycan in cartilage repair process. Under normal circumstance, tissue inhibitor of metalloproteinases (TIMPs) are activated to inhibit MMP activity (Kapoor et al. [2011](#page-44-7)). When the symbiosis is disrupted, proteoglycan aggregation and aggrecan concentration will decrease as a result of overwhelming MMP. At the same time, structural changes in collagenous frameworks cause swelling in aggrecan molecules and increase in water content (Roughley and Mort [2014](#page-47-7)). These deteriorations reduce the stifness of matrix and ability of self-repair. Subsequently, death of chondrocytes would occur and contributes to signifcant cartilage damage. The destruction of matrix structure also leads to subchondral bone changes in terms of density, sclerosis, formation of cysts and osteophytes (Goldring and Goldring [2010](#page-43-2)).

2.2 Subchondral bone

Subchondral bone is a thin cortical lamellae located beneath the calcifed cartilage layer where its role is to facilitate the force distribution and reduce the shear stress on articular cartilage. For instance, adaptive process of bone modelling and remodeling play vital role in maintaining the good responsiveness of joint. Bone remodeling comprises of bone resorption by osteoclasts at damaged bone site and generation of new bone by osteoblastic precursors on the resorbed surface. Likewise, bone modeling continues to drive change in bone architecture and volume via direct apposition to existing bone surface due to skeletal adaption to the stressor. Together with articular cartilage, both components are actively preserving the homeostasis of healthy joint environment (Li et al. [2013](#page-45-6)).

When the strain threshold is beyond the normal adaptive process, disruption to normal bone modelling and remodeling cause delay in new bone formation which weaken the bone structure (Stewart and Kawcak [2018\)](#page-48-5). Subchondral bone volume and density changes are indicative biomarkers to the modifcation of bone architecture. As the pathological events progress, the subchondral bone plate becomes thicker, which afects the ability of articular cartilage to withstand mechanical loading. The deformation causes horizontal clefts within the deep zone of cartilage as well as other pathological features such as sclerosis, osteophytes, bone shape alternation and bone cysts (Barr et al. [2015](#page-41-3)). Even though our knowledge about the pathogenesis of knee OA is advancing, there are still much questions about the underlying mechanisms and their relationships which requires further clinical investigations (Sharma et al. [2013\)](#page-47-8).

3 Knee bone segmentation

Knee OA-afected bone endures consistent loss of mineralization, causing it sensitives to structural deformation (Neogi [2012](#page-45-7)). Some radiologically visible structural changes such as osteophytes, bone marrow lesions (BMLs) and subchondral bone attrition (SBA) are good biomarkers for OA-related clinical trials. A study has reported that subchondral BMLs were apparent across knee regions with increased biomechanical loading (Hunter et al. [2006](#page-44-8)) whereas other studies showed that development of BMLs was related to cartilage loss (Davies-Tuck et al. [2010;](#page-42-6) Neogi et al. [2009](#page-46-4); Wluka et al. [2009](#page-49-3)). Bone segmentation is needed to support the discovery and characterization of these biomarkers.

Specifcally, purposes of knee bone segmentation are refected in the following applications: to produce bone-cartilage interface (BCI) in order to extract cartilage tissue from bone surface (Fripp et al. [2007](#page-43-3); Kashyap et al. [2016;](#page-44-9) Yin et al. [2010\)](#page-49-4), to quantify and monitor the changes of bone shape and surface associated with structural deformations (Neogi et al. [2013](#page-46-5)), and to compute bone model to investigate the efect of biomechanical stress at diferent localized knee sites (Paranjape et al. [2019](#page-46-6)). An example of 2D bone structure and segmentation result is shown in Fig. [4](#page-6-1). Because knee bone has regular shape and big anatomical size, bone segmentation is easier than cartilage segmentation. At the end of this

Fig. 4 The position and anatomical size of knee bones compared to other tissues give advantages to knee bone segmentation. **a** Sagittal view of knee joint with femur (FB), tibia (TB) and patella (PB) at the center of image, **b** knee bone is the biggest structure of knee joint with consistent shape (white arrows: FB; red arrows: TB), **c** segmented femur (FB) and tibia (TB) usually have better boundary delineation

section, complete lists of classical and deep learning-based knee bone segmentation models were provided in Tables [2](#page-8-0) and [3](#page-10-0), respectively.

3.1 Deformable model‑based methods

An active contour is defned by a collection of points along the curve, $X(s) = (X(s), Y(s)), s \in [0,1],$ which is governed by either parametric or geometric information available in the image. Parametric (Cohen [1991](#page-42-7); Kass et al. [1988](#page-44-10)) and geometric (Caselles et al. [1993,](#page-41-4) [1997;](#page-41-5) Malladi et al. [1995](#page-45-8)) deformable models difer in terms of the evolving curves and surface representations. For instance, parametric deformable models represent curves and surfaces explicitly in their parametric form as an energy minimizing and dynamic force formulation, whereas geometric deformable models represent the evolving curves and surfaces implicitly as a function of level set.

Active contours model (ACM) (Kass et al. [1988\)](#page-44-10) is the benchmark deformable model in image segmentation. Deformation of active contour is equivalent to minimizing an energy function, ε (*X*), which comprises of internal and external spline force as shown below:

$$
\varepsilon(X) = \varepsilon_{\text{int}}(X) + \varepsilon_{\text{ext}}(X) \tag{1}
$$

The formulation aims to identify a parameterized curve that minimizes the weighted sum of both spline force. The internal spline force, $\varepsilon_{int}(X)$, controls the elasticity of contour deformation based on contour tension and rigidity. The external spline force, $\varepsilon_{\text{ev}}(X)$, matches the boundary of deformable model toward the targeted object. On the other hand, evolution of geometric curves is independent of parameterization. The model relies on geometric measures such as the unit normal and curvature along the normal direction to form the representation function. Given a moving curve $\gamma(p, t) = [X(p, t), Y(p, t)]$, where *p* is any parameterization, t is time, N is its inward unit normal and κ is its curvature, evolution of curve can be described as:

$$
\frac{\partial \gamma}{\partial t} = V(\kappa)N\tag{2}
$$

where $V(\kappa)$ is known as a speed function that determines the speed of curve evolution.

In addition, primary deformable model has been extended by incorporating prior shape information. Some prominent extensions include statistical shape model (SSM) (Heimann and Meinzer [2009\)](#page-44-11), active shape models (ASM) (Cootes and Taylor [1992\)](#page-42-8) and active appearance models (AAM) (Cootes et al. [2001](#page-42-9)). Intuitively, these deformable models usually involve training to acquire details of shape variability or appearance feature about the targeted object. The infusion of priori knowledge can be performed via manual interaction such as placing a set of landmark points to form a point distribution model (PDM).

Due to its shape consistency and size advantages, deformable model was extensively used in knee bone segmentation. These deformable models include active contour model (ACM) (Guo et al. [2011;](#page-44-12) Lorigo et al. [1998;](#page-45-9) Schmid and Magnenat-Thalmann [2008](#page-47-9)), statistical shape model (SSM) (Fripp et al. [2007;](#page-43-3) Seim et al. [2010](#page-47-10); Wang et al. [2014](#page-48-6)) and active appearance model (AAM) (Neogi et al. [2013;](#page-46-5) Williams et al. [2010b](#page-48-7)). Semiautomatic hybrid geodesic active contour was implemented in both Lorigo et al. [\(1998](#page-45-9)) and Guo et al. ([2011\)](#page-44-12). Classical active contours was sensitive to the location of contour placement (it would fail when the contour was placed too far from target object) and lacked the convergence to boundary concavities (Abdelsamea et al. [2015](#page-40-1)). Besides, it often leaked in the event of varied intensity across the trabecular bone areas and noisy boundary. Initially,

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ASD Average Surface Distance, RMSD Root Mean Square Surface Distance, SD Standard Deviation *ASD* Average Surface Distance, *RMSD* Root Mean Square Surface Distance, *SD* Standard Deviation

ASD Average Surface Distance, *IoU* Jaccard Index, *HD* Hausdorf Distance, *RMSD* Root Mean Square Surface Distance, *SD* Standard Deviation

texture information was added into the model to compensate the weakness of intensity gradient-based energy function (Lorigo et al. [1998](#page-45-9)). Then, a statistical overlap constrain was introduced to the active contour stopping function to overcome boundary leaking (Guo et al. [2011\)](#page-44-12). A performance comparison between both models showed that the later (Dice Similarity Coefficient (DSC): 0.94) outperformed the former (DSC: 0.89).

Fripp et al. ([2007\)](#page-43-3) built three separate 3D SSM models for femur, tibia and patella with adapted initialization from existing atlas. The surface related to the atlas was propagated to the knee image through afne transform obtained from aligning the atlas to the knee image. In total, there were 2563, 10,242 and 10,242 correspondence points on the surface of femur, tibia and patella, respectively. Then, pose and shape parameters of the propagated surface were trained to estimate the pose and shape variation inside the SSM (Fripp et al. [2007\)](#page-43-3). Similar automatic bone segmentation model was found in Seim et al. [\(2010](#page-47-10)), where SSMs of tibia and femur were generated. Since SSM could generate robust bone model, it was frequently used to extract BCI from surface of bone model. Another application of shape model was to predict the onset of radiographic knee OA. Neogi et al. [\(2013](#page-46-5)) trained the AAM by using 96 knees to learn the shape variation and graylevel texture of femur, tibia and patella. Then, these information were encoded as principal components. A total of 69, 66 and 59 principal components for femur, tibia and patella bone were created to generate the AAM models (Neogi et al. [2013](#page-46-5)).

