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Deep learning-based automated detection of human knee joint's synovial fluid from magnetic resonance images with transfer learning

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Abstract: As an analytic tool in medicine, particularly in radiology, deep learning is gaining much attention and opening a new way for disease diagnosis. Nonetheless, it is rather challenging to acquire large-scale detailed labelled datasets in the field of medical imaging. In fact, transfer learning provides a possible way to resolve this issue to a certain extent such that the parameter learning of a neural network starts with its pre-trained weights learned from a large-scale dataset of certain similar task, and fine-tunes on a small comprehensively annotated dataset for the particular target task. The main aim of this study is to apply the deep learning model to detect the synovial fluid of human knee joint from magnetic resonance images. A specialized convolutional neural network architecture is proposed for automated detection of human knee joint's synovial fluid. Two independent datasets are used in the training, development, and evaluation of the proposed model. It is demonstrated by the experimental results that the proposed model obtains high sensitivity, specificity, precision, and accuracy to the detection of human knee joint's synovial fluid. As a result, this proposed approach provides a novel and feasible way for automating and expediting the synovial fluid analysis.

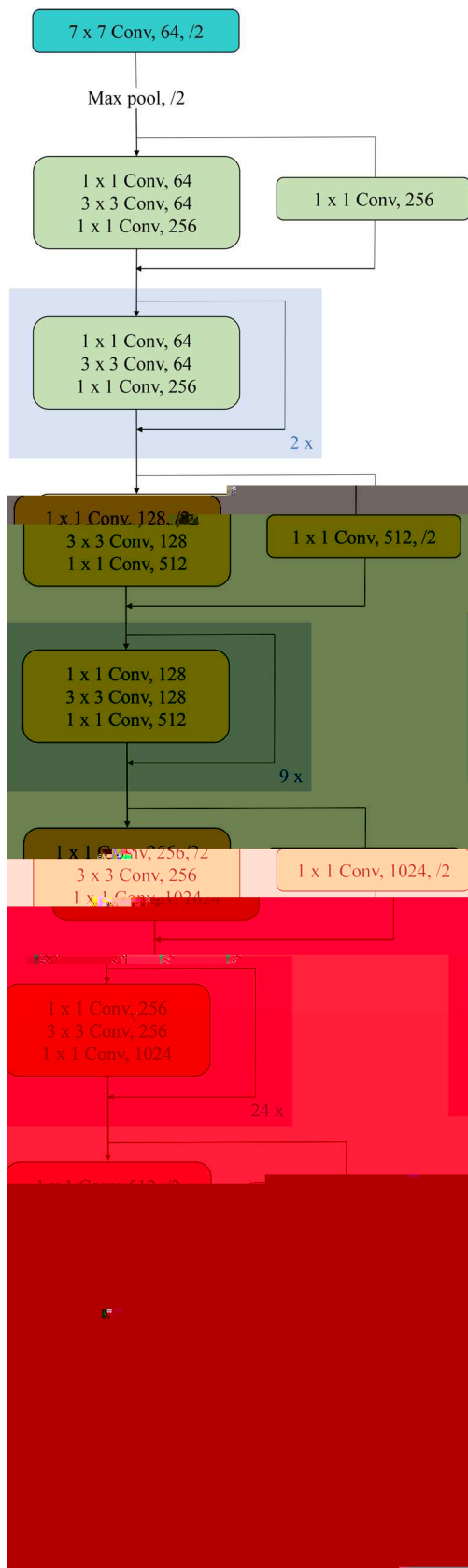## 1 Introduction

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Fig. 1 *Layout of the proposed CNN architecture. Note that all convolutional layers are followed by ReLU [33] and batch normalisation [34] (not included in the diagram). 'FC' signifies fully connected layer*
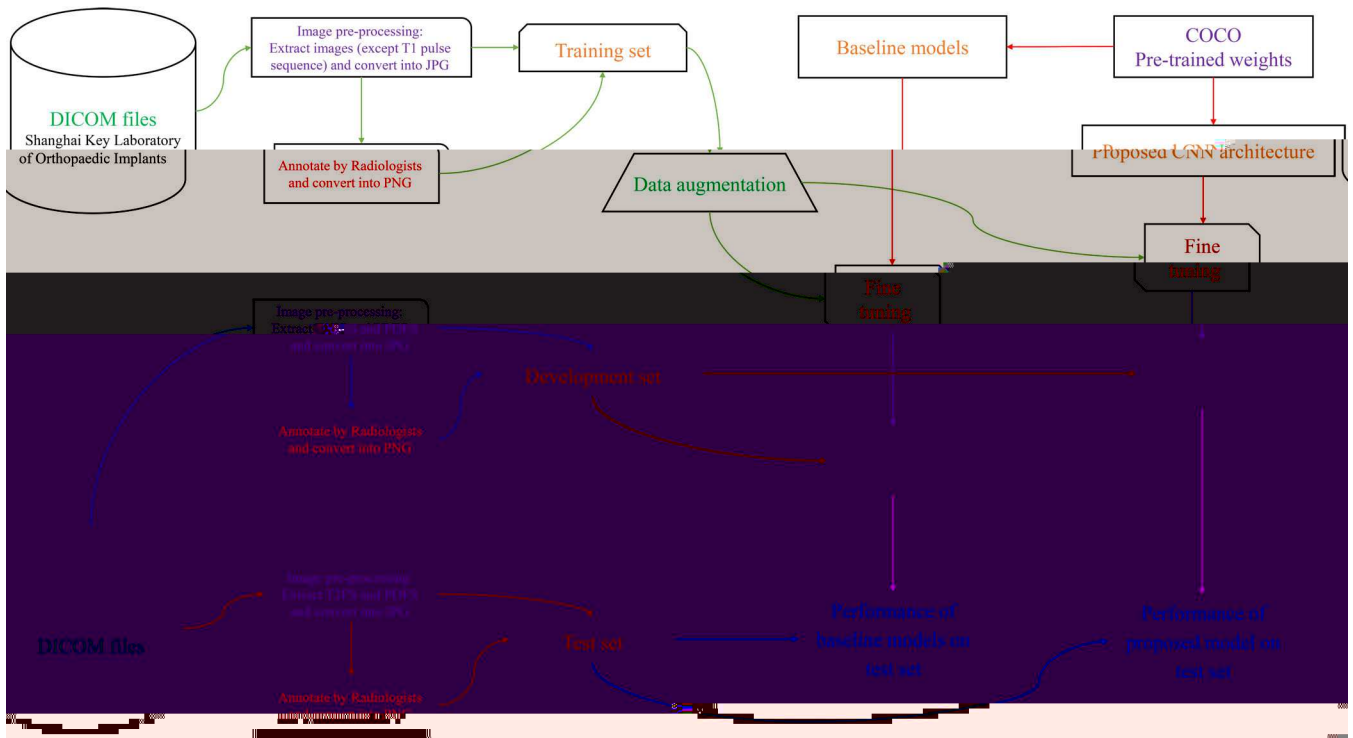
Fig. 2 *Automated deep learning-based human knee joint's synovial fluid detection pipeline. For training set: extract all pulse sequences except T1 from 49 subjects. For development and test sets: extract coronal proton-density weighting with fat suppression (PDFS), sagittal PDFS, and transverse T2 weighting with fat suppression (T2FS) from 15 subjects for development and 25 subjects for evaluation*

