SquidNet: A Novel GAN-based Algorithm for the Color Normalization of Histopathological Images

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The role of deep learning in the recognition of morphological structures in histopathological data is heavily stunted by extreme variations that may exist in the datasets that these deep learning models are trained on. In order to mitigate this data-side bias, color normalization algorithms are utilized, allowing datasets to exhibit less variation. Such a normalization typically results in better model performances. However, color normalization (CN) algorithms typically only use one target image as a reference, and use this singular target image to generalize an entire dataset. Therefore, normalized datasets are oftentimes not complete reflections of an aligned staining pattern. However, general adversarial networks, or GANs, generate plausible data and effectively replicate or modify a source image while being trained and learning regularities from another dataset. So, GANs hold the potential to more effectively color normalize by mapping features from dataset to dataset. A novel GAN architecture was custom-built from scratch for the purpose of generating color normalized, high-quality histopathological images. The proposed SquidNet leverages two discriminator networks and novel augmentation techniques. 3 state-of-the-art CN algorithms were utilized to compare to SquidNet: Reinhard, Macenko, and Vahadane. The 4 CN techniques each normalized 4 different datasets, with each dataset containing diverse staining patterns and being compiled from multiple laboratories and organ types. A U-Net segmentation algorithm was used to segment each of the datasets, and the dice score coefficient (DSC) was used to compare the results of each run. It was determined that the novel SquidNet algorithm outperformed current conventional, state-of-the-art techniques.

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