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Estimating biological age from retinal imaging: a scoping review

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ABSTRACT

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Background/Aims The emerging concept of retinal age, a biomarker derived from retinal images, holds promise in estimating biological age. The retinal age gap (RAG) represents the difference between retinal age and chronological age, which serves as an indicator of deviations from normal ageing. This scoping review aims to collate studies on retinal age to determine its potential clinical utility and to identify knowledge gaps for future research.

Methods Using the Preferred Reporting Items for Systematic Reviews and Meta-Analyses checklist, eligible non-review, human studies were identified, selected and appraised. PubMed, Scopus, SciELO, PsycINFO, Google Scholar, Cochrane, CINAHL, Africa Wide EBSCO, MedRxiv and BioRxiv databases were searched to identify literature pertaining to retinal age, the RAG and their associations. No restrictions were imposed on publication date.

Results Thirteen articles published between 2022 and 2023 were analysed, revealing four models capable of determining biological age from retinal images. Three models, 'Retinal Age', 'EyeAge' and a 'convolutional network-based model', achieved comparable mean absolute errors: 3.55, 3.30 and 3.97, respectively. A fourth model, 'RetiAGE', predicting the probability of being older than 65 years, also demonstrated strong predictive ability with respect to clinical outcomes. In the models identified, a higher predicted RAG demonstrated an association with negative occurrences, notably mortality and cardiovascular health outcomes.

Conclusion This review highlights the potential clinical application of retinal age and RAG, emphasising the need for further research to establish their generalisability for clinical use, particularly in neuropsychiatry. The identified models showcase promising accuracy in estimating biological age, suggesting its viability for evaluating health status.

INTRODUCTION

The number of elderly individuals is rising, leading to an increased burden on healthcare services and society. Ageing changes are heterogenous, with substantial variation in health impacts of ageing across populations, individuals and tissues.¹ 2 Thus, biological ageing markers have emerged to better represent the ageing process and predict functional capability.

WHAT IS ALREADY KNOWN ON THIS TOPIC

 \Rightarrow Retinal age has emerged as a promising ageing biomarker capable of determining biological age from retinal images.

WHAT THIS STUDY ADDS

⇒ This study presents a comprehensive scoping review of current literature concerning retinal age and the retinal age gap (RAG), highlighting the reproducible association between advanced RAG and increased mortality and cardiovascular disease risk.

HOW THIS STUDY MIGHT AFFECT RESEARCH, PRACTICE OR POLICY

 \Rightarrow The findings underscore the paucity of knowledge on this topic, advocating for further research in this area to determine the potential clinical use of retinal age as a biomarker.

Retinal age, an imaging-based biomarker, provides an estimate of biological age derived from retinal fundus photographs.³⁴ The rationale for retinal age as a biomarker stems from the retina's shared embryological origin with the central nervous system (CNS)^{[5](#page-4-2)} and microvascular structure, which is closely related to that of the brain, heart and kidney. 6^{7} Although retinal imaging has largely been used by ophthalmologists for understanding and treatment of ocular disease,^{[8](#page-4-4)} predictive retinal ageing extends utility of retinal fundus imaging by applying deep learning (DL).

The introduction of the retinal age gap (RAG), the difference between calculated retinal age and chronological age, provides a valuable metric for assessing normal ageing deviations. Compared with traditional biomarker approaches, criticised for their cost, invasiveness, time-consuming nature and suboptimal accuracy, application of retinal age models provides a cost-effective, non-invasive and readily accessible way of estimating biological age, 9^{10} particularly suited to large-scale population studies.

To date, there is no review on the reliability of retinal age as a biomarker. Although several biomarker reviews have included retinal age as one of many biological age estimators, they have not provided a comprehensive summary of the accuracy, practical utilisation or relevance of retinal ageing models. This scoping review seeks to consolidate what is known about retinal age, while identifying gaps for future research.

Specifically, this review aims to answer:

- ► How extensive is the current literature pertaining to retinal age and RAG?
- How many models exist? How accurate are they?
- ► Does this biomarker have clinical associations? Does it exhibit clinical utility?
- ► What are pressing future directions for research?

