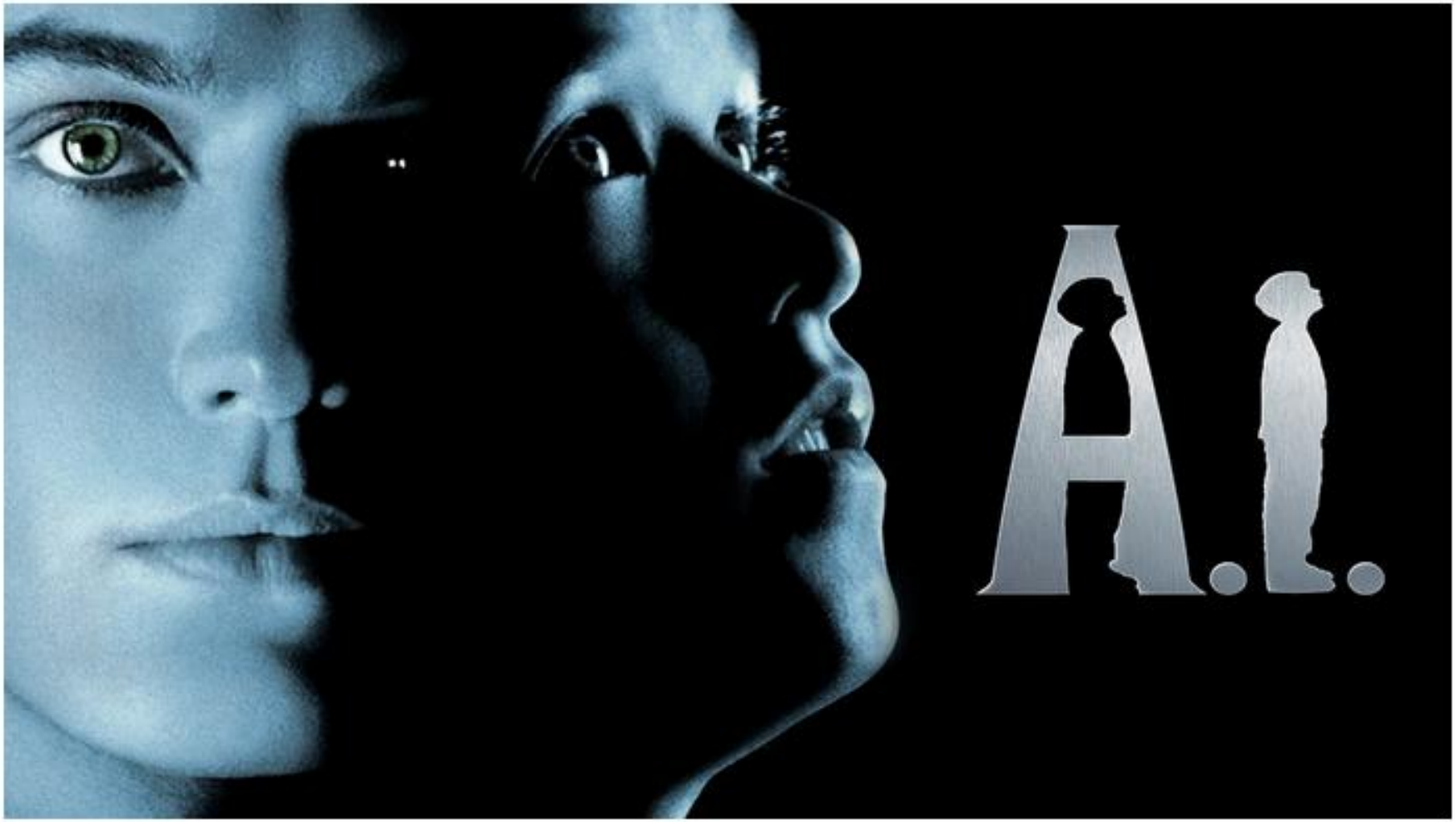
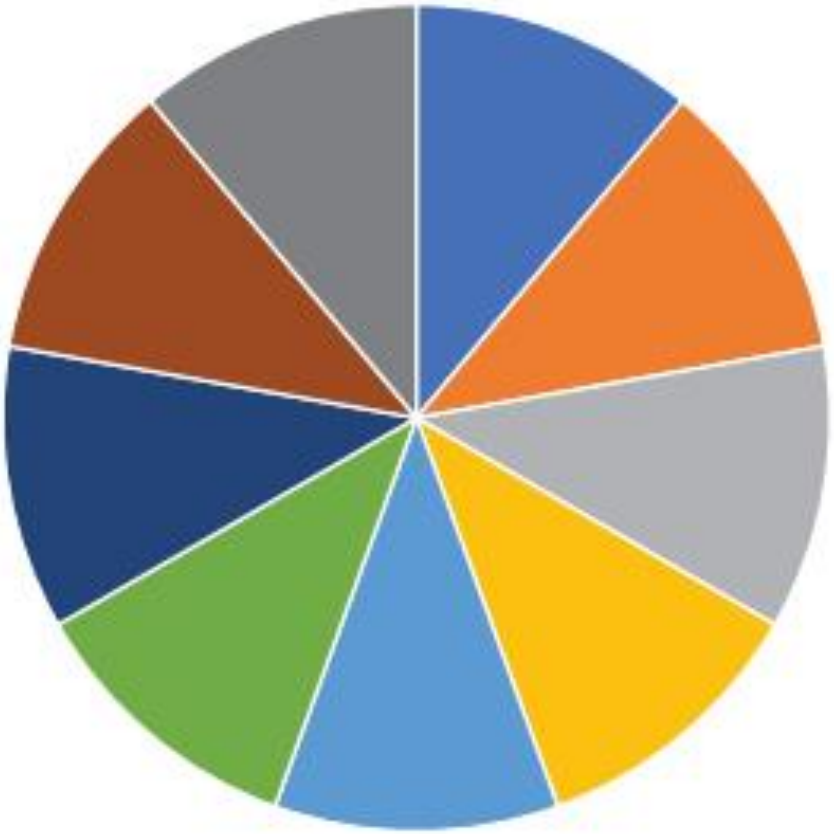
ΕΡΧΕΤΑΙ ΤΟ ΤΕΛΟΣ ΤΗΣ ΠΑΡΑΔΟΣΙΑΚΗΣ…ΙΑΤΡΙΚΗΣ;;;