3.2 Graph‑based methods

Graph-based method treats an image as a graph, $G = (V, E)$ where the pixel is denoted as node, $v \in V$ and the relationship between two neighboring nodes is denoted by edge, $e \in E \subseteq V \times V$. Every edge is assigned by a weight, *w*, which is extracted from value difference between two nodes v_i and v_j . Retrospectively, graph segmentation started to gain attention after the normalized cut (Jianbo and Malik [2000](#page-44-14)) and *s*∕*t* graph cuts (Boykov and Jolly [2001\)](#page-41-8) were published. In this context, the partition of graph is known as a "cut". A general graph-based binary segmentation will partition the graph into two subgraphs i.e. *g_m* and *g_n*, where *g_m* ∪ *g_n* = *V* and *g_m* ∩ *g_n* = ∅, by minimizing the degree of dissimilarity across g_m and g_n . We calculate the dissimilarity as the total weight of the edges that have been removed:

$$
cut(g_m, g_n) = \sum_{p \in g_m, q \in g_n} w(p, q)
$$
\n(3)

where v_{g_m} and v_{g_n} are nodes in two disjoint subgraphs.

In practice, achieving an optimal "cut" is a non-trivial task. The solution requires minimizing an energy function, which is known to be NP-hard. Wu and Leahy [\(1993](#page-49-6)) proposed to divide the graph into *K* sub-graphs based on Max-fow min-cut theorem. The theorem defnes a maximum fow from node *s* to node *t* is equivalent to the minimum cut value (minimal cost) that separates *s* and *t*. In order to obtain the optimal solution, the algorithm would recursively search for every potential cut that divide the two nodes with minimal cost (Wu and Leahy [1993](#page-49-6)). Nonetheless, the algorithm is biased to segmenting small fraction of nodes. Normalized cut has been proposed by Jianbo and Malik [\(2000](#page-44-14)) to address this problem.

The *s*∕*t* graph cuts for binary image segmentation was formulated based on maximum fow algorithm with addition seeds as hard constraint. Users need to mark some pixels as "foreground" or "background" to represent the designated terminal nodes *s* (source) and *t*

(sink), respectively. The aim is to attain an optimal cut that severs the edges between these two types of terminal nodes. Hence, a minimal cost may correspond to a segmentation with a desirable balance of boundary and regional properties (Boykov and Funka-Lea [2006](#page-41-9)). The segmentation energy of graph cuts, *E*(*A*), is defned as:

$$
E(A) = \lambda \sum_{p \in \mathcal{P}} R_p(A_p) + \sum_{\{p,q\} \in \mathcal{N}} B_{\{p,q\}} \cdot \delta(A_p, A_q)
$$
(4)

where $A = (A_1, \ldots, A_p, \ldots, A_{|\mathcal{P}|})$ is label vector assigned to pixel *p* in $\mathcal{P}, R_p(\cdot)$ is the regional term of *A* and *B* is the boundary term of *A* Coefficient $\lambda > 0$ controls a rel regional term of *A* and $B_{\{p,q\}}$ is the boundary term of *A*. Coefficient $\lambda \geq 0$ controls a relative importance of the regional term, $R_p(\cdot)$, versus boundary term, $B_{\{p,q\}}$. The regional term, $R_p(\cdot)$, assumes that the individual penalties for assigning pixel p to "foreground" and "background", correspondingly. For example, $R_p(\cdot)$ may reflect on how the intensity of pixel *p* fts into a known intensity mode (e.g. histogram) of the "foreground" and "background". Meanwhile, the boundary term measures the penalty of discontinuity between pixel *p* and *q*.

Other prominent graph-based segmentation methods include random walks (Grady [2006\)](#page-44-15), intelligent scissors (Mortensen and Barrett [1998\)](#page-45-12) and Live Wire (Falcao et al. [2000\)](#page-42-15). The segmentation model can be automatic or interactive. Several studies (Ababneh et al. [2011](#page-40-2); Kashyap et al. [2018](#page-44-16); Park et al. [2009;](#page-46-7) Shim et al. [2009b;](#page-47-12) Yin et al. [2010](#page-49-4)) have implemented graph cuts to extract knee bone from MR image. Shim et al. [\(2009b](#page-47-12)) has implemented semiautomatic graph cuts to segment femur, tibia and patella. To localize the search space during the segmentation, user needed to place scribbles on region of interest as hard constraint. The authors only compared the efficiency of graph cuts with manual segmentation and the model's accuracy performance was not available (Shim et al. [2009b](#page-47-12)). Besides, classical semiautomatic graph cuts model depend heavily on seeds to initialize and refne the segmentation, which led to substantial amount of manual intervention.

In Park et al. (2009) (2009) and Ababneh et al. (2011) (2011) , automatic graph cuts segmentation models were proposed. To replace manual seed deployment, extra priori information was required to complement the lack of discriminative power faced by classical graph cuts energy function. Park et al. [\(2009](#page-46-7)) proposed to incorporate shape obtained from shape template into their model, and decomposed translation, rotation and scale parameters for shape prior confguration. Then, branch-and-mincut algorithm was repetitively computed to optimize the decomposition. In addition, low intensities of bone tissues was taken as intensity prior to further improve the segmentation accuracy (Park et al. [2009](#page-46-7)). Ababneh et al. ([2011\)](#page-40-2) proposed a multi-stage bone segmentation framework. At initial stage, the image was divided into $n \times n$ square blocks and classified into background and non-background blocks based on a set of features extracted from training data. Then, these image blocks were treated as seeds to initiate the graph cuts algorithm while several GLCM-derived features were exported into the construction of energy function (Ababneh et al. [2011](#page-40-2)). Both improved graph cuts models have registered DSCs of 0.958 (Park et al. [2009\)](#page-46-7) and 0.941 (Ababneh et al. [2011](#page-40-2)).

3.3 Atlas‑based methods

An atlas is defned as a reference model with labels related to the anatomical structures. These labels contain useful priori information to describe certain anatomical structure. Example of priori information includes topological, shape and positional details of the structure, as well as spatial relationship between them. Atlas registration,

selection and propagation are three fundamental steps in atlas-based segmentation. Given precise point-to-point correspondence from an image to pre-constructed atlas, the methods are capable of segmenting image with poor relation between regions and pixel's intensities due to difuse boundary or image noise. The process of coordinate mapping is known as registration. For an image, *I*, and an atlas, *A*, the correspondence is defined as a coordinate transformation *T* that maps any specific image coordinates, $\boldsymbol{\mathbf{x}}$ in the domain of *I* onto the atlas, *A*. The mapping is given below:

$$
I(\mathfrak{x}) \to A(T(\mathfrak{x})) \tag{5}
$$

Overall, there are four atlas selection methods: single atlas, the best atlas, averageshape atlas and multiple atlas (Rohlfng et al. [2005\)](#page-47-13). Single atlas method uses an individual segmented image. The selection can be random or based on certain criterion such as quality of image. The best atlas chooses the most desirable atlas from a set of atlases. In order to identify an optimal segmentation from the results of diferent atlases, one could check the image similarity by using normalized mutual information (NMI) and magnitude of deformation after registration. Compared to previous methods, the averaged shape atlas maps all original individual images onto a common reference to produce an average image. Then, the original images are mapped onto the frst average to produce a new average. The mapping process occurs iteratively until convergence. Multiple atlases approach applies diferent atlases onto a raw image. Then, the segmentations are combined into a fnal segmentation based on "Vote Rule" decision fusion.

Several research groups have utilized multiple templates to perform knee bone segmentation (Dam et al. [2015;](#page-42-10) Lee et al. [2014](#page-44-13); Shan et al. [2014](#page-47-11)). Due to the overlapping tibiofemoral boundary after segmentation, direct cartilage segmentation was challenging. Therefore, an initial bone segmentation would serve as shape prior to guide successive cartilage segmentation. Lee et al. (2014) (2014) applied non rigid registration to align all templates to target image and selected the best matched template. Then, a locally weighted vote approach with local structure analysis was deployed to generate label fusion. Instead of intensity similarity metrics, the new voting scheme used cartilage model as local reference to generate probability of correspondence to compute the target label. As a result, it was able to avoid poor accuracy attributed to magnetic feld inhomogeneity (Lee et al. [2014\)](#page-44-13). The bone segmentation model has reported an average surface distance error of 0.63 mm for femur and 0.53 mm for tibia, which were lower than other bone-cum-cartilage segmentation models.

Dam et al. ([2015\)](#page-42-10) introduced a multiatlas pre-registration as a source of training before *k*NN-based classifcation of cartilage voxels. During the training process, a rigid registration would transform a given atlas to a common training space to enable the determination of region of interest (ROI) for each anatomical structure and feature extraction (Dam et al. [2015](#page-42-10)). Based on a set a features from Folkesson et al. ([2007\)](#page-43-5), *k*NN classifer would classify the voxels within the ROI instead of whole image. The structure-wise ROI identifcation reduced the computation cost of classifers but construction of atlas was a daunting task. Plus, segmentation accuracy would depend on several other factors, such as high quality registration to create precise structure-wise ROI and reliability of features used to perform classifcation. In this model, only tibia was segmented from knee images, which gave DSC of 0.975 on 30 training data.

