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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒ The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐ A description of all covariates tested
☐	☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒ For null hypothesis testing, the test statistic (e.g. F, t, r) with confidence intervals, effect sizes, degrees of freedom and P value noted *Give P values as exact values whenever suitable.*
☒	☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	Data from a teledermatology service were de-identified prior to transfer to study investigators.
Data analysis	The deep learning framework (TensorFlow v1.15.0) used in this study is available at https://www.tensorflow.org/; the training framework (Estimator) is available at https://www.tensorflow.org/guide/estimators; the deep learning architecture (Inception-v4) is available at: https://github.com/tensorflow/models/blob/master/research/slim/nets/inception_v4.py.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The de-identified teledermatology data used in this study are not publicly available due to restrictions in the data-sharing agreement.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences   ☐ Behavioural & social sciences   ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	The 80/20 development/validation split was determined a priori without sample size calculations. The number of skin conditions (26) was chosen such that at least 100 examples per skin condition (based on preliminary labels) would be available for model development, and a projected 25 examples per skin condition for model validation.
Data exclusions	Several pre-determined exclusion criteria were applied. First, cases with multiple skin conditions or not diagnosable were excluded from the study. Second, from the validation sets, cases from repeat visits of a patient in the development dataset were excluded to avoid bias.
Replication	The deep learning system is an ensemble of 6 trained models. The spread in tuning set performance between the 6 trained models was measured at 1-3%.
Randomization	Validation set B cases were randomly subselected from validation set A using stratified random sampling to enrich for rarer skin conditions.
Blinding	The skin condition mapping were established by dermatologists who were blinded to the predictions of the deep learning system.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Human research participants

Policy information about studies involving human research participants

Population characteristics	De-identified data from cases submitted to a teledermatology service. Baseline variables are reported in Table 1, but briefly on the development and validation sets, patients were aged 40-43 on average, with 62-64% female, and the most common diagnoses were eczema, psoriasis, and acne. Post-visit treatment data were not available.
Recruitment	All consecutive adult cases in the time period (2010-2018) were used, excluding those with multiple skin conditions or not diagnosable (as in exclusion criteria above).
Ethics oversight	The protocol was reviewed by Advarra IRB (Columbia, MD), which determined that it was exempt from further review under 45 CFR 46.

Note that full information on the approval of the study protocol must also be provided in the manuscript.