



An Improved UNet++ Architecture for Deep Learning based Segmentation of Kidneys and Cysts in Autosomal Dominant Polycystic Kidney Disease (ADPKD)

Chetana Krishnan, Graduate Student, University of Alabama at Birmingham; Emma Schmidt; Ezinwanne Onuoha, MS; Michal Mrug, MD; Carlos E Cardenas, PhD; Harrison Kim, PhD

Introduction

UNet++, an enhanced version of UNet, incorporates nested skip connections (NSC), batch normalization (BN), and deep supervision to improve feature extraction and accuracy. However, the UNet++ encoder lacks sufficient feature extraction in small regions of interest (ROIs), leading to inadequate feature fusion during up-sampling and reduced accuracy due to the absence of proper feature normalization. We propose a new architecture called sUNet++, replacing BN with switching normalization (SN) to avoid batch effects and integrate residual blocks in the encoder and decoder. NSCs are replaced with concatenated skip connections (CSC). We compared this architecture with gUNet++, employing group normalization.

Hypothesis

Our hypothesis posits that SN identifies suitable normalization techniques for each layer based on their importance, while residual blocks propagate essential features through skip connections. CSCs improve gradient flow and information propagation. This mitigates performance degradation, allowing the network to learn residual mappings and retain information across layers, resulting in improved segmentation.

Methods

To validate our hypothesis, we trained UNet++, sUNet++, and gUNet++ on T2-weighted MRI images of 95 ADPKD patients, utilizing a total of 756 3D kidney images (604 for training, 76 for validation, and 76 for testing). Preprocessing, cropping, and slicing techniques were applied to generate 2D training samples, resulting in approximately 69,000 samples. The task involved segmenting kidneys and cysts. The models were trained for 50 epochs using a patch-wise approach. Data augmentation techniques were employed to increase the training samples. Leaky ReLU was the activation function. Performance was evaluated using the Dice similarity coefficient (DSC), Hausdorff distance (HD), and Intersection over Union score (IoU).

Results

As summarized in Table 1, sUNet++ achieved higher accuracy than UNet++ for both kidney and cyst segmentation. Moreover, sUNet++ exhibited the highest minimum dice score, indicating superior individual dice performance and success in cases where UNet++ failed. Although gUNet++ showed better performance for kidneys, it was less suitable for cyst segmentation. Notably, sUNet++ required fewer model parameters, converged faster, and demanded less training and inference time. Figure 1 shows the representative test kidney and cyst boundaries determined by sUNet++, gUNet++, and UNet++. Figure 2 illustrates the importance layers of sUNet++ and UNet++.

Conclusion

sUNet++ addresses the challenge of learning normalization in deep learning by dynamically selecting normalizations and statistics for each layer, offering architectural flexibility, and adaptability to varying batch sizes, and eliminating the reliance on sensitive hyperparameters.

Statement of Impact

sUNet++ can improve the diagnosis, treatment planning, and monitoring of ADPKD by detecting early changes in cysts.