ΡΗΓΟΠΟΥΛΟΣ ΔΗΜΗΤΡΗΣ

ΚΑΘΗΓΗΤΗΣ ΔΕΡΜΑΤΟΛΟΓΙΑΣ-ΑΦΡΟΔΙΣΙΟΛΟΓΙΑΣ



Artificial Intelligence (2001) by Stanley Kubrick and Steven Spielberg



- Drug development
- Health montoring
- Managing medical data
- Disease diagnostics
- Digital consultation
- Personalized treatment
- Analysis of health plans
- Surgical treatment
- Medical teratment

Journal of Family Medicine and Primary Care July 2019

App Store Preview

Epocrates 12+

Drug/Disease Clinical Support

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Screenshots

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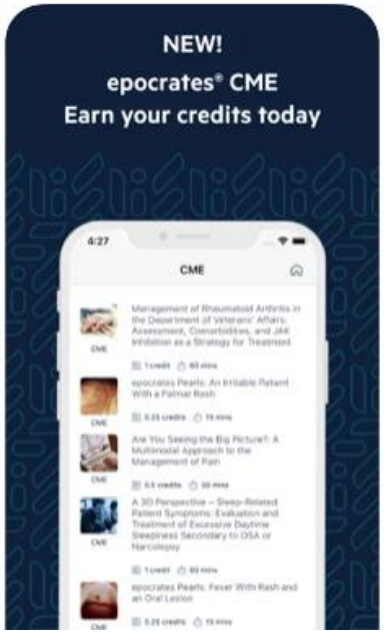
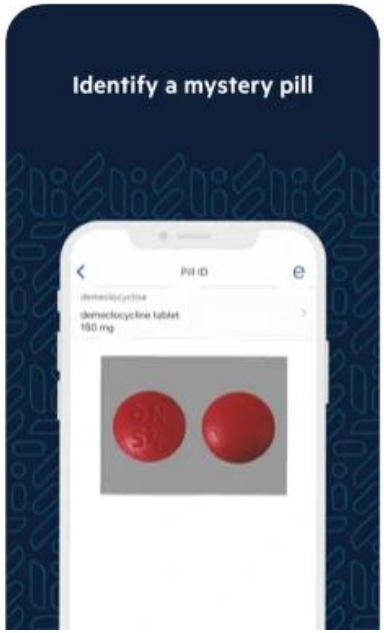
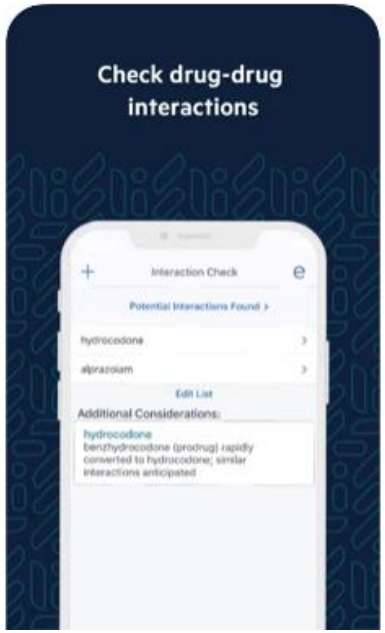
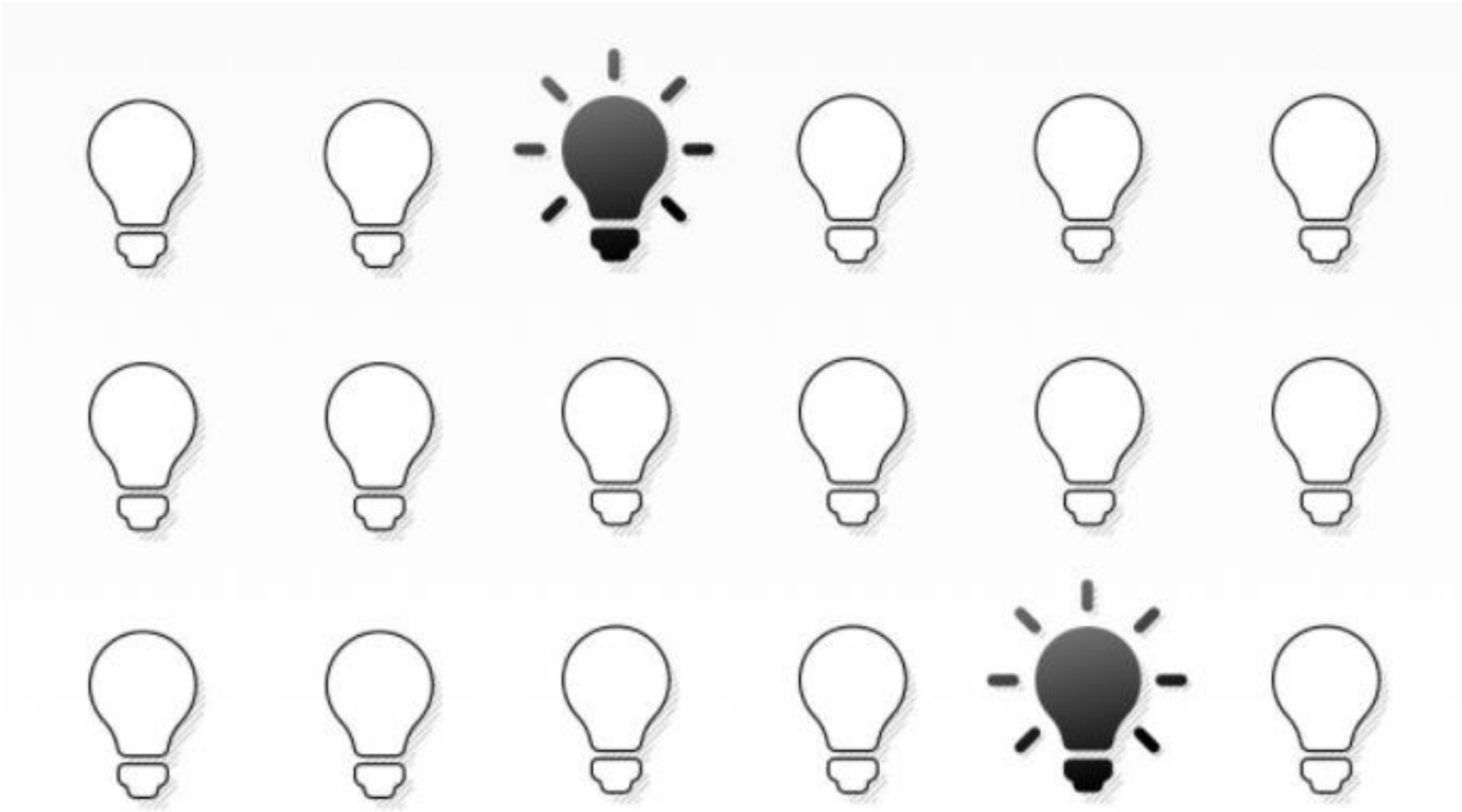




