

False Positive Reduction for Lung Nodule Analysis

The current solution uses a Wide Residual Network architecture [1].

The full Luna2016 CT scan image dataset has been resampled to an isotropic resolution [2] [3]. Furthermore, to deal with the significant class imbalance in the dataset (i.e.: of the 551065 candidates, only about 1186 were labeled as nodules), the "negative" class (the most common class in our case) has been under-sampled and the "positive" class has been augmented (through random rotation, zoom, translation, crop). This has resulted in a 75-25 class distribution. For each candidate, three orthogonal (2D) slices are selected and fed to the same network [2].

For model training, 10-fold cross-validation has been used.

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[1] Zagoruyko, S., & Komodakis, N. (2016). Wide Residual Networks.
<https://arxiv.org/pdf/1605.07146.pdf>

[2] Moira Berens, Robbert van der Gugten, Michael de Kaste, Jeroen Manders, and Guido Zuidhof (2016). ZNET - Lung Nodule Detection
http://luna16.grand-challenge.org/serve/public_html/pdfs/ZNET_NDET_160831.pdf/

[3] <https://www.kaggle.com/gzuidhof/data-science-bowl-2017/full-preprocessing-tutorial>