3.4 Miscelleneous segmentation methods

Other knee bone segmentation models were found to be using edge and thresholding (Lee and Chung [2005\)](#page-44-17), ray casting (Dodin et al. [2011\)](#page-42-11), and level set (Dalvi et al. [2007;](#page-42-12) Gandhamal et al. [2017](#page-43-4)). Lee and Chung [\(2005\)](#page-44-17) proposed a multi-stage knee bone segmentation model with a series of edge detection, thresholding and contrast enhancement to enhance the contrast of bone edges and extract bone boundary information. The information was incorporated into region grow algorithm to perform a fnal segmentation. Then, the model was evaluated by using 40 knees but the presentation of result was not clear (Lee and Chung [2005\)](#page-44-17). Meanwhile, Dodin et al. [\(2011\)](#page-42-11) has imported the ray casting algorithm, which was typically used to create solid geometry model in computer graphic, into knee bone segmentation. The algorithm decomposed knee image into multiple surface layers via Laplacian operators. At each surface layer, the algorithm relied on a set of localization points known as "observers" as input to project the ray pattern at diferent angles and derived the cylindrical pattern of bone. The model was able to capture local bone irregularities such as osteophytes, which might be taken as error by shape-based methods. Eventually, the model was validated on a larger data size of 161 images and has reported DSC of 0.94 for femur and 0.92 for tibia (Dodin et al. [2011\)](#page-42-11).

In a similar fashion, Dalvi et al. (2007) (2007) (2007) and Gandhamal et al. (2017) (2017) (2017) have implemented level set in their knee bone segmentation models. Specifcally, Dalvi et al. ([2007\)](#page-42-12) used a region growing algorithm to undersegment the knee bone and followed by segmentation refnement via Laplacian level set algorithm. It was validated by using sensitivity (Sens) and specifcity (Spec) evaluation metrics on two healthy subjects. Gandhamal et al. ([2017\)](#page-43-4) proposed a hierarchical knee bone segmentation model. At preprocessing stage, the image intensity was transformed by a sigmoid-alike function to improve the contrast between soft and hard tissues. Then, two automatic seeds was identifed to represent the femur and tibia, and used to initiate a novel distance-regularized level-set evolution (DRLSE) algorithm to extract the bone regions. Once the evolution completed in one slice, geometric centroids of the level set function would be updated and used in successive slices. The limitation of this level-set function, for instance, was that it would stop if the area of the earlier segmented bone region was less than 100 pixels. Therefore, the algorithm would perform badly in very small bone region as well as when the bone was separated into two regions.

In conclusion, there were two key highlights. First, segmentation models in this category were independent on any training dataset or user interaction, which were diferent from shape-, atlas-, graph-, and machine learning-based methods. To ensure the model remained automatic, the learning gap was flled by a variety of preprocessing and image property learning procedures instead. Second, diferent strategies have been adopted to attain the fnal bone segmentation based on modifed image properties. While these models were able to overcome common anatomical features of bone, their suitability would depend heavily on tissue and image property of the image. Besides, some models required predefned threshold values. Consequently, it could be hard to generalize these models to dataset of larger size in comparison to modern machine learning techniques, especially deep learning.

3.5 Classical machine learning‑based methods

General machine learning framework comprises of data and prediction algorithm. The data is a set of observations used during the training and testing while prediction algorithm learns descriptive data pattern to perform certain classifcation task. Classical machine learning uses a set of discriminative handcrafted features to describe the object of interest and fed to a classifer to assign image pixel to the most likely label. The family of machine learning is wide; comprising of supervised learning, unsupervised learning, semi-supervised learning and reinforcement learning. Noteworthy, supervised and unsupervised learning represent two dominant clusters of learning algorithms which can be applied to any machine learning.

Supervised learning studies the relationship between an input space *x* and a label (output) space *y*. Given a set of labels $\{0,1, ..., L\}$, the model acquires the functional relationship between the input and label $f : x \rightarrow y$, where the mapping *f* is a classifier by taking training data, $(X_1, Y_1), \ldots, (X_n, Y_n) \in x \times y$, as source of learning. Supervised learning is commonly applied for regression and classifcation problems. Common supervised learning algorithms include:

- 1. Decision Tree (Quinlan [1986\)](#page-46-8): The algorithm is in a form of tree structure with branches and nodes. Each leaf node represents a class label and each branch represents the outcome. The algorithm will hierarchically sort attributes from the root of the tree until it reaches a leaf node.
- 2. Naïve Bayes (Rish [2001](#page-46-9)): The algorithm applies Bayes' Theorem, which assumes that features are statistical independent. The classifcation is performed based on conditional probability of an occurrence of an outcome derived from the probabilities imposed on it by the input variables.
- 3. Support Vector Machine (Cortes and Vapnik [1995\)](#page-42-16): A margin is defned as the distance between two supporting vectors which are separated by a hyperplane. Larger margin implies smaller classifcation errors. Thus, the algorithm aims to draw the most suitable margins in which the distance between each class and the nearest margin is maximized.
- 4. Ensemble Learning (Rokach [2010\)](#page-47-14): A method to aggregate multiple weak classifers to construct a strong classifer. Important ensemble learning algorithms include boosting and bagging.

On the other hand, there is no labeled data in unsupervised learning. So unsupervised model draws inferences from input data based on similarities and redundancy reduction during the training. Clustering and association rule are two well-known types of unsupervised learning. Popular unsupervised learning algorithms include:

- 1. *k*-Means (MacQueen [1967\)](#page-45-13): This clustering algorithm groups data into *k* clusters based on their homogeneity. An individual mean value represents the center of each cluster. During the implementation, data values will be assigned to the most likely class label based on their proximity to the nearest mean with the least error function.
- 2. Principal Component Analysis (Jollife [2002\)](#page-44-18): This method aims to reduce of dimensionality of data by fnding a set of mutually un-correlated linear low dimensional data representations which have largest variance. This linear dimensionality technique is useful in exploring the latent interaction between the variable in an unsupervised setting.

Bourgeat et al. [\(2007](#page-41-6)) extracted additional texture features from phase information of MR image to consider magnetic property of tissue. The features were fed into a multiscale support vector machine (SVM) framework. An image subsampling process would classify the voxels from coarse-to-fne representation. In total, 40,000 voxels were extracted from 4 training images. In order to maintain the segmentation quality, contour refnement was performed to eliminate jaggy boundary from the segmented bones (Bourgeat et al. [2007](#page-41-6)). Fabian et al. ([2015\)](#page-42-13) applied random forest (RF) classifier with bagged decision trees of 20 trees to segment the femur. Only 5% of the femur voxels and 5% of the non-femur voxels from each data were selected to train the classifer by using a set of features that included spatial location, volumetric mean, volumetric variance, volumetric entropy, skewness, kurtosis, edge and Hessian (Fabian et al. [2015](#page-42-13)). Nonetheless, the classifcation accuracy relied heavily on the quality of labeled data, which indicated the major limitation faced by classical machine learning.

3.6 Deep learning‑based methods

Deep learning is a powerful machine learning model equipped with automatic hierarchical feature representation learning ability. General architecture comprises of input layer, hidden (feature extraction) layers and output (classifcation) layer (Goceri [2018\)](#page-43-6). A comparison between classical machine learning and deep learning is shown in Fig. [5.](#page-17-0) Major architectures of deep learning (LeCun et al. [2015](#page-44-2)) are convolutional neural network (CNN), recurrent neural network (RNN), recursive neural network and unsupervised pretrained networks (UPN). Among these networks, CNN is well suited to image processing applications such as object detection, image classifcation and segmentation. During model training, the value of each node is estimated by parameterizing weights through convolutional flters and the objective function is then optimized via backpropagation.

A list of deep learning-based knee bone segmentation is indicated here: (Almajalid et al. [2019;](#page-40-3) Ambellan et al. [2019;](#page-41-7) Cheng et al. [2020](#page-42-14); Lee et al. [2018](#page-45-11); Liu et al. [2018a](#page-45-10); Zhou et al. [2018](#page-49-5)). In general, knee bone segmentation model adopts CNN architecture with some modifications. Liu et al. [\(2018a\)](#page-45-10) built a 10-layers SegNet framework with discarded fully connected layer after the decoder network, to perform pixelwise semantic labelling on 2D knee image. The processed labels were fed to the marching cube algorithm to generate 3D simplex mesh. Then, the simplex mesh was sent to 3D simplex deformable process with each individual segmentation objects being separately refned based on the source image (Liu et al. [2018a\)](#page-45-10). Lastly, performance of the model was compared to U-net. Because Seg-Net removed fully connected layer, the model has lower number of parameters. Besides, SegNet performed a nonlinear upsampling; hence, credential features and boundary delineation could be better reconstructed. Later, Zhou et al. [\(2018](#page-49-5)) extended the model into multiple tissue segmentation by using conditional RF to perform multiclass classifcation. The model has reported DSC accuracy of 0.97 for femur, 0.962 for tibia and 0.898 for patella (Zhou et al. [2018](#page-49-5)).