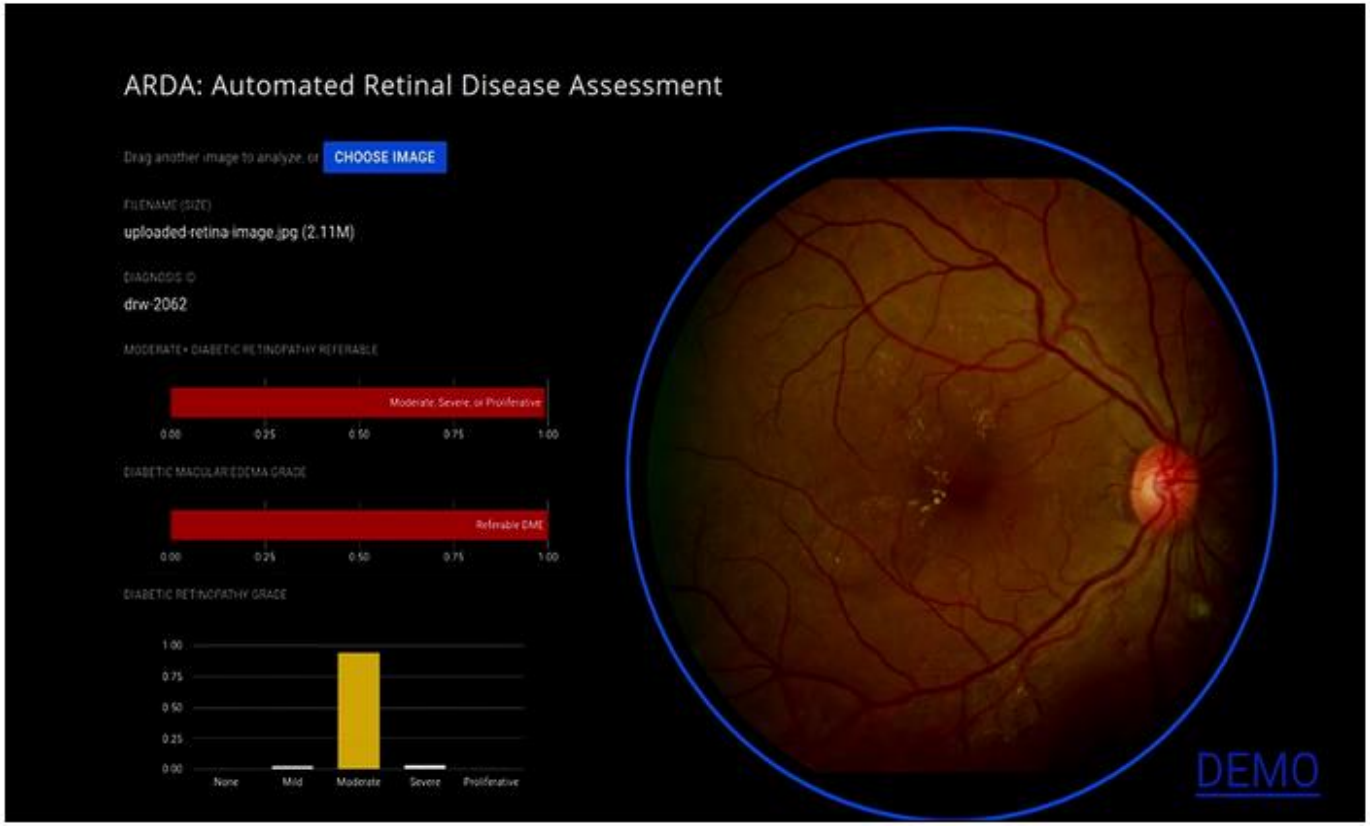


Χειρουργική

Αναγνώριση πιθανότερων υποψήφιων να νοσήσουν

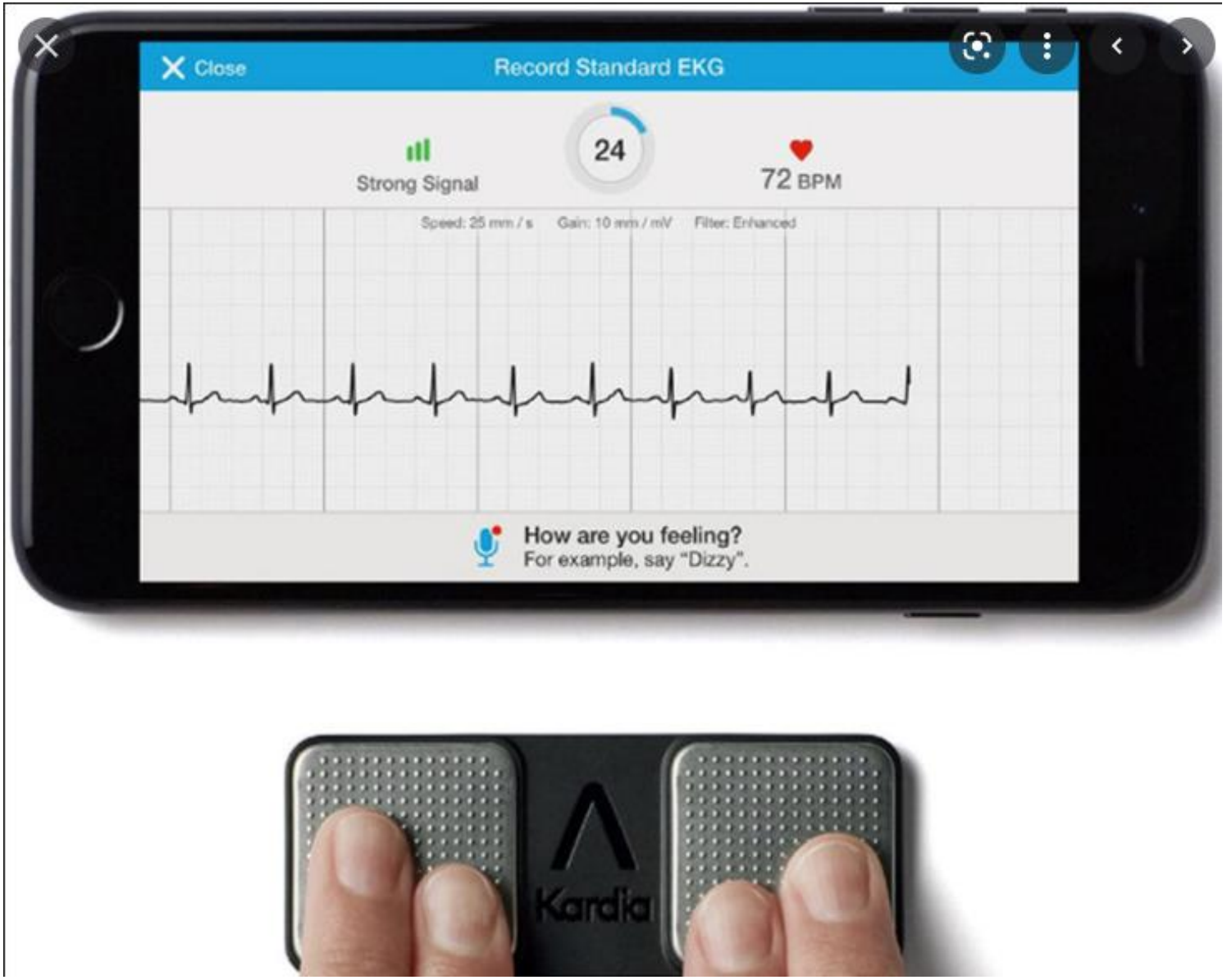


Ταχύτερη ανάπτυξη φαρμάκων



Lily Peng MD, Ph.D. & Product Manager at Google Research, studied and developed a tool to detect Diabetic Retinopathy. This diseases is one of the leading causes of blindness in the world. It can be treated if detected in time but in some parts of the world like India, there is a shortage of eye doctors, and 45% of patients suffer vision loss before being able to receive a diagnosis.

A.I software may help spot early signs of oesophageal cancer



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Original Article

Analysis of Machine Learning Techniques for Heart Failure Readmissions

Bobak J. Mortazavi, PhD; Nicholas S. Downing, MD; Emily M. Bucholz, MD, PhD; Kumar Dharmarajan, MD, MBA; Ajay Manhapra, MD; Shu-Xia Li, PhD; Sahand N. Negahban, PhD*; Harlan M. Krumholz, MD, SM*

Background—The current ability to predict readmissions in patients with heart failure is modest at best. It is unclear whether machine learning techniques that address higher dimensional, nonlinear relationships among variables would enhance prediction. We sought to compare the effectiveness of several machine learning algorithms for predicting readmissions.

Methods and Results—Using data from the Telemonitoring to Improve Heart Failure Outcomes trial, we compared the effectiveness of random forests, boosting, random forests combined hierarchically with support vector machines or logistic regression (LR), and Poisson regression against traditional LR to predict 30- and 180-day all-cause readmissions and readmissions because of heart failure. We randomly selected 50% of patients for a derivation set, and a validation set comprised the remaining patients, validated using 100 bootstrapped iterations. We compared C statistics for discrimination and distributions of observed outcomes in risk deciles for predictive range. In 30-day all-cause readmission prediction, the best performing machine learning model, random forests, provided a 17.8% improvement over LR (mean C statistics, 0.628 and 0.533, respectively). For readmissions because of heart failure, boosting improved the C statistic by 24.9% over LR (mean C statistic 0.678 and 0.543, respectively). For 30-day all-cause readmission, the observed readmission rates in the lowest and highest deciles of predicted risk with random forests (7.8% and 26.2%, respectively) showed a much wider separation than LR (14.2% and 16.4%, respectively).

