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Primary Category: Musculoskeletal
Secondary Category: Machine Learning

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04) Automated Analysis of Muscle Quantitative Imaging Biomarkers for Muscle Quantity and Quality Using Convolutional Neural Networks

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FIGURE (RECOMMENDED)

http://abstract.rsna.org/uploads/2019/19015012/19015012_i28y.jpg

PURPOSE

To automate quantification of muscle quantity and quality using a cascaded system of convolutional neural networks (CNNs) applied opportunistically to chest and abdominal CT.

METHOD AND MATERIALS

A combination of public and internal non-contrast CT scans were used to train CNNs. 328 public low-dose chest CT scans from the National Lung Screening Trial (NLST) and 258 internal abdomen and pelvis CT scans of healthy kidney donors were collected. Hand-drawn left paraspinal muscle (LSPM) segmentations at the level of T12 were created using custom software. 80% of the scans were used to train and 20% were used for validation.

A fully automated system of cascaded CNNs was developed to (1) identify the axial location of the T12 slice from sagittal slices, and (2) predict the axial T12 left paraspinal muscle segmentation. Axial slice selection performance was evaluated against the mean absolute error, and segmentations were evaluated on dice scores.

LSPM segmentations yielded the following muscle quantitative imaging biomarkers (mQIBs): skeletal muscle cross sectional area (SMA), muscle radiation attenuation (SMRA), percentage muscle (SMT), lean muscle (SML), fatty muscle (SMF) and intermuscular adipose (IMAT). Agreement between manual and predicted mQIB metrics was analyzed using Bland-Altman analysis. Composite network performance metrics and mQIB metrics were compared using two-tailed unpaired Student's t-tests to determine if cohort means were significantly different ($p < 0.05$).

RESULTS

Mean absolute T12 axial slice selection error for the NLST (21.7 mm +/- 10.9 mm) and internal data (18.9 mm +/- 8.3 mm) were significantly different. There was no significant difference between T12 LSPM dice scores for the NLST (0.92 +/- 0.03) and internal data (0.93 mm +/- 0.03). SMA, SMRA, SMT, and SML values were significantly greater and SMF and IMAT values were significantly lower for the internal dataset when compared to those from the NLST dataset reflecting higher muscle quantity and quality.

CONCLUSION

Convolutional neural networks are a feasible approach for automating quantification of muscle mass and quality, and are able to distinguish between healthy and older patients with chronic disease at risk for sarcopenia.

CLINICAL RELEVANCE/APPLICATION

The quantification of mQIBs reflecting skeletal muscle mass and quality can be fully-automated using a cascaded system of CNNs, and should facilitate the diagnosis of sarcopenia.

FIGURE (OPTIONAL)

**** no data entered ****

Disclosures:

Nothing to disclose:	Dustin Brown
Consultant, Arterys Inc Consultant, IBM Corporation	Brian Hurt
Nothing to disclose:	Brady Huang
Nothing to disclose:	Leon Lenchik
Nothing to disclose:	Robert Boutin
Founder, Arterys, Inc Consultant, Arterys, Inc Shareholder, Arterys, Inc Speaker, Bayer AG Research Grant, Bayer AG Speaker, General Electric Company Research Grant, General Electric Company	Albert Hsiao

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