Ambellan et al. [\(2019](#page-41-7)) adopted the concept of slice-wise segmentation from Liu et al. ([2018a](#page-45-10)) and added SSM as extra feature into their 2D/3D U-net based bone segmentation model. The purpose of SSM was to overcome the holes in segmentation masks due to poor intensity contrast or image artifacts as well as to remove false positive voxels from femur and tibia that were detected at the outside of typical range of osteophytic growth. By utilizing 60 training shapes, the model has attained excellent DSC of 0.986 for femur and 0.985 for tibia (Ambellan et al. [2019\)](#page-41-7). Notwithstanding, the good performance was achieved at

the expense of huge computational resources and localized training. For instance, generalpurpose graphic cards with smaller memory were not capable to support the 3D convolution, so it wouldn't be easy to extend the model to process larger dataset without suitable graphic card. Besides, the 3D model was trained on small subvolumes of $64 \times 64 \times 16$ voxels along the bone contours to reduce computational burden and compensated the inability of SSM to provide osteophytic details. The training option, however, compromised the surrounding voxel intensity and texture feature.

In recognition of abovementioned limitations, Cheng et al. [\(2020](#page-42-14)) proposed a simplifed CNN model, known as holistically nested network (HNN), to segment femur and patella bones. HNN eliminated the decoding path to form a forward-feeding network; and reduced the graphic card computational size. Plus, the network was trained on whole knee image by using a 1×1 convolution at first layer (to produce fine details such as edge) until a 32×32 convolution at ffth layer (to produce coarse details such as shape of bone; thereby, acquiring both local and global contextual information. At the end, a weighted fusion layer was developed to average the probability map at each layer and successively computed the fnal prediction (Cheng et al. [2020\)](#page-42-14). Although the authors tried to perform a comprehensive validation against current state-of-art, it was hindered by the type of bone selection (immature bone vs mature bone; and diferent bone compartment) and the absence of public groundtruth. Moreover, it is noteworthy that training of deep learning model is computationally heavy in spite of its better robustness. According to Ambellan et al. ([2019\)](#page-41-7), implementation of deep learning model on large scale data image of 50,000 would consume 43 weeks on a single computational node, which explicitly highlighted the expansive cost of computation. Some researchers have simplifed CNN architecture to reduce complexity, but the issue still required further analysis.

Fig. 5 Segmentation of knee bone by using **a** classical machine learning and **b** deep learning. Feature engineering of classical machine learning involves handpicked feature representations and mapping. On the other hand, deep learning uses multiple hidden layers to extract hierarchical feature representations

4 Knee cartilage segmentation

Knee cartilage segmentation from MR image produces cartilage model, which is used in a broad range of OA-related studies: imaging biomarkers analysis (Hafezi-Nejad et al. [2017;](#page-44-19) Schaefer et al. [2017](#page-47-15); Shah et al. [2019;](#page-47-16) Williams et al. [2010a](#page-48-8)), classification and detection of knee OA progression (Ashinsky et al. [2017;](#page-41-10) Ashinsky et al. [2015](#page-41-11); Chang et al. [2018;](#page-41-12) Almajalid et al. [2019a;](#page-40-4) Tiulpin et al. [2019](#page-48-9)), biomechanical modeling (Liukkonen et al. [2017b\)](#page-45-14) and stimulation of cartilage degeneration (Liukkonen et al. [2017a;](#page-45-15) Mononen et al. [2019,](#page-45-16) [2016;](#page-45-17) Peuna et al. [2018](#page-46-10)). To date, cartilage segmentation remains an active research problem because knee cartilage has very thin structure at a few millimeters wherein some extremely thin areas are measured in submillimeter. Examples of knee cartilage geometry complexity are shown in Fig. [6.](#page-19-0) Moreover, femoral, tibial and patellae cartilage have distinctively diferent and changing shapes across the slides.

Some medical image analysis tools (Akhtar et al. [2007;](#page-40-5) Bonaretti et al. [2020;](#page-41-13) Duryea et al. [2016;](#page-42-17) Gan et al. [2014a](#page-43-7); Iranpour-Boroujeni et al. [2011\)](#page-44-20) were developed to preprocess knee image, segment the cartilage and quantify knee OA progression via imaging biomarkers. Established medical image analysis consultancy such as Imorphics (based in Manchester, UK), ArthroVision (based in Montreal, Canada) and Chondrometrics (based in Ainring, Germany) caters to the need of medical image analysis service. Complete lists of classical cartilage segmentation model were given in Table [4](#page-20-0) (semiautomatic) and Table [5](#page-22-0) (fully automatic). An updated list of deep learning-based knee cartilage segmentation models was given in Table [6](#page-25-0).

4.1 Region‑based methods

Region growing exploits the homogeneity property of neighboring pixels' values. Often, users need to place an initial set of seed points $S_i = \{S_1, S_2, ..., S_n\}$. Then, the algorithm will start to expand to neighboring pixels in search for homogenous pixels (Adams and Bischof [1994\)](#page-40-6). Let *T* be the set of all pixels which are adjacent to at least one of the pixels in S_i

$$
T = \left\{ x \notin \bigcup_{i=1}^{n} S_i | nb(x) \cap \bigcup_{i=1}^{n} S_i \neq \emptyset \right\}
$$
 (6)

where $nb(x)$ is the set of immediate neighbors of the pixel x. The search will continue updating the mean of corresponding region and expand until the similarity criterion is breached. Common similarity criterion includes intensity or image texture. Classical region growing is not good at coping with inhomogeneous image property landscape of knee image. As a result, researchers need to combine region growing with other image processing techniques in their segmentation models.

Pakin et al. [\(2002](#page-46-11)) applied region growing to obtain an initial segmentation of knee cartilage from image background. A subsequent two-class local clustering voting mechanism was introduced to determine the class of unlabeled regions based on their proximity to knee bone and contrast diference at the region boundaries. Lastly, surface mesh was generated to produce a 3D cartilage model (Pakin et al. [2002](#page-46-11)). While the model has reported an accuracy of 98.87%, it was validated on a MR image of knee only. Cashman et al. [\(2002](#page-41-14)) proposed a multistage region growing-based knee cartilage segmentation model. At preprocessing stage, image noise was fltered with median flter and background image was removed by using edge detection and thresholding. Then, a recursive region grow method

would pre-segment the image to produce a bone-plus-cartilage region mask, where the bone region would be subtracted to leave-out cartilage (Cashman et al. [2002](#page-41-14)). Similar work was found at Riza et al. ([2019\)](#page-47-17).

Region growing was one of the earliest segmentation algorithm implemented in knee cartilage segmentation. Although it was simple to use, direct implementation was computational heavy. Further, knee images were infamous for weak tissue boundaries; causing potential under- or oversegmentation. Signifcant amount of manual intervention was required throughout the segmentation to fll in discontinued boundary during edge detection, to place seed points inside bone region during pre-segmentation and to eliminate any residual non-cartilage pixels adhering to the outside of cartilage. Furthermore, perfor-mance of region growing methods (Pakin et al. [2002](#page-46-11); Riza et al. [2019](#page-47-17)) were not properly validated. These limitations question the applicability of region growing to be extended to large patient groups.

4.2 Deformable model‑based methods

Application of traditional ACM in knee cartilage segmentation model could be found in Stammberger et al. [\(1999](#page-48-10)), Lynch et al. ([2000\)](#page-45-18), Duryea et al. ([2007\)](#page-42-18) and Brem et al. ([2009\)](#page-41-15). As highlighted in Sect. [3.1,](#page-7-0) traditional ACM was sensitive to initialization and suffered from poor convergence performance of the contour for concave boundaries. Some improvement works were proposed. Gradient Vector Flow (GVF) was integrated into ACM to resolve abovementioned problems but the model was still vulnerable to poor tissue contrast or blur cartilage boundary (Tang et al. [2006](#page-48-11)). Carballido-Gamio et al. [\(2005](#page-41-16)) used Bezier spline to control active contour formation. The Bezier spline was created by manually inserting control points inside the cartilage. Then, local information acquired from the initial control points would update the Bezier spline until it reached the articular surface. The model also took into consideration the disconnected cartilage boundary; hence, it was more robust to weak boundary problem (Carballido-Gamio et al. [2005\)](#page-41-16). Meanwhile, Ahn et al. ([2016\)](#page-40-7) applied level set contour as an active contour. At initialization phase, 20 normal knee templates were used to estimate the initial contour in level set. The energy function was designed to consider local regions while spatial information from the templates was incorporated into the energy function to minimize the effect of noise (Ahn et al. [2016](#page-40-7)).

Fig. 6 Illustrations of anatomical complexity demonstrated by knee cartilage. **a** Irregular cartilage structure with diffuse boundary (white arrowheads). **b** Thin cartilage structure (white arrowheads) adds more challenges to segmentation process. **c** Efusion between at patellofemoral cartilage (white arrows) adds ambiguity to segmentation accuracy. **d** Narrow tibiofemoral boundary (white arrows) hardens the segmentation of tibial and femoral cartilage

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PD Proton Density, VC Volume of Cartilage, *Thc* Thickness of Cartilage, AC Area of Cartilage Surface, *tAB* Total Area of Subchondral Bone, *RMS* Root Mean Square, CV
Coefficient of Variation, SD Standard Deviation *PD* Proton Density, *VC* Volume of Cartilage, *ThC* Thickness of Cartilage, *AC* Area of Cartilage Surface, *tAB* Total Area of Subchondral Bone, *RMS* Root Mean Square, *CV* Coefficient of Variation, *SD* Standard Deviation

VOE±SD: 18.82±6.006 (F),

19.81±6.072 (TC), 21.19±6.594 (PC)

ASD Average Surface Distance, VOE Volumetric Overlap Error, SD Standard Deviation *ASD* Average Surface Distance, *VOE* Volumetric Overlap Error, *SD* Standard Deviation

Apart from ACM, researchers also apply ASM for cartilage segmentation. The model requires user to place *n* landmark points, $\{(x_1, y_1), (x_2, y_2), \dots, (x_n, y_n)\}$ on cartilage boundary (see Fig. [7\)](#page-28-0), which is arranged as a 2*n* element vector, $X = (x_1, \dots, x_n, y_1, \dots, y_n)^T$. The landmarking process is repeated on a stack of *N* training images to produce a cloud of landmark points. These shapes are aligned in a common model coordinate frame by using the Procrustes algorithm. Then, principal component analysis (PCA) is implemented on the set of vectors $\{X_i\}$. An affine transformation will be defining the position, (X_t, Y_t) , orientation, θ , and scale, s , of the model in knee image frame.