4 Experimental results

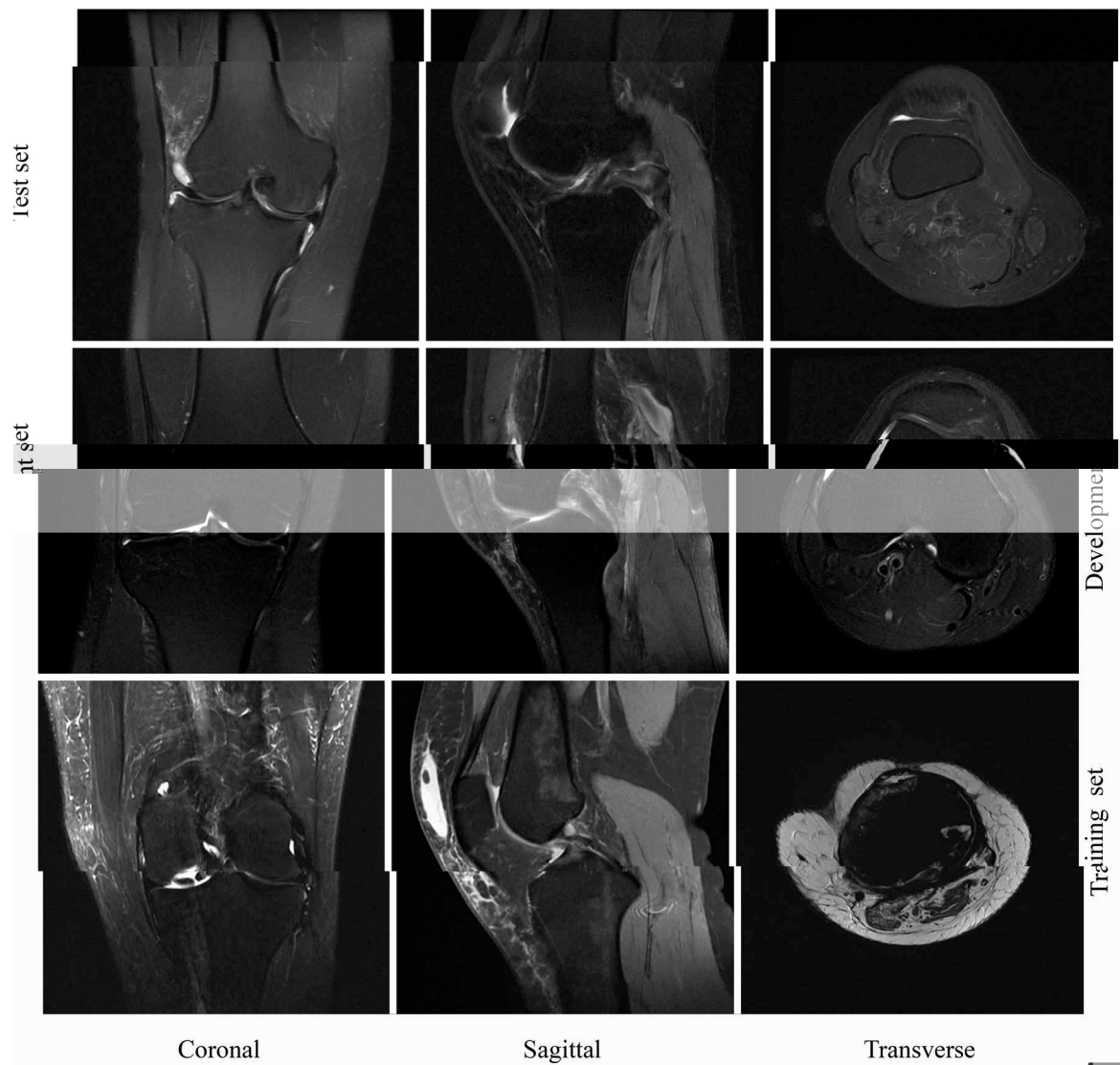### 4.1 Training setting

4.2 Hyperparameter configuration

Fig. 3 *Typical training, development, and test MR images of human knee joint of coronal (left), sagittal (middle), and transverse (right) planes*

Table 1 Training time and hyperparameter configuration of the proposed and baseline models

CNN architecture	Learning algorithm	Learning rate	Mini-batch size	Epochs	Dropout rate	Data augmentation	No. of subjects	Total training time (hours)
baseline model-1	momentum	2×10^{-4}	1	~400	0.3	horizontal flip, crop image, crop to aspect ratio, pixel value scale, rotation, adjust brightness, adjust contrast, adjust hue, adjust saturation, distort colour, and black patches	49	**~37.50**
baseline model-2		3×10^{-4}						~81.57
baseline model-3								~182.16
baseline model-4								~127.53
proposed model								~140.15