METHODS

Protocol and registration

A scoping review is suited to expand what is known about retinal age, as it allows synthesis of current literature. A protocol was developed for this purpose and registered on Open Science Forum (available at: [https://osf.io/](https://osf.io/fse75/) [fse75/](https://osf.io/fse75/) DOI 10.17605/OSF.IO/FSE75). The format for this review is based on the Preferred Reporting Items for Systematic Reviews and Meta-Analyses for Scoping Reviews (PRISMA-ScR) checklist and has made use of the Janna Briggs Institute Manual for Evidence Synthesis.

Eligibility criteria

All published literature, and preprints of primary studies of retinal age in adults were included for analysis. No limitations were imposed for publication language or date.

Search

A literature search of the following electronic databases was conducted from 17 to 19 June 2023: PubMed, Scopus, Cochrane Library, CINAHL, SciELO, Google Scholar, PsycINFO, Africa Wide EBSCO Host, MedRxiv and BioRxiv. A librarian assisted with formulating the search strategy. Initial search terms for the PubMed database included the non-MESH terms, "retinal age" AND "association", which were further refined to ((retinal age [Text Word]) OR (retinal age gap [Text Word])) AND (((association) OR (link)) OR (biomarker)) and adapted for each database searched. Refer to [online](https://dx.doi.org/10.1136/bmjophth-2024-001794) [supplemental appendix 1](https://dx.doi.org/10.1136/bmjophth-2024-001794) for full search strategy used.

Selection

A two-stage selection process was employed. Articles identified through the search strategy were deduplicated. Two reviewers (MJG, S-MK) independently screened titles and abstracts to ascertain eligibility and relevance, using the predetermined inclusion and exclusion criteria. For publications that met inclusion criteria, these criteria were re-applied to the full-text articles. When discrepancies in reviewers' ratings were observed, a coordinating investigator (JI) conducted a final review to determine inclusion eligibility. Citations within included articles

Figure 1 The Preferred Reporting Items for Systematic Reviews and Meta-Analyses diagram outlines the selection process for studies included in this scoping review.

were scanned to identify additional articles suitable for inclusion. Email updates for Google Scholar were enabled to capture newly published literature between the search date and the writing phase. Subsequent articles found were subjected to the same review process.

Data charting process

Data were extracted from the suitable articles using a spreadsheet developed by reviewers. Data extracted included title, publication date, authors, study design, study aims, model type, model development, outcome of interest and key findings.

RESULTS

Selection of sources

The PRISMA flow diagram [\(figure](#page-1-0) 1) outlines the selection process. The search strategy yielded 342 articles (online supplemental appendix 1). After application of inclusion criteria, 41 full-text articles were examined for eligibility. Four articles published after the literature search date were considered for inclusion. A total of 13 articles met criteria for inclusion in this review.

Characteristics of the articles

All articles included for review were published between 2022 and 2023. [Online supplemental appendix 2](https://dx.doi.org/10.1136/bmjophth-2024-001794) presents a summary of the studies.

Narrative review of study findings

All included studies used DL algorithms for retinal age analysis. Four distinct models capable of determining biological age from fundus photographs are outlined. Their training, validating and testing processes are described below.

Model development and accuracy

Three models can predict age from retinal images, namely: '*Retinal Age*',⁴ '*EyeAge*'^{[11](#page-4-7)} and '*convolutional network-based model*'[.12](#page-4-8) A fourth biological ageing model, '*RetiAGE*',^{[3](#page-4-1)} estimates the probability of an individual being older than 65 years.