Active Shape Model Algorithm Summary:

1. Calculate the mean of the data

 $\widetilde{X} = \frac{1}{N} \sum_{i=1}^{N} X_i$

2. Calculate the covariance of the data

 $S = \frac{1}{N-1} \sum_{i=1}^{N} (X_i - \tilde{X})(X_i - \tilde{X})^T$

- 3. Compute the eigenvectors, P_i and corresponding eigenvalues, λ_i of the covariance matrix. Each eigenvalue gives the variance of the data about the mean in the direction of the corresponding eigenvector
- 4. Select the *m* largest eigenvalues where *m* is the number of mode of variation
- 5. Approximate the linear shape model given the eigenvectors $\{P_i\}$ and shape parameters *b*

 $X \approx \widetilde{X} + \sum_{m} \mathcal{P}_{m} b_{m}$

- 6. Update the parameters pose parameters (X_t, Y_t, s, θ) and shape parameters *b*
- 7. Repeat until convergence

Solloway et al. [\(1997](#page-48-13)) placed 42 around the cartilage boundary and 22 landmark points around the endosteal surface of femoral condyles to produce a 2D femoral cartilage ASM model. In total, 10 modes of variations were utilized to derive the mean shape approximation. The model has achieved CV of 2.8% for cartilage thickness measurement (Solloway et al. [1997\)](#page-48-13). However, the shape variation fexibility was often constraint by the number of principal components extracted from the diagonal of the covariance matrix, which depend on the number of training shapes. As a result, traditional ASM sufered from over-restrictive shape variation and problematic re-initialization in knee cartilage segmentation.

To overcome these limitations, two studies have integrated additional feature information during the training of shape model. González and Escalante-Ramírez [\(2013](#page-43-11)) has tested Hermite transform, Haar- and Sym-5 wavelet transform on the *x* and *y* coordinate directions of the contour in an attempt to capture more information from the contours at diferent spatial resolutions. The Sym-5 wavelet transform based model has reported the best DSC score of 0.8329 with 16 training samples (González and Escalante-Ramírez [2013](#page-43-11)). In another study, González and Escalante-Ramírez ([2014\)](#page-43-12) has combined texture features from Local Binary Patterns (LBP) into ASM. The texture information from each landmark point was computed into LBP histogram. Unfortunately, the model only produced DSC of 0.8132. (González and Escalante-Ramírez [2014](#page-43-12)). Accordingly, diferent modifed ASM models failed to demonstrate apparent accuracy attainment, instead these models continued to rely on handpicked feature and number of training samples. Although direct performance comparison between diferent deformable models is not available, neither a single deformable model nor modifed deformable model seems to be able to cope with frequent changes in cartilage structure.

Fig. 7 Traditional ASM sufers from over-restrictive shape variation. In practice, users are required to place substantial amount of landmark points on curved cartilage boundary (**a**). However, scrupulous landmarking does not guarantee desirable result and refnement is needed (**b**)

4.3 Graph‑based methods

Graph cuts defnes a segmentation as an optimization of energy cost function problem. Bae et al [\(2009](#page-41-17)) and Shim et al. [\(2009a](#page-47-18)) have applied classical graph cuts to segment knee cartilage of 20 and 10 subjects, respectively. User scribbles were utilized as hard constraint and the segmentation has reported good DSC accuracy of 94.3%. However, both works did not address the notorious smallcut problem and image noise problem sufered by the algorithm. Besides, classical graph cuts does not support multiclass segmentation.

To address abovementioned limitations, a hierarchical segmentation model known as Layered Optimal Graph Segmentation of Multiple Objects and Surfaces (LOGISMOS) was proposed by Yin et al. ([2010\)](#page-49-4). The model approximated the interaction between interacting surfaces of diferent objects by utilizing prior knowledge about knee structure, which was infused as multi-surface interaction constraint and multi-objective interactive constraint during graph construction. The former analyzed the relationship between bone and surrounding soft tissue inclusive of cartilage, while the latter analyzed the relationship between bone and cartilage. The design of cost function was essential to accommo-date all pretrained information (Yin et al. [2010](#page-49-4)). Unfortunately, the cost function in original LOGISMOS failed to capture the regionally-specifc appearance of the surrounding menisci, muscle bone and other anatomies; which caused certain intensity profle of normal cartilage areas to be mistaken as pathological case. An extension of LOGISMOS with Just Enough Interaction (JEI) was introduced in Kashyap et al. [\(2018](#page-44-16)) to rectify the cost function.

Another type of graph-based method, random walks models the segmentation problem as looking for solution to Dirichlet problem. In theory, a harmonic function that satisfes the boundary condition will minimize the Dirichlet integral. Thus, the probability of unlabeled pixel belongs to each label class could be computed by solving a system of linear equations.

Random Walks Algorithm Summary:

- 1. Map the image intensity value, *g*, to edge weights, *w*, for two pixels *i* and *j* in lattice structure
- $w_{ij} = exp(-\beta(g_i g_j)^2)$ where β is a free parameter
- 2. Organize the nodes into two sets, V_M (labeled nodes) and V_U (unlabeled nodes) such that $V_M \cup V_U = V$ and $V_M \cap V_U = \emptyset$
- 3. Obtain a set of V_M labeled pixels with *K* labels via interactive or automatic approach
- 4. Defne the set of labels for the labeled pixels as a function
- $Q(v_j) = s, \forall v_j \in V_M$ where $s \in \mathbb{Z}, 0 < s < K$
- 5. Define the $|V_M| \times 1$ vector for each label, *s*, at node $v_j \in V_M$ as

 $m_j^s = \begin{cases} 1 & \text{if } Q(v_j) = s \\ 0 & \text{if } Q(v_i) \neq s \end{cases}$ 0 *if* $Q(v_j) \neq s$

6. Resolve the combinatorial Dirichlet problem for each label

 $L_Ux^s = -B^Tm^s$

Because random walks is robust to weak boundary problem, it can overcome the diffuse boundary observed in pathological cartilage. Thorough analyses were conducted to analyze the performance of random walks for knee cartilage segmentation (Gan and Sayuti [2016](#page-43-13); Gan et al. [2017](#page-43-8),[2019](#page-43-9),[2018](#page-43-14),[2014b](#page-43-15), [c\)](#page-43-16). The model was evaluated against manual segmentation. As shown in Fig. [8](#page-30-0), classical random walks relied heavily on seed points' locations to provide local information about knee structure (Gan et al. [2017\)](#page-43-8). Subsequently, an improved model was developed, which demonstrated DSC accuracy of 0.94, 0.91 and 0.88 for normal femoral, tibial and patellae cartilage, as well as 0.93, 0.88 and 0.84 for pathological femoral, tibial and patellae cartilage (Gan et al. [2019](#page-43-9)).

In summary, design of energy function plays an infuential role in developing graphbased methods. A majority of the graph-based methods' energy function in knee cartilage segmentation aimed to partition the graph through min-cut concept. However, minimization of the energy function was always a daunting task due to various issues such as smallcut and binary segmentation problem. Besides, incorporation of user interaction to provide priori knowledge was ubiquitous in both advanced graph model such as LOGISMOS and other simpler graph-based models. User-specifc markers was manually inserted through scribbles or boundary points. The priori knowledge was essential to initialize and modify the segmentation (Bowers et al. [2008;](#page-41-18) Gan et al. [2017](#page-43-8), [2019;](#page-43-9) Gougoutas et al. [2004\)](#page-43-10) as well as to compensate the lacking of cost function (Kashyap et al. [2018](#page-44-16)). Consequently, graph-based methods were often plagued with overdependence on user interaction in order to attain desirable segmentation results.

4.4 Atlas‑based methods

Diferent from previously discussed segmentation methods, atlas-based segmentation makes use of priori knowledge from labeled training images to segment the target image. Because the atlas is directly created by expert, the priori information is rich of discriminative details about the location, shape, object class, priori probabilities and topological details of target object. Given that the knee cartilages are sharing similar texture and spatial features, as well as ill-defned boundary with surrounding soft tissues, atlas-based methods is expected to excel in knee cartilage segmentation. Still, atlas-based methods are not

^{7.} Compute a final segmentation by assigning to each node, v_i , the label corresponding to $max_s(x_i^s)$, where the probabilities at any node will sum to unity, $\sum_s x_i^s = 1, \forall v_i \in V$

without any disadvantage. Creation of atlas can be time- and resources consuming, and small number of atlas image can potentially lead to overftting problem.