Conclusions—Machine learning methods improved the prediction of readmission after hospitalization for heart failure compared with LR and provided the greatest predictive range in observed readmission rates. **(*Circ Cardiovasc Qual Outcomes*. 2016;9:629-640. DOI: 10.1161/CIRCOUTCOMES.116.003039.)**

Key Words: computers ■ heart failure ■ machine learning ■ meta-analysis ■ patient readmission

High rates of readmission after hospitalization for heart failure impose tremendous burden on patients and the healthcare system.[1–3] In this context, predictive models facilitate identification of patients at high risk for hospital readmissions and potentially enable direct specific interventions toward those who might benefit most by identifying key risk factors. However, current predictive models using administrative and clinical data discriminate poorly on readmissions.[4–8] The inclusion of a richer set of predictor variables encompassing patients' clinical, social, and demographic domains, while improving discrimination in some internally validated studies,[9] does not necessarily markedly improve discrimination,[10] particularly in the data set to be considered in this work. This richer set of predictors might not contain the predictive domain of variables required, but does represent a large set of data not routinely collected in other studies.

Another possibility for improving models, rather than simply adding a richer set of predictors, is that prediction might improve with methods that better address the higher order interactions between the factors of risk. Many patients may have risk that can only be predicted by modeling complex relationships between independent variables. For example, no available variable may be adequately explanatory; however,

Received May 26, 2016; accepted October 17, 2016.

From the Section of Cardiovascular Medicine, Department of Internal Medicine (B.J.M., N.S.D., E.M.B., K.D., H.M.K.), Department of Psychiatry and the Section of General Medicine, Department of Internal Medicine (A.M.), and Robert Wood Johnson Foundation Clinical Scholars Program, Department of Internal Medicine, Yale School of Medicine, and Department of Health Policy and Management (H.M.K.), Yale School of Public Health, New Haven

Ο προηγμένος αλγόριθμος SmartGuard στο σύστημα MiniMed 780G αυτοματοποιεί και εξατομικεύει τη χορήγηση βασικής ινσουλίνης προσαρμόζοντάς την αυτόματα κάθε πέντε λεπτά, 24 ώρες την ημέρα.

DOI: 10.1111/sdi.12915

REVIEW ARTICLE

Seminars in Dialysis WILEY

Artificial intelligence enabled applications in kidney disease

Sheetal Chaudhuri[1,2] | Andrew Long[2] | Hanjie Zhang[3] | Caitlin Monaghan[2] | John W. Larkin[2] | Peter Kotanko[3,4] | Shashi Kalaskar[2] | Jeroen P. Kooman[1] | Frank M. van der Sande[1] | Franklin W. Maddux[2] | Len A. Usvyat[2]

[1]Maastricht University Medical Center, Maastricht, The Netherlands

[2]Fresenius Medical Care, Waltham, MA, USA

[3]Renal Research Institute, New York, NY, USA

[4]Icahn School of Medicine at Mount Sinai, New York, NY, USA

Correspondence
Len A. Usvyat, 920 Winter St, Waltham, MA 02451, USA.
Email: len.usvyat@fmc-na.com

Funding information
Fresenius Medical Care provided resources to support this review.

Abstract

Artificial intelligence (AI) is considered as the next natural progression of traditional statistical techniques. Advances in analytical methods and infrastructure enable AI to be applied in health care. While AI applications are relatively common in fields like ophthalmology and cardiology, its use is scarcely reported in nephrology. We present the current status of AI in research toward kidney disease and discuss future pathways for AI. The clinical applications of AI in progression to end-stage kidney disease and dialysis can be broadly subdivided into three main topics: (a) predicting events in the future such as mortality and hospitalization; (b) providing treatment and decision aids such as automating drug prescription; and (c) identifying patterns such as phenotypical clusters and arteriovenous fistula aneurysm. At present, the use of prediction models in treating patients with kidney disease is still in its infancy and further evidence is needed to identify its relative value. Policies and regulations need to be addressed before implementing AI solutions at the point of care in clinics. AI is not anticipated to replace the nephrologists' medical decision-making, but instead assist them in providing optimal personalized care for their patients.

Seminars in Dialysis. 2021;34:5–16.