4.3 Evaluation and comparison
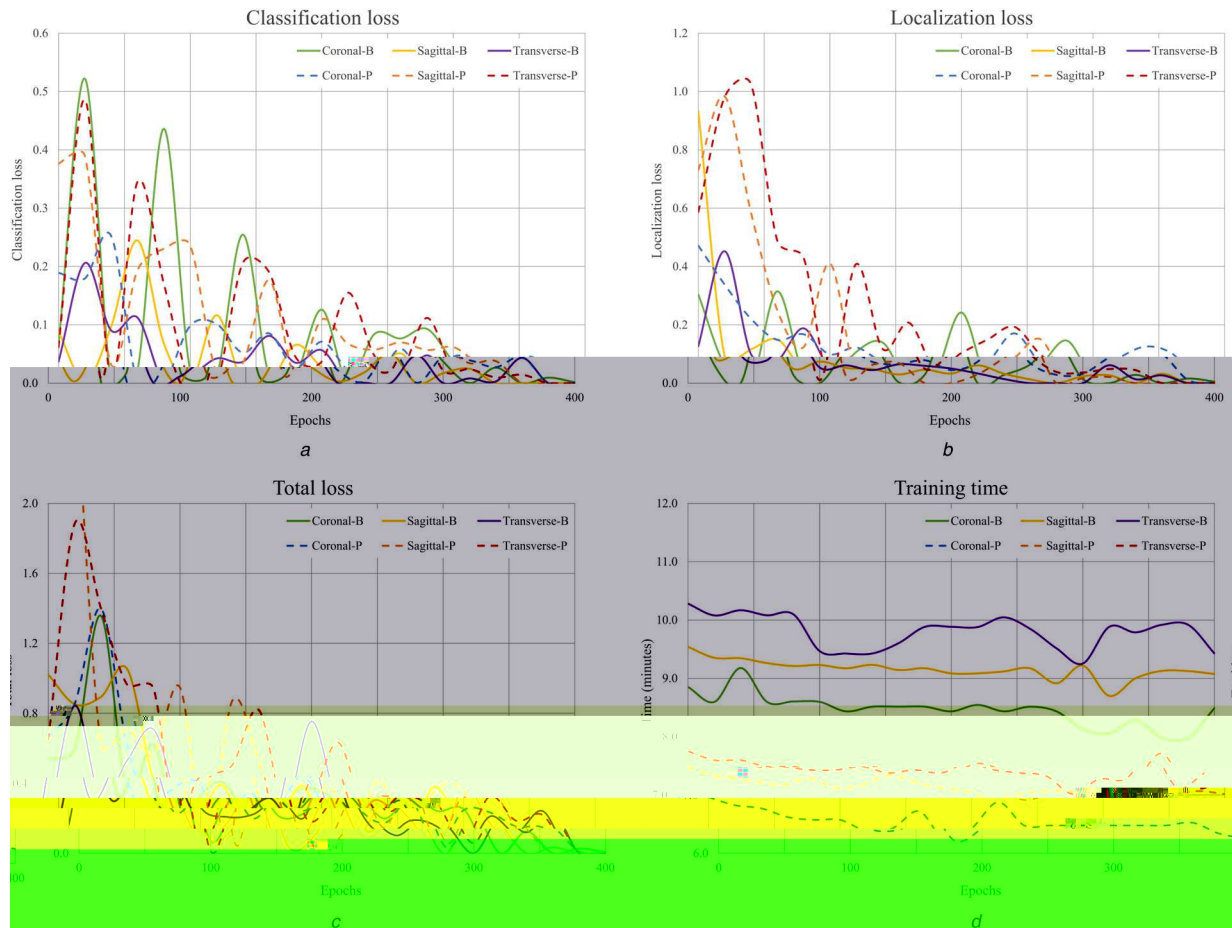
Fig. 4 *Comparison of proposed and baseline models in coronal, sagittal, and transverse planes*
(a)   (b)   (c)   (d)

Table 2 Development losses of the proposed and baseline models in coronal, sagittal, and transverse planes