There are common four atlas selection methods, namely single atlas (which selects a reference image from a set of labeled images), the best atlas (which identify the most suitable labeled image from the set), averaged-shape atlas (which constructs an averaged atlas from a set of labeled images), and multiple atlases (which registers every individual labeled image to the test image independently). The preceding three selection approaches were not robust enough though, so most studies have employed the multiple atlas method in knee cartilage segmentation model (Carballido-Gamio and Majumdar [2011;](#page-41-19) Dam et al. [2015;](#page-42-10) Lee et al. [2014](#page-44-13); Liu et al. [2015](#page-45-19); Shan et al. [2012a,](#page-47-20) [2012b,](#page-47-19) [2014](#page-47-11); Tamez-Peña et al. [2012\)](#page-48-14). The main role of atlas was to provide spatial prior to guide an automatic multilayer knee cartilage segmentation model at initialization stage.

Among these works, Shan's research group has conducted a pipeline of studies to investigate the most suitable atlas-assisted probabilistic classifcation segmentation structure (Shan et al. [2012a,](#page-47-20) [2012b](#page-47-19), [2014](#page-47-11)). Priori information was transferred from the atlas to test image via non-rigid image registration. Interestingly, the concept was somehow similar to the classical machine learning-based methods, which we would discuss later. Compared to other atlas-based models, their fnal model (Shan et al. [2014](#page-47-11)) have registered the best DSC score of 0.856 for femoral cartilage and 0.859 tibial cartilage on a group of 155 subjects. A major disadvantage of atlas-based method, however, was its dependence on registration method and anatomical similarity between the atlas and the subject to achieve good performance.

4.5 Classical machine learning‑based methods

Given its anatomical complexity, classifcation of cartilage is a daunting task indeed. Folkesson et al. ([2007\)](#page-43-5) has published one of the earliest classification model by using two binary *k*NN classifers to segment the femoral and tibial cartilage. The feature learning was a computational heavy process. Approximately 500,000 training voxels for background, 120,000 voxels for tibia cartilage and 300,000 voxels for femoral cartilage were involved. To alleviate this issue, human knowledge prior about the location of the cartilage was predefned at the initialization stage (Folkesson et al. [2007\)](#page-43-5). Even though the model reported DSC of 0.80, it became the benchmark for future classifcation-based knee cartilage segmentation model.

Fig. 8 Infuence of seeds' positions on cartilage segmentation using random walks. **a**, **c** Placement of label seeds on knee image to indicate the cartilage and non-cartilage tissues. **b**, **d** Over- and undersegmentation occur due to imprecise location of seeds

Numerous multi-stage/multi-level (Dodin et al. [2010;](#page-42-19) Lee et al. [2011](#page-44-21); Öztürk and Albayrak [2016;](#page-46-12) Pang et al. [2015;](#page-46-13) Wang et al. [2014;](#page-48-6) Zhang et al. [2013](#page-49-7)) classifcation models have employed diferent approaches such as bone pre-segmentation to derive BCI (Lee et al. [2011](#page-44-21); Wang et al. [2014\)](#page-48-6), SVM based edge classifcation (Pang et al. [2015](#page-46-13)), utilization of four types of image contrast to extract rich features (Zhang et al. [2013\)](#page-49-7) and subsampling of background voxels to enable feasible *k*NN classifcation (Öztürk and Albayrak [2016](#page-46-12)). Because diferent researchers were restricted to their own classifcation strategies, their models' architectures varied signifcantly according to the image feature, spatial priors, imaging sequence type and cartilage type. Consequently, these models lacked the generalizability to unseen pathological features in knee image. Further, handpicked features were subjective to the training data; these concerns severely undermined the robustness of classifcation models.

For example, Öztürk and Albayrak ([2016\)](#page-46-12) applied central coordinate computation and one-versus-all classifcation. During the training, subsampling processes were adopted to eliminate abundant background voxels step-by-step and helped to increase computational feasibility. A total of 150 features were extracted. At the testing, separate *k*NN classifers were used to classify femoral, tibial and patellae cartilage. Despite its complexity, the model merely achieved DSC of 0.826 for femoral cartilage, 0.831 for tibial cartilage and 0.726 for patellae cartilage. In Zhang et al. ([2013\)](#page-49-7), T1-weighted FS SPGR, T2/T1-weighted FIESTA, T2/T1-weighted IDEAL GRE waster and fat imaging sequence were used to exploit spectral correlation among diferent imaging sequences. But the model has reported very big results variance; depending on the inclusion of number of features (DSC ranged from 0.019 to 0.880) and classifcation models (DSC ranged from 0.456 to 0.880).

4.6 Deep Learning‑based methods

Recently, artifcial intelligence (AI), especially deep learning, has emerged as a popular research topic (Goceri and Goceri [2017\)](#page-43-17). Deep learning uses convolutional flters to extract deep features and fed the concatenated feature vector into dense layer (see Fig. [9](#page-32-1)). Large number of studies (Ambellan et al. [2019](#page-41-7); Norman et al. [2018a;](#page-46-17) Panflov et al. [2019](#page-46-18); Prasoon et al. [2013;](#page-46-15) Raj et al. [2018;](#page-46-16) Tack and Zachow [2019](#page-48-15); Tan et al. [2019;](#page-48-16) Xu and Niethammer [2019](#page-49-8)) which used deep learning in knee cartilage segmentation were published. In particular, CNN architecture has received the most research attention. For example, a U-net architecture of 4 convolutional layers and kernel filter of 5×5 for 2D CNN and $5 \times 5 \times 5$ for 3D CNN was adopted in Ambellan et al. ([2019\)](#page-41-7). In Prasoon et al. [\(2013](#page-46-15)), three CNN models were computed from xy-, -yz, and $-zx$ planes respectively with a kernel size of 5×5 . Meanwhile, a 3D CNN with 5 convolutional layers and $3 \times 3 \times 3$ kernel filter was adopted in Tack and Zachow [\(2019](#page-48-15)).

Among these works, some have added extra improvements to enhance the accuracy of existing models. Given that U-net failed to segment low contrast areas, Ambellan et al. ([2019\)](#page-41-7) imported shape information from SSM to fll in holes and sub-holes in segmentation masks. A better segmentation accuracy of 85.6–89.9% (DSC) was reported at the expense of laborious SSM construction. On the other hand, Panflov et al. ([2019\)](#page-46-18) attempted two regularization techniques, namely mix-up and unsupervised domain adaptation (UDA) to improve the robustness of their U-net model. Unfortunately, their investigation showed mixed results, and even performance deterioration when both mix-up and UDA were combined together.

Tan et al. [\(2019](#page-48-16)) introduced a deep learning segmentation framework which integrated collaborative multi-agent learning mechanism to label cartilage and discriminator to determine output cartilage label. A V-net with 3 convolutional layers and 2×2 kernel filters served as the fundamental of segmentation model. Their work has reported high accuracy of $0.900 + 0.037$ for femoral cartilage, $0.889 + 0.038$ for tibial cartilage and $0.880 + 0.043$ for patellae cartilage. Another deep learning segmentation, DeepAtlas (Xu and Niethammer [2019\)](#page-49-8) proposed a joint learning mechanism from weakly supervised image registration and semi-supervised segmentation learning. The authors have adopted a U-net structure. During the learning mechanism, an anatomy similarity loss would compute the segmentation dissimilarity through matching segmentations between the target image and the warped moving image in order to guide the model training. Despite the authors claimed the DeepAtlas would beneft from fewer manual segmentations during model training, it suffered from lower accuracy performance i.e. DSC of $81.19 \pm 3.47\%$ and complex learning objective function.

Many deep learning-based segmentation models were validated on more than one dataset. For example, DeepAtlas was validated on the OAI dataset and OASIS-TRT dataset (brain MR images), while Tack and Zachow[\(2019](#page-48-15)) and Ambellan et al. [\(2019](#page-41-7)) utilized SKI10, OAI Imorphics and OAI Zuse Institute Berlin (ZIB) dataset to evaluate their models' performance. However, a real problem in medical image analysis was the lack of largescale annotated image data with high quality (Goceri [2019](#page-43-18)). To segment knee cartilage, research groups have to either train their CNN models from scratch by utilizing small amount of labelled images or build a large in-house training dataset. The former could easily lead to overftting problem while the latter would incur substantial fnancial and expert resources. Another concern associated with deep learning model was the enormous computational memory requirement, which was implicitly refected through the selection of 2D slice-by-slice segmentation option in most knee cartilage segmentation models.

5 Evaluation of computational segmentation models

In 2010, SKI10 was announced in Grant Challenge Workshop organized by MICCAI [\(https](https://ski10.org) [://ski10.org](https://ski10.org)) to promote a common evaluation framework among segmentation models by using a public dataset. A total of 170 research teams have registered and the best research team has reported an averaged total score of 75.73 (Ambellan et al. [2019](#page-41-7)). Besides, evaluation were localized into subregions in many cartilage segmentation studies (see Fig. [10](#page-34-0)). Given a broadly diversifed types of segmentation models, it is hard to systematically evaluate their performance as a whole. Therefore, in following sub-sections, we analyzed performance of these models from the perspective of 1) deep learning against classical segmentation models, and 2) biomarkers in computational models.