The '*Retinal Age*' model was trained and validated on 19 200 fundus photographs from 11 052 healthy UK Biobank (UKB) participants, a dataset comprising over 500 000 individuals between the ages of 40 and 69 years at recruitment. The model underwent fivefold crossvalidation, achieved a mean absolute error (MAE) of 3.55 and Pearson's correlation coefficient (R) between estimated age and chronological age of 0.80 .^{[4](#page-4-6)} The '*EyeAge*' model was trained on 217 289 images from 100 692 individuals with a mean age of 54 years in the EyePACS dataset, validated on 54 292 images from 25 238 individuals within the same dataset and tested in both the UKB and EyePACS datasets. The model achieved an MAE of 3.30, and a Pearson's R of 0.87 for the UKB test dataset, with corresponding figures of 2.86 and 0.95 for EyePACS.[11](#page-4-7) The '*convolutional network-based model*' was trained on 98 400 photos from patients diagnosed with diabetes, aged 40–90 years, who were enrolled in the Retisalud programme of the Canary Islands Health Service. To validate the model, 1000 images from the dataset were

used, achieving a MAE of 3.97. The '*RetiAGE*' model was trained on 116 312 photographs from 36 432 participants of the Korean Health Screening Study with a mean age of 54 years and validated on 12 924 unseen photos from 4048 participants from the same dataset. An internal test on 32 318 photos of 10 171 participants achieved an area under the receiver operating characteristic (AUROC) curve of 0.968 and an area under the precision-recall curve (AUPRC) of 0.83. When applied to the UKB, the model achieved an AUROC of 0.756 and an AUPRC of 0.399 with a correlation of 0.62 between '*RetiAGE*' and chronological age.³

Clinical utility and model associations

RAG, previously defined, has conventionally been used as the metric for assessing clinical utility and performance of retinal ageing models in reflecting biological ageing. Eleven papers using two models, '*Retinal Age*' and '*convolutional network-based model*', have been published with RAG as the outcome measure of interest. [Table](#page-2-0) 1 summarises the clinical utility of the four identified retinal ageing models.

Ten association analyses were conducted using '*Retinal Age*' to explore the relationship between RAG and agerelated parameters, within the UKB. The introductory study, highlighting the development of the model, revealed a significant association of a 2% increase in mortality risk for each 1-year increase in RAG.^{[4](#page-4-6)} Beyond the risk stratification for mortality, several prospective studies have highlighted associations for each 1-year increase in RAG with a 10% increase of Parkinson's disease,^{[13](#page-5-0)} a 4% increase of stroke,¹⁴ a 3% increase of incident cardiovascular disease, 15 a 10% increase in risk

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of incident kidney failure¹⁶ and a 7% increased risk of diabetic retinopathy in patients with diabetes. 17 Several cross-sectional studies using '*Retinal Age*' explored the associations between lifestyle diseases and RAG. Central ω obesity,^{[18](#page-5-5)} higher glycaemia levels¹⁹ and metabolic syndrome^{[20](#page-5-7)} were associated with higher RAGs, while a study aimed at correlating RAG with cardiovascular health metrics—comprising 7 metrics with a total score of 14—found that each 1-unit increase in cardiovascular health score was associated with a 13% decrease in calcu-lated RAG.^{[21](#page-5-8)}

'*EyeAge*' evaluated its clinical performance by calculating EyeAge Acceleration, determined akin to RAG, as the difference between EyeAge (reflecting retinal age) and chronological age. In the UKB, adjusted '*EyeAge*' achieved an all-cause mortality HR of 1.03, while RAG (referred to as EyeAge Acceleration) was associated with a higher risk of chronic obstructive pulmonary disease, myocardial infarction, elevated systolic blood pressure and fluid intelligence scores. Additionally, a genomewide association study performed found candidate genes identified for EyeAge acceleration are associated with eye function and age-related disorders.¹¹

The '*convolutional network-based model*' determined, from a case-control study in patients with diabetes from the Retisalud programme, that higher RAG was associated with more severe, progressive diabetic retinopathy.[12](#page-4-8) Although more severe, progressive diabetic retinopathy cannot simply be equated with ageing, this echoes findings of '*Retinal Age*' in patients with diabetes.^{[17](#page-5-4)}