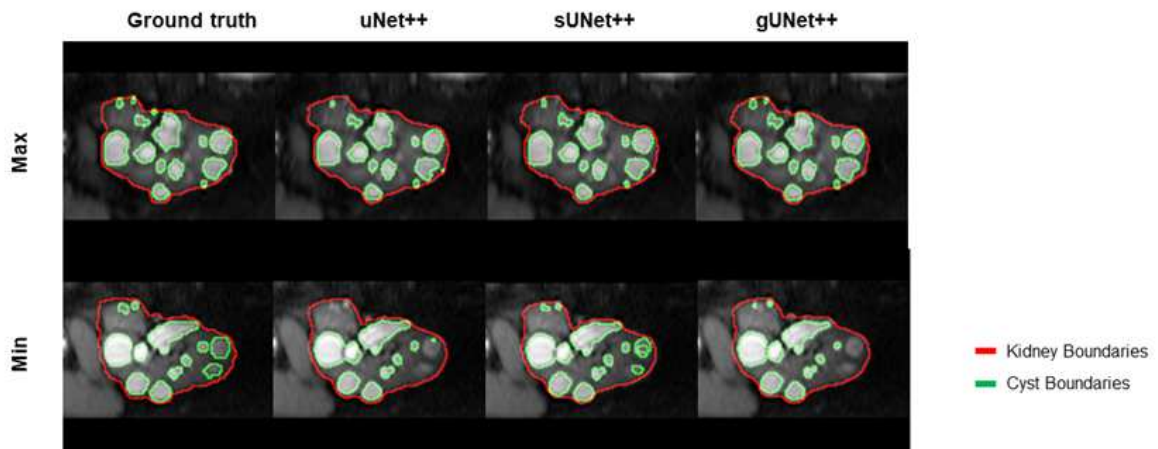


Figure 1. Ground truth Vs predicted kidney and cyst segmentation. Two representative images showing best (max) and moderate (min) performance on the test set, respectively, with kidney (red line) and cyst (green line) boundaries determined by our semi-automatic method (ground truth, first column) and all three models (second to fourth columns) sUNet++ demonstrates improved boundary, edge localization, and enhanced accuracy in capturing collided cyst edges. The replacement of concatenated skip connections enables the preservation of high-resolution edge information by establishing direct paths for information flow between corresponding encoder and decoder layers. This is advantageous for transferring learning to a different task.

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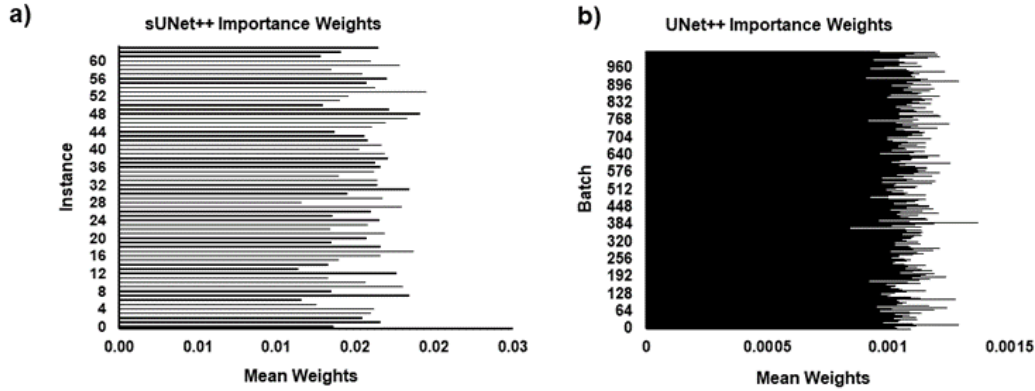


Figure 2. Importance weights. a) The model weight distribution per instance for sUNet++. b) The model weight distribution per batch for UNet++. sUNet++ has fewer model parameters and the concatenated skip connections combined all the layers with equal importance to one single layer to avoid complexity. This reduces redundancy and helps in faster convergence and training. UNet++ with batch normalization considers all the batches irrespective of importance thus leading to re-learning the same features causing overfitting on training. The mean weights are higher in sUNet++ for fewer parameters compared to UNet++ thus having improved representative learning thus removing batch effects.

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Model	ROI	IoU Score	HD (mm)	Test DSC	Min Test DSC	Max Test DSC	Training Time / Epoch (s)	Inference Time (min ± sec)
UNet++	Kidney	0.88±0.47	1.35±0.95	0.93±0.35	0.70	0.97	217±5	05±23
	Cyst	0.77±0.43	1.52±0.78	0.86±0.42	0.71	0.92	220±7	07±14
sUNet++	Kidney	0.90±0.44	1.38±0.94	0.94±0.35	0.84	0.98	110±3	04±12
	Cyst	0.77±0.47	1.30±0.90	0.87±0.42	0.76	0.93	116±6	04±34
gUNet++	Kidney	0.88±0.46	1.43±0.91	0.93±0.34	0.74	0.97	203±4	05±09
	Cyst	0.76±0.44	1.53±0.79	0.86±0.43	0.65	0.93	218±9	05±16

Table 1. Performance Metrics. Intersection over union (IoU) score, Hausdorff distance (HD), and test Dice similarity score (DSC) of UNet++ and proposed models based kidney and cyst segmentation, together with its training time per epoch, and inference time to predict the boundaries of all test images.

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Keywords

Skip connections; Normalization; Image segmentation; Polycystic kidney disease; UNet++; Residual staging