Fig. 9 Convolution performed on DESS knee image

5.1 Performance of deep learning versus classical segmentation models

The standard practice to assess the performance of computational knee segmentation model is by comparing the segmentation results against groundtruth. Because groundtruth is often created by expert through manual segmentation, there is a scarcity of public groundtruth to assess diferent segmentation models in global domain. Among the statistical evaluation metrics (see Table [7](#page-35-0)), DSC was extensively applied metric in classical and deep learning segmentation models, especially cartilage segmentation to evaluate the degree of agreement between groundtruth and segmentation. Besides, two surface distance evaluation metrics were frequently used in bone segmentation i.e. average symmetric surface distance (ASD) and root-mean-square symmetric surface distance (RMSD). To compute the measurement, each surface boundary voxel of the segmentation was compared to the closest boundary voxel in groundtruth and Euclidean distance diference was derived and stored in a list.

A number of fully automatic segmentation models overlapped either 2D or 3D segmented cartilage (Ahn et al. [2016;](#page-40-7) Dodin et al. [2010](#page-42-19); Folkesson et al. [2007;](#page-43-5) Liu et al. [2015;](#page-45-19) Öztürk and Albayrak [2016](#page-46-12); Tamez-Peña et al. [2012](#page-48-14); Zhang et al. [2013\)](#page-49-7) or segmented bone (Ababneh et al. [2011](#page-40-2); Bourgeat et al. [2007;](#page-41-6) Fabian et al. [2015](#page-42-13); Fripp et al. [2007](#page-43-3); Gandhamal et al. [2017](#page-43-4); Wang et al. [2014\)](#page-48-6) with groundtruth to validate the accuracy of their models. Overall, classical cartilage segmentation models' DSC ranged from 70 to 88% while classical bone segmentation models' DSC ranged from 90 to 97%. In semiautomatic cartilage segmentation models, both DSC (Gan et al. [2017](#page-43-8), [2019;](#page-43-9) Liukkonen et al. [2017b;](#page-45-14) Shim et al. [2009a](#page-47-18)) and CV (Bae et al. [2009;](#page-41-17) Bowers et al. [2008](#page-41-18); Brem et al. [2009;](#page-41-15) Duryea et al. [2007;](#page-42-18) Gougoutas et al. [2004](#page-43-10); Lynch et al. [2000](#page-45-18); Stammberger et al. [1999](#page-48-10); Tang et al. [2006](#page-48-11)) were two equally important evaluation metrics. DSCs of semiautomatic cartilage segmentation models ranged from 80 to 94% and CV was measured from the perspective of diferent observers (inter-observer), within observer (intra-observer), diferent subjects, and different scans. The result details of CV could be referred to Table [4](#page-20-0). Despite semiautomatic cartilage segmentation models have achieved better DSC results than fully automatic segmentation models, the number of knees in the former was small, attributed to the need of expert to supervise the segmentation. On the other hand, the highest DSC score attained by bone segmentation model was 97%. The high accuracy of segmented bone model enables researchers (Dam et al. [2015;](#page-42-10) Lee et al. [2014](#page-44-13); Shan et al. [2014](#page-47-11); Wang et al. [2014;](#page-48-6) Yin et al. [2010\)](#page-49-4) to exploit the spatial relationship between bone and cartilage surface and facilitate subsequent cartilage segmentation.

Overall, deep learning-based cartilage and bone segmentation models attained DSC ranged from 80–90% and 97–98%, respectively. In both cases, deep learning models did not demonstrate apparent performance superiority compared to classical segmentation models. There are three key highlights about deep learning-based segmentation models. First, deep learning models demonstrated greater consistency compared to classical segmentation models. Besides, deep learning models were more robust to huge amount of image dataset. Tack and Zachow([2019\)](#page-48-15) used 1378 subjects in their knee cartilage segmentation model while Ambellan et al. ([2019\)](#page-41-7) used 507 images in their knee bone segmentation model. Both were the largest sample size to date and it was unprecedented in classical segmentation models. Third, diferent research groups used their own groundtruth data during training even though their data originated from the OAI or MOST dataset. As a result, there was no regularization to assess and control the quality of annotated data. This

Fig. 10 (Left) Coronal view of DESS knee image showing division of femorotibial subregions i.e. central lateral femoral cartilage (cLFC), central tibial cartilage (cLTC), lateral tibia (LTB) and medial tibia (MTB). (Right) Cartilage plate maps detailing diferent subregions on femoral and tibial cartilage where "a" denotes anterior, "p" denotes posterior, "i" denotes interior, "e" denotes external and "c" denotes central (Eckstein and Peterfy [2016](#page-42-2))

also explained the varied accuracies among deep learning models, despite using similar architecture and amount of training data.

5.2 Biomarkers in computational segmentation models

Biomarker is defned as any anatomic, physiologic, or molecular parameter detachable with one or more imaging methods used to help establish the presence and/or severity of disease (Smith et al. [2003\)](#page-47-21). In clinical knee OA research, morphological biomarkers are derived from cartilage and bone 3D models to replace traditional endpoint clinical trials in assessing and validating the morphology and functionality of cartilage tissue in vivo. Morphological biomarkers (see Table [8](#page-37-0)) were analyzed over a certain range of time point to identify the pattern of joint degradation. Notably, cartilage endures greater degradation at weightbearing locations. Wluka et al. ([2002\)](#page-48-17) investigated cartilage volume loss at weight bearing lateral and medial tibial plateau regions in a two time points study. Based on 132 patients with symptomatic OA, tibial cartilage reported an annual volumetric loss of approximately 5% (Wluka et al. [2002\)](#page-48-17). Pelletier et al. [\(2007](#page-46-19)) conducted a 24-months follow-up quantitative MRI subregional (diferent segments of femoral condyle and tibial plateau) study of 107 patients. Overall, the fndings showed that medial region experienced greatest cartilage

volume loss. Central region of the medial tibial plateau (cartilage loss: -84.2 ± 72.4 mm/ $-15.0 \pm 12.0\%$) and of the medial femoral condyle (cartilage loss: -87.9 ± 90.4 mm/ -12 . $0 \pm 11.5\%$) (Pelletier et al. [2007\)](#page-46-19). Meanwhile Eckstein et al. [\(2015](#page-42-20)) have analyzed cartilage thickness loss at tibiofemoral cartilage over 24 months (Eckstein et al. [2015\)](#page-42-20).

5.2.1 Semiautomatic segmentation models

It is standard to test the responsiveness of a knee joint segmentation model by computing test–retest coefficient of variation (CV) via repeated measurements of biomarkers over certain time frame. A number of semiautomatic segmentation models (Akhtar et al. [2007](#page-40-5); Bae et al. [2009;](#page-41-17) Brem et al. [2009;](#page-41-15) Carballido-Gamio et al. [2005](#page-41-16); Cashman et al. [2002;](#page-41-14) Duryea et al. [2014;](#page-42-21) Duryea et al. [2007;](#page-42-18) Tang et al. [2006](#page-48-11)) were analyzed comprehensively in this manner. An early semiautomatic segmentation models by Waterton et al. [\(2000](#page-48-18)) has repeated the measurement of femoral cartilage volume over a time point range of three weeks. The assessment has reported a test–retest CV of 1.6% (Waterton et al. [2000](#page-48-18)). Brem et al. ([2009\)](#page-41-15) computed RMS CV of VC, ThC, AC, tAB to quantify test–retest reproducibility. Based on 12 knees, the paired analyses root mean square CV ranged from 0.9–1.2% for VC, 0.3–0.7% for AC, 0.6–2.7% for tAB and 0.8–1.5% for ThC. Duryea et al. [\(2014](#page-42-21)) tested the responsiveness of their segmentation processing tool by measuring the cartilage volume loss at localized fxed region, which reported standardized response mean (SRM) of −0.52 at largest region (Duryea et al. [2014\)](#page-42-21). However, the number of data used in these studies were usually small.

Moreover, semiautomatic segmentation results are infuenced by experience of operators. These operators comprise of musculoskeletal experts, radiologists or clinicians with musculoskeletal subspecialty. Hence, conventional reproducibility analysis, which involves two to three experts, will be divided into inter- and intra-observer reproducibility. Intraobserver reproducibility measures the agreement of repeated results produced by each expert while inter-observer measures the agreement among result produced by experts. For example, reliability of graph cuts-based segmentation model (Bae et al. [2009\)](#page-41-17) was validated on variation error of VC produced by two radiologists. The model reported high inter-observer reproducibility of $1.29 \pm 1.05\%$ and $1.67 \pm 1.14\%$ for radiologist 1 and 2 and intra-observer reproducibility of $1.31 \pm 1.26\%$ and $1.70 \pm 1.72\%$ for session 1 and 2, respectively. Duryea et al. [\(2007](#page-42-18)) measured the CV of their image segmentation software based on VC and ThC. The fndings showed higher inter-observer variance (VC: 2.5–8.6%) (ThC: 1.9–5.2%) than intra-reader variance (VC: 1.6–2.5%) (ThC: 1.2–1.9%).

5.2.2 Fully automatic segmentation models

Only a few automatic knee segmentation models evaluated the longitudinal reproducibility of morphological biomarkers. Tamez-Pena et al. (2012) conducted comprehensive accuracy (in terms of mean diference) and test–retest precision evaluation of cartilage volume, thickness, and curvature biomarkers by using healthy and OA knees. Dam et al. [\(2015](#page-42-10)) evaluated the precision of cartilage volumes by using the OAI, CCBR and SKI10 dataset. Both models were tested against manual segmentation. In Tamez-Pena et al. (2012), the accuracy evaluation was localized into subregional areas: femur (F), femoral trochlea (FT), the central medial femur (cMF), the posterior medial femur (pMF), the central lateral femur (cLF), the posterior lateral femur (pLF), the medial tibia (MT), and the lateral tibia (LT). The mean accuracy for volume ranged from -0.2% for the pLF to 4.1\$ for the femur,

 $\frac{1}{2}$ in $\frac{1}{2}$ and $\frac{1}{2}$ research (Eclectein et al. 2006) **Table 8** Nomenclature of cartilage and bone biomarkers commonly used in knee OA research (Eckstein et al. [2006](#page-42-22)) $\frac{1}{2}$ markare á $\frac{1}{2}$ $\frac{1}{2}$ J. L. Table 8 Nr

the thickness accuracies ranged from -2.2% for the CMF to 10.4% for the MT, the curvature accuracies ranged from -5.2% for the MT to -2.1% for the cMF. The large variance in thickness biomarker indicated that some degree of atlas bias were introduced into the segmentation process.