DOI: 10.1111/sdi.12915

REVIEW ARTICLE

Seminars in Dialysis WILEY

Artificial intelligence enabled applications in kidney disease

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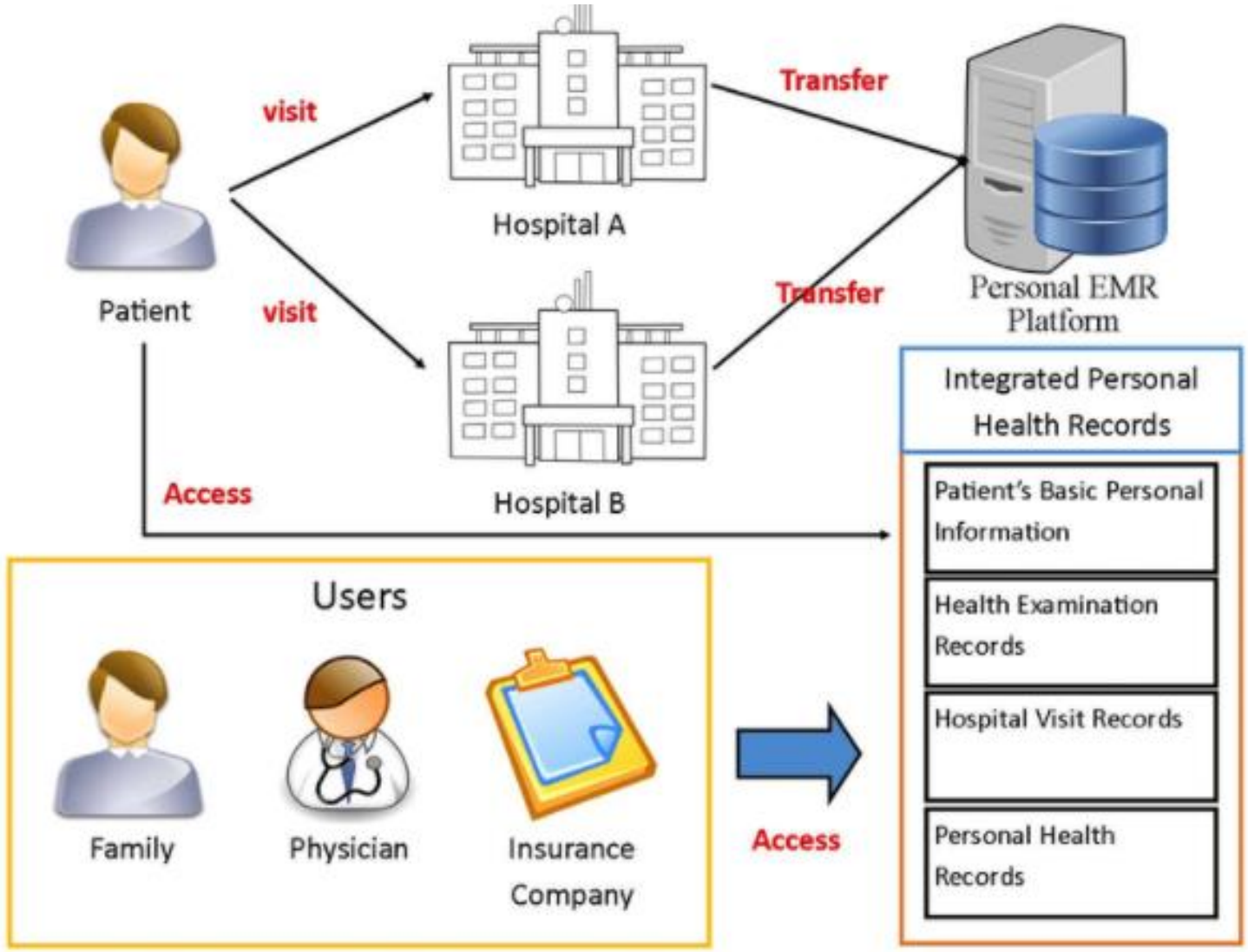
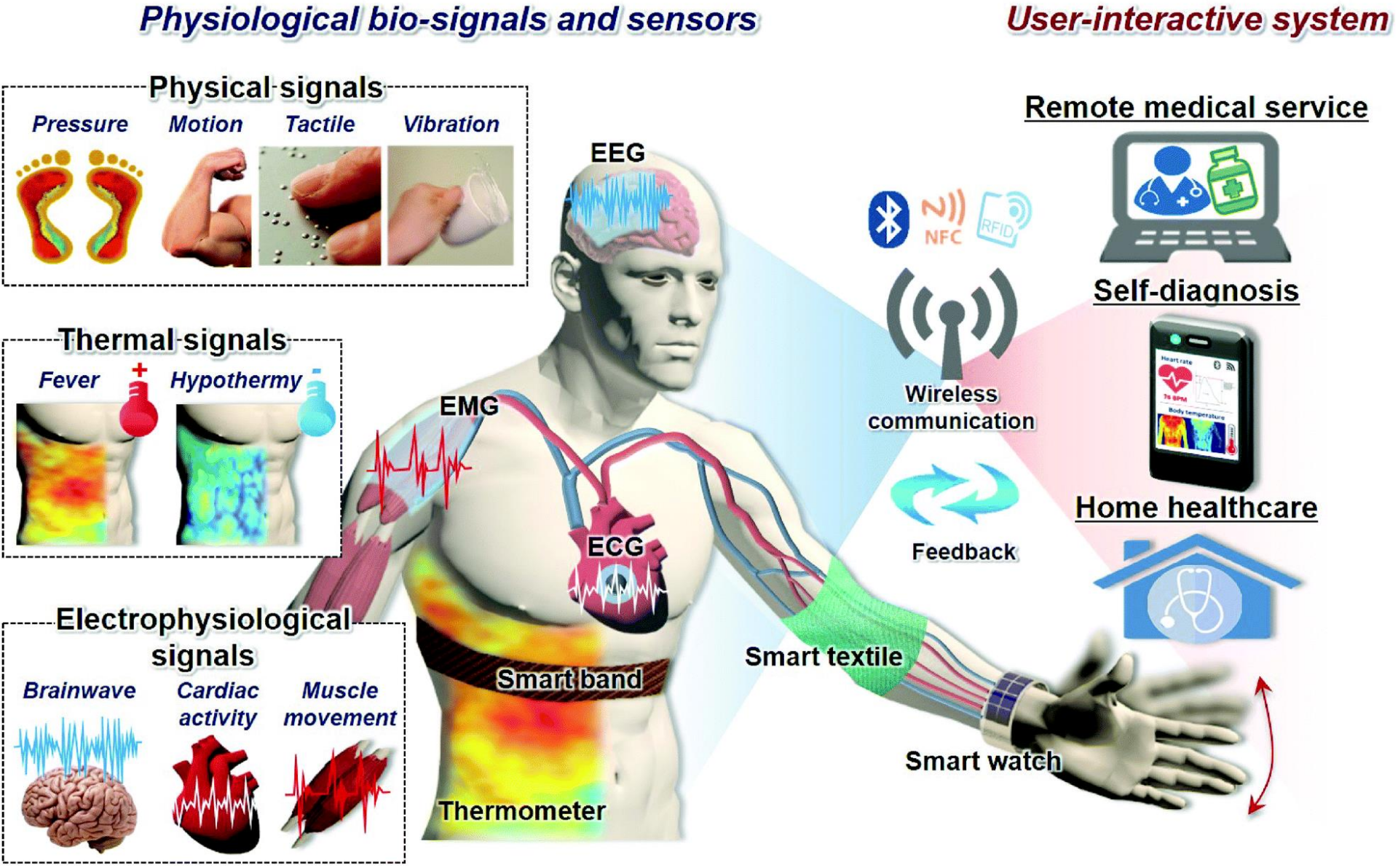
Seminars in Dialysis. 2021;34:5–16.