'*RetiAGE*' also used the UKB to assess its clinical performance. In contrast to '*Retinal Age*' and '*convolutional network-based model*', which used RAG for outcome assessment, '*RetiAGE*' directly investigated its association with different age-related outcomes. Individuals placed in higher quartiles of '*RetiAGE*' were considered to have accelerated ageing. Comparing individuals in the fourth quartile group with those in the first quartile, there was a 67% higher risk of 10-year all-cause mortality, a 142% higher risk of cardiovascular-related mortality and a 60% higher risk of cancer-related mortality after adjusting for chronological age and other established ageing biomarkers.^{[3](#page-4-1)}

Saliency maps

Features that drive retinal ageing estimates were identified for '*Retinal Age*' and '*RetiAGE*'. '*Retinal Age*' retrieved attention maps using guided Grad-CAM, 22 to highlight pixels in the input retinal fundus image based on their contributions to the final evaluation. Areas around retinal vessels are highlighted, indicating that retinal microvasculature is used by the DL model for age prediction[.4](#page-4-6) '*RetiAGE*' generated saliency maps to localise anatomy contributing to retinal ageing. They indicate that '*RetiAGE*' focuses on the macula, optic disc and retinal vessels for age determination.^{[3](#page-4-1)}

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DISCUSSION

This study aimed to appraise existing research using retinal photography to develop biological ageing markers. We sought to determine the accuracy of retinal age prediction models, evaluate their ability to reflect age-related parameters and explore their clinical associations. This scoping review identified models which estimate chronological age from retinal images with moderate to high accuracy and identified several age-related associations.

Four models are currently available to estimate biological age from retinal images, all based on DL algorithms: '*Retinal Age*',^{[4](#page-4-6)} '*EyeAge*',¹¹ '*convolutional network-based* model^{[12](#page-4-8)} and '*RetiAGE*'.³ '*Retinal Age*', '*EyeAge*' and '*convolutional network-based model*' were trained to predict numerical chronological age from retinal images, while '*RetiAGE*' was trained to predict the probability of an individual being older than 65 years.

All models were trained and validated using a single dataset, predominantly comprising Caucasian or Asian populations. To enhance robustness, both '*EyeAge*' and '*RetiAGE*' underwent additional internal testing on previously unseen images from the training and validation cohort. For model testing and outcome assessment, the UKB was used by three models: '*Retinal Age*', '*EyeAge*' and '*RetiAGE*'. While the four identified models demonstrated comparable accuracy and performance, it is important to highlight inconsistent reporting of performance metrics, with some pertaining to validation performance, and others test performance. Consequently, the generalisability of these models is uncertain, warranting further work to assess their applicability across diverse populations.

Nevertheless, using retinal age models to predict mortality and morbidity carries significant clinical implications. A key finding from these 13 selected papers emphasises that accelerated ageing, calculated as RAG, age acceleration or other indices, consistently correlates with mortality risk across three models. 3411 In addition, '*Retinal Age*' and '*EyeAge*' show associations with cardiovascular disease, while '*Retinal Age*' and '*convolutional network-based model*' show connections with the risk of diabetic retinopathy in patients with diabetes. These findings highlight the potential of retinal age as an informative tool for quantifying risk of mortality and cardiovascular morbidity. However, no clinical trials have yet explored the utility or feasibility of the models, a crucial aspect for determining their clinical relevance. Furthermore, factors associated with higher RAG, including glycaemic status,¹⁹ central obesity¹⁸ and metabolic syndrome,²⁰ suggest that RAG may provide valuable insight into lifestyle habits and traits that accelerate ageing.

Reporting of characteristics of populations used for training age prediction models is important. Only '*Retinal Age*' mentions training on healthy populations, a key distinction if one wishes to consider biological age equal to chronological age. The health status of the population used for training '*EyeAge*' and '*RetiAGE*' remains undisclosed, while '*convolutional network-based model*' used

data from patients with diabetes. This may confound the effects of diabetes on apparent ageing, with age itself. Such discrepancies could spark controversy over whether these three retinal age models are accurate predictors of biological age, demanding a standardised procedure for developing biological age.