Since neural networks models have greater extraction power through hidden layers, some (Hafezi-Nejad et al. [2017;](#page-44-19) Shah et al. [2019](#page-47-16)) have trained the model as a longitudinal clinical tool to obtain insight about the progression of knee OA. Hafezi-Nejad et al. ([2017\)](#page-44-19) used a multilayer perceptron (MLP) model to predict the medial joint space loss (JSL) progression by using 24-months changes of cartilage volume loss in fve knee plates and anthropometric parameters. The last layer would produce the prediction (importance value) of JSL progression based on association with cartilage degradation at diferent knee plates. Base on the fndings, lateral femoral cartilage was the most predictive of medial JSL progression (average importance value: 0.191; range 0.177–0.204). By using a population of 3910 MR images, Shah et al. [\(2019](#page-47-16)) investigated the cartilage thickness change at four diferent knee points according to three demographic variables i.e. age, sex and body mass index. For instance, the use of neural network enables researchers to investigate the physiological variation of cartilage with respect to various anthropometric variables, and analyze their relationships through multivariate analysis.

6 Discussion and conclusion

Advancement of AI technology has spurred the rise of new machine learning techniques. Inspired by promising accuracy outcomes demonstrated by deep learning-based segmentation models, deep learning has been extended to a wide range of computer-aided diagnosis applications such as classifcation (Antony et al. [2017;](#page-41-20) Chang et al. [2018](#page-41-12); Górriz et al. [2019;](#page-43-19) Norman et al. [2018b;](#page-46-20) Pedoia et al. [2019;](#page-46-21) Thomas et al. [2020](#page-48-19); Tiulpin et al. [2019](#page-48-9), [2018\)](#page-48-20) and detection (Lim et al. [2019;](#page-45-20) Liu et al. [2018b\)](#page-45-21) in radiographs and MRI-based knee OA studies. The ultimate goal is to detect and halt the progression of knee OA at early stage, where the cartilage degeneration remains reversible.

Classifcation is the process where an algorithm outputs the probability of a label for a given input image. Related knee OA-specifc applications include grading of OA by radiography (Antony et al. [2017](#page-41-20); Górriz et al. [2019;](#page-43-19) Norman et al. [2018b](#page-46-20); Thomas et al. [2020;](#page-48-19) Tiulpin and Saarakkala [2019](#page-48-21); Tiulpin et al. [2018\)](#page-48-20), grading of OA by MRI (Pedoia et al. [2019\)](#page-46-21), predicting the progression of OA by radiography (Tiulpin et al. [2019](#page-48-9)), and predicting knee pain by MRI (Chang et al. [2018\)](#page-41-12). Based on the literature, quantifcation of OA severity via end-to-end deep neural network is vital to provide more precise computeraided diagnosis to support clinicians in grading the severity of OA patients. Prior to deep learning, Ashinsky et al. [\(2015](#page-41-11)) has implemented Weighted Neighbour Distance using Compound Hierarchy of Algorithm Representing Morphology (WND-CHRM) algorithm (Shamir et al. [2008\)](#page-47-22), an open source classical machine learning software dedicated to biological image analysis, to classify normal and pathological knee images.

Antony et al. [\(2017](#page-41-20)) utilized a FCN to localize the knee joint and trained a CNN model to classify the OA severity grade. The CNN model has apparently outperformed classical WND-CHRM, producing classifcation results of 60.3% and 29.3–34.8%, respectively. On a test set of 3,146 training images and 1,300 testing images from the OAI, and 2020 training images and 900 testing images, the jointly trained model has attained precision score of 0.68 for KL grade 0, 0.32 for KL grade 1, 0.53 for KL grade 2, 0.78 for KL grade 3

and 0.81 for KL grade 4. The essence of this work consolidated the baseline state-of-art for the application of deep learning models in this feld, and opened up rooms for further enhancement to the model. Noteworthy, attention mechanism was implemented in subsequent classifcation-orientated deep learning models (Górriz et al. [2019;](#page-43-19) Norman et al. [2018b;](#page-46-20) Thomas et al. [2020;](#page-48-19) Tiulpin et al. [2018](#page-48-20)) to refne the weights of feature and improve the prediction. A latest attention-mechanism related model has achieved precision score of 0.73 for KL grade 0, 0.38 for KL grade 1, 0.71 for KL grade 2, 0. 82 for KL grade 3 and 0.87 for KL grade 4 (Thomas et al. [2020\)](#page-48-19).

In addition to classifcation, an early detection model was developed by Lim et al. ([2019\)](#page-45-20) to predict the occurrence of OA in patients aged 50 years and above. The architecture consisted of a deep neural network with eight hidden layers and trained along with lifestyle- and health status-associated risk factors. Based on a sample size of 5479 subjects, the proposed model showed an Area Under Curve (AUC) of 76.8%. Nonetheless, the accuracy of this predictive model was limited to patients with determined OA disease, while patients under OA treatment were excluded from the model training. Hence, future models shall consider this limitation as well as other detail decision parameter such as physiological signals. On the other hand, a cartilage lesion detection model was developed by using two CNN models i.e. the former for cartilage segmentation and the latter to detect structural abnormalities on the segmented cartilage. To train the classifcation model, a total of 17,395 cartilage image patches were extracted from knee cartilage of 175 patients by a musculoskeletal radiologist; in which 2642 image patches were classifed as cartilage lesions and the remaining 14,753 image patches were classifed as normal cartilage. The model has reported a high AUC of 0.917 and 0.914 in two rounds of evaluations (Liu et al. [2018b\)](#page-45-21).

Along with abovementioned deep learning-based classifcation and detection models, simulation of cartilage degeneration signifes another future direction of computer-aided diagnosis of knee OA. Herewith, we have presented important publications related to the development of knee cartilage degeneration simulation model (Liukkonen et al. [2017a;](#page-45-15) Mononen et al. [2019,](#page-45-16) [2016](#page-45-17)). Initial simulation algorithm (Mononen et al. [2016\)](#page-45-17) was built on a computational fnite element model, which took into account the stress distribution across the cartilage and change of collagen stifness in cartilage, to estimate the alternations in cartilage tissue properties with time. Fibril reinforced poroviscoelastic (FRPVE) material was chosen to mimic the cartilage tissue. Patient-specifc gait cycle experiment would provide the biomechanical stress loading information across diferent time points. The collagen fbril damage would happen at cartilage region where the tensile tissue stress exceeded a threshold limit of 5 MPa. The initial degeneration algorithm, however, was limited to tibiofemoral compartment and two subject groups i.e. normal weight and obese.

Since, a follow-up study was conducted to validate the performance of this cartilage degeneration stimulation algorithm by separating clinically healthy but obese subjects, diagnosed frim the baseline radiographs, into KL grade 2 and 3 based on the predicted level of cartilage degeneration (Liukkonen et al. [2017a](#page-45-15)). Twenty one subjects were involved in this study. In femoral cartilage model, an AUC of 0.94 and 0.84 was reported in predicting the cartilage KL grade 3 and 2, respectively. Meanwhile, in tibial cartilage model, AUC of 0.90 and 0.80 were reported in predicting the cartilage KL grade 3 and 2, respectively. In Mononen et al. ([2019](#page-45-16)), a template-based approach was introduced to substitute the previous patient-specifc approach. Anatomical dimensions were measured from 21 subjects to create templates from these subjects. Then, matching of template were conducted via minimum RMSE of anatomical dimension between the subject of interest and templates (multiple templates) or minimum RMSE of anatomical

dimension between each subject and all templates (one template). An optimal template model was scaled to match anatomical dimension for the subject of interest and eventually, the scaled templated model was simulated along with the simplifed gait loading. Interestingly, the approach with one template and the average meniscus support was statistically able to separate all KL grade groups to each other.

Existing research direction focuses on biomarkers to quantify the pattern of knee OA progression wherein nee segmentation serves as the cornerstone in knee OA research pipeline. Early segmentation models applied interaction from human expert for guidance but led to inter- and intra-observer ambiguity and heavy reliance on manual intervention. Then, substantial amount of attention has shifted to fully automatic segmentation models. Learning power of fully automatic segmentation models was limited to subjective feature selection, optimization and knowledge prior information. Consequently, these models failed to generalize to bigger dataset size. Nowadays, AI has transformed knee OA research direction toward prediction and early detection, given that deep learning has demonstrated great potential in terms of generalizability, robustness and versatility. Besides, it is noteworthy that advanced diagnostic applications are gradually becoming the future state-of-art. To embrace future challenges, more investigations are needed to validate the clinical applicability of deep learning models.

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Compliance with ethical standards

Conficts of interest The authors declare that they have no confict of interest.

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