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Skin cancer, the most common human malignancy^{1,2,3}, is primarily diagnosed visually, beginning with an initial clinical screening and followed potentially by dermoscopic analysis, a biopsy and histopathological examination. Automated classification of skin lesions using images is a challenging task owing to the fine-grained variability in the appearance of skin lesions. Deep convolutional neural networks (CNNs)^{4,5} show potential for general and highly variable tasks across many fine-grained object categories^{6,7,8,9,10,11}. Here we demonstrate classification of skin lesions using a single CNN, trained end-to-end from images directly, using only pixels and disease labels as inputs. We train a CNN using a dataset of 129,450 clinical images—two orders of magnitude larger than previous datasets¹²—consisting of 2,032 different diseases. We test its performance against 21 board-certified dermatologists on biopsy-proven clinical images with two critical binary classification use cases: keratinocyte carcinomas versus benign seborrheic keratoses; and malignant melanomas versus benign nevi. The first case represents the identification of the most common cancers, the second represents the identification of the deadliest skin cancer. The CNN achieves performance on par with all tested experts across both tasks, demonstrating an artificial intelligence capable of classifying skin cancer with a level of competence comparable to dermatologists. Outfitted with deep neural networks, mobile devices can potentially extend the reach of dermatologists outside of the clinic. It is projected that 6.3 billion smartphone subscriptions will exist by the year 2021 (ref. 13) and can therefore potentially provide low-cost universal access to vital diagnostic care.

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Contributions

A.E. and B.K. conceptualized and trained the algorithms and collected data. R.A.N., J.K. and S.S. developed the taxonomy, oversaw the medical tasks and recruited dermatologists. H.M.B. and S.T. supervised the project.

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Ethics declarations

Competing interests

The authors declare no competing financial interests.

Additional information

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Extended data figures and tables

Extended Data Figure 1 Procedure for calculating inference class probabilities from training class probabilities.

Illustrative example of the inference procedure using a subset of the taxonomy and mock training/inference classes. Inference classes (for example, malignant and benign lesions) correspond to the red nodes in the tree. Training classes (for example, amelanotic melanoma, blue nevus), which were determined using the partitioning algorithm with maxClassSize = 1,000, correspond to the green nodes in the tree. White nodes represent either nodes that are contained in an ancestor node’s training class or nodes that are too large to be individual training classes. The equation represents the relationship between the probability of a parent node, u , and its children, $C(u)$; the sum of the child probabilities equals the probability of the parent. The CNN outputs a distribution over the training nodes. To recover the probability of any inference node it therefore suffices to sum the probabilities of the training nodes that are its descendants. A numerical example is shown for the benign inference class: $P_{\text{benign}} = 0.6 = 0.1 + 0.05 + 0.05 + 0.3 + 0.02 + 0.03 + 0.05$.

Extended Data Figure 2 Confusion matrix comparison between CNN and dermatologists.

Confusion matrices for the CNN and both dermatologists for the nine-way classification task of the second validation strategy reveal similarities in misclassification between human experts and the CNN. Element (i, j) of each confusion matrix represents the empirical probability of predicting class j given that the ground truth was class i , with i and j referencing classes from [Extended Data Table 2d](#). Note that both the CNN and the dermatologists noticeably confuse benign and malignant melanocytic lesions—classes 7 and 8—with each other, with dermatologists erring on the side of predicting malignant. The distribution across column 6—inflammatory conditions—is pronounced in all three plots, demonstrating that many lesions are easily confused with this class. The distribution across row 2 in all three plots shows the difficulty of classifying malignant dermal tumours, which appear as little more than cutaneous nodules under the skin. The dermatologist matrices are each computed using the 180 images from the nine-way validation set. The CNN matrix is computed using a random sample of 684 images (equally distributed across the nine classes) from the validation set.

Extended Data Figure 3 Saliency maps for nine example images from the second validation strategy.

a–i, Saliency maps for example images from each of the nine clinical disease classes of the second validation strategy reveal the pixels that most influence a CNN’s prediction. Saliency maps show the pixel gradients with respect to the CNN’s loss function. Darker pixels represent those with more influence. We see clear correlation between the lesions themselves and the saliency maps. Conditions with a single lesion (**a–f**) tend to exhibit tight saliency maps centred around the lesion. Conditions with spreading lesions (**g–i**) exhibit saliency maps that similarly occupy multiple points of interest in the images. **a**, Malignant melanocytic lesion (source image: <https://www.dermquest.com/imagegallery/large/020114HB.JPG>). **b**, Malignant epidermal lesion (source image: <https://www.dermquest.com/imagegallery/large/001883HB.JPG>). **c**, Malignant dermal lesion (source image:

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a, Identical plots and results as shown in [Fig. 3a](#), except that dermatologists were asked if a lesion appeared to be malignant or benign. This is a somewhat unnatural question to ask, in the clinic, the only actionable decision is whether or not to biopsy or treat a lesion. The blue curves for the CNN are identical to [Fig. 3. b](#), [Figure 3b](#) reprinted for visual comparison to **a**.

Extended Data Table 1 Disease-partitioning algorithm

Extended Data Table 2 General validation results

PowerPoint slides

- [PowerPoint slide for Fig. 1](#)
- [PowerPoint slide for Fig. 2](#)
- [PowerPoint slide for Fig. 3](#)
- [PowerPoint slide for Fig. 4](#)

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