| CNN architecture	Plane	No. of subjects	RPN loss		Box classifier loss	
			Localisation loss	Objectness loss	Classification loss	Localisation loss
baseline model-1	coronal	15	0.1024	0.1841	0.0801	0.0391
	sagittal		0.1108	0.2254	0.1012	0.0512
	transverse		0.0269	0.1722	0.0465	0.0212
	overall		0.0800	0.1939	0.0759	0.0372
baseline model-2	coronal		0.1547	0.2470	0.0942	0.0462
	sagittal		0.1834	0.3978	0.1057	0.0530
	transverse		0.0493	0.1884	0.0477	0.0215
	overall		0.1291	0.2773	0.0825	0.0402
baseline model-3	coronal		0.1084	0.2309	0.0764	0.0341
	sagittal		0.1446	0.3247	0.1108	0.0636
	transverse		0.0346	0.1576	0.0541	0.0196
	overall		0.0959	0.2377	0.0804	0.0391
baseline model-4	coronal		0.1344	0.2056	0.1068	0.0483
	sagittal		0.1940	0.3794	0.1287	0.0635
	transverse		0.0288	0.1151	0.0831	0.0471
	overall		0.1191	0.2334	0.1062	0.0529
proposed model	coronal		0.1239	0.1870	0.1026	0.0463
	sagittal		0.1801	0.3906	0.0979	0.0642
	transverse		0.0383	0.1212	0.0632	0.0266
	overall		0.1141	0.2329	0.0879	0.0457
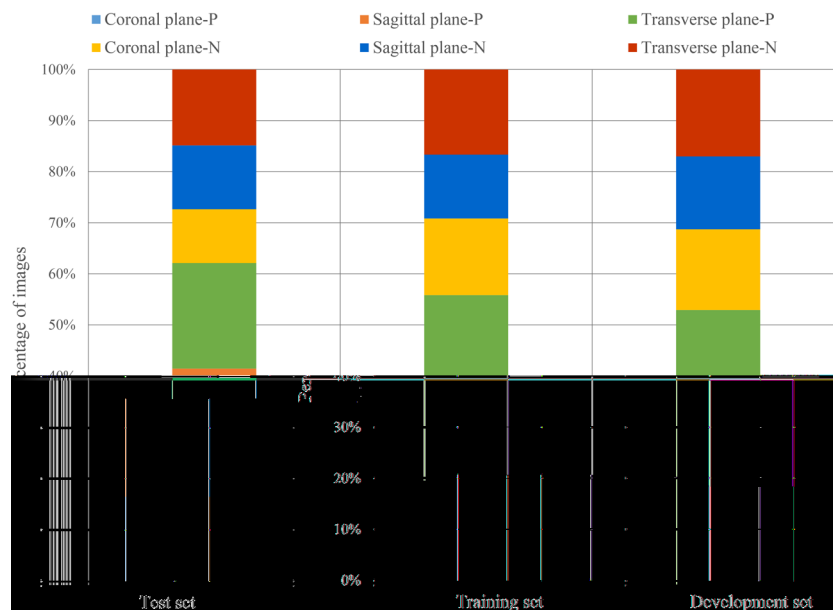
Fig. 5 *Percentages of synovial fluid images in coronal, sagittal, and transverse planes for training, development, and test sets. 'P' denotes for positive example and 'N' denotes for negative example of synovial fluid*
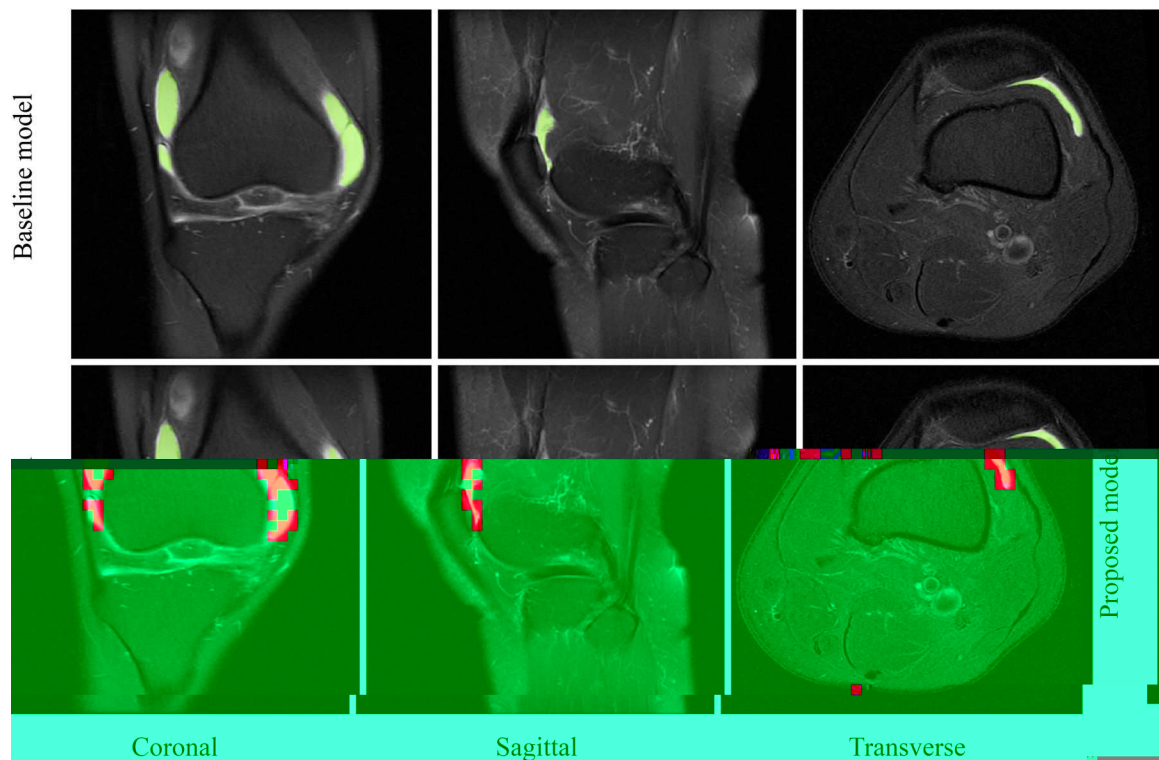

Fig. 6 *Successful detection of human knee joint's synovial fluid instances in coronal (left), sagittal (middle), and transverse (right) planes of the baseline model-3 and proposed model*

4.4 Discussion

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