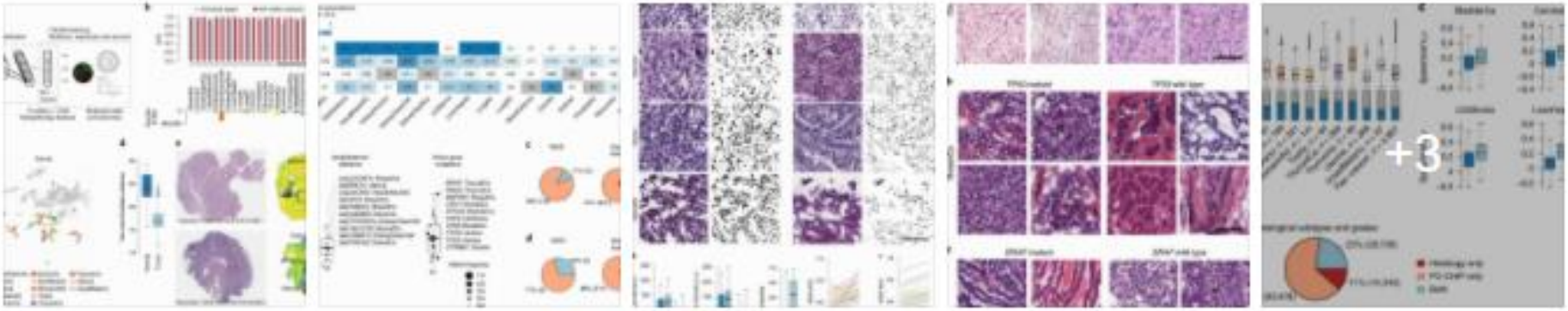
Scenario of personal electronic medical record platform.


Physiological bio-signals and sensors
User-interactive system
Physical signals
Pressure
Motion
Tactile
Vibration
Thermal signals
Fever
Hypothermy
Electrophysiological signals
Brainwave
Cardiac activity
Muscle movement
EEG
EMG
ECG
Smart band
Thermometer
Smart textile
Smart watch
NFC
RFID
Wireless communication
Feedback
Remote medical service
Self-diagnosis
Home healthcare

85 αισθητήρες

Nanowear Receives FDA 510(k) Platform Clearance to Implement Forthcoming AI-based Diagnostics in its Closed Loop Hospital-at-Home Network.

Nanowear Company Profile - MedTech Innovatorhttps://medtechinnovator.org