Additionally, these models were trained on a limited set of retinal features with only two models, '*Retinal Age*' and '*RetiAGE*', producing saliency maps to identify features used for age assessment. This links to concerns about regulatory compliance and interpretability of the use of artificial intelligence in healthcare.²³ ²⁴ However, both models alluded to retinal microvasculature being a key component of age ascertainment, indicating that retinal age may reflect ageing related to vascular status. This is supported by the finding that retinal age models are particularly associated with cardiovascular health. 321 To improve understanding of retinal features that align with biological age, advanced visualisation techniques are imperative.

The application of retinal age models in predicting neuropsychiatric diseases is relatively underexplored. Given that the retina is an extension of the CNS, it offers a unique and accessible 'window' to visualise cerebral neuronal health.^{[7](#page-4-9)} Studies have found that changes in the retina, most notably thinning in the retinal nerve fibre layer, may be associated with certain neuropsychiatric and neurodegenerative diseases.²⁵ In our review, only one paper using the '*Retinal Age*' model explored RAG in the realm of neuropsychiatry, specifically in the context of Parkinson's disease, leaving this area underexplored.¹³ As neurodegeneration is an important aspect of ageing, future studies should concentrate on improving our understanding of the connections between retinal age and neuropsychiatric conditions.

Several limitations of this scoping review deserve emphasis. Publications in non-indexed journals and other 'grey literature' may have been missed. Insufficient data availability precluded quantitative synthesis using meta-analytic statistical techniques. As more literature becomes available, conducting a more extensive review may unveil more diverse associations of retinal age, mechanisms for associations and possibly link retinal age to other biomarkers. Strengths of our study included its development according to a predefined protocol, and application of the PRISMA-ScR.

In conclusion, this scoping review identified four retinal ageing models derived from retinal images, linking advancing RAGs with mortality and cardiovascular disease. It highlights the scarcity of data in the realm of neuropsychiatry, emphasises the need for standardised procedures in developing retinal ageing models and shows that testing across different datasets is crucial to improve the generalisability and utility of the models. Improving our understanding of the biological underpinnings of how these models determine age may too improve their reliability in reflecting ageing processes. Nevertheless, the evidence highlights the potential of retinal age as a biomarker, suggesting its viability as a valuable, cost-effective tool for evaluating health status.

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Supplementary Materials

Appendix 1:

Search of Published Works Databases

Preliminary search strategy formulated on Pubmed.

Initial search terms included: retinal age, retinal age gap, association, link, biomarker.

Search of Preprint Databases

Appendix 2: **Table 1: Cross Sectional Studies – Data Extraction**

increase of hyperglycaemia (OR=1.06. 95% CI:1.04-1.07), p<0.001). When compared to participants with RAG in lower quartile, the risk of MetS was significantly increased by 10% in the 3rd quartile and 14% in the 4th quartile (OR=1.10, 95% CI:1.01-1.21, p=0.030, OR=1.14, 95% CI: 1.03-1.26, p=0.012)

Table 2: Prospective Studies – Data Extraction

Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) Checklist

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1

JBI = Joanna Briggs Institute; PRISMA-ScR = Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews.

* Where *sources of evidence* (see second footnote) are compiled from, such as bibliographic databases, social media platforms, and Web sites.

† A more inclusive/heterogeneous term used to account for the different types of evidence or data sources (e.g., quantitative and/or qualitative research, expert opinion, and policy documents) that may be eligible in a scoping review as opposed to only studies. This is not to be confused with *information sources* (see first footnote). ‡ The frameworks by Arksey and O'Malley (6) and Levac and colleagues (7) and the JBI guidance (4, 5) refer to the process of data extraction in a scoping review as data charting*.*

§ The process of systematically examining research evidence to assess its validity, results, and relevance before using it to inform a decision. This term is used for items 12 and 19 instead of "risk of bias" (which is more applicable to systematic reviews of interventions) to include and acknowledge the various sources of evidence that may be used in a scoping review (e.g., quantitative and/or qualitative research, expert opinion, and policy document).

From: Tricco AC, Lillie E, Zarin W, O'Brien KK, Colquhoun H, Levac D, et al. PRISMA Extension for Scoping Reviews (PRISMAScR): Checklist and Explanation. Ann Intern Med. 2018;169:467–473. doi: 10.7326/M18-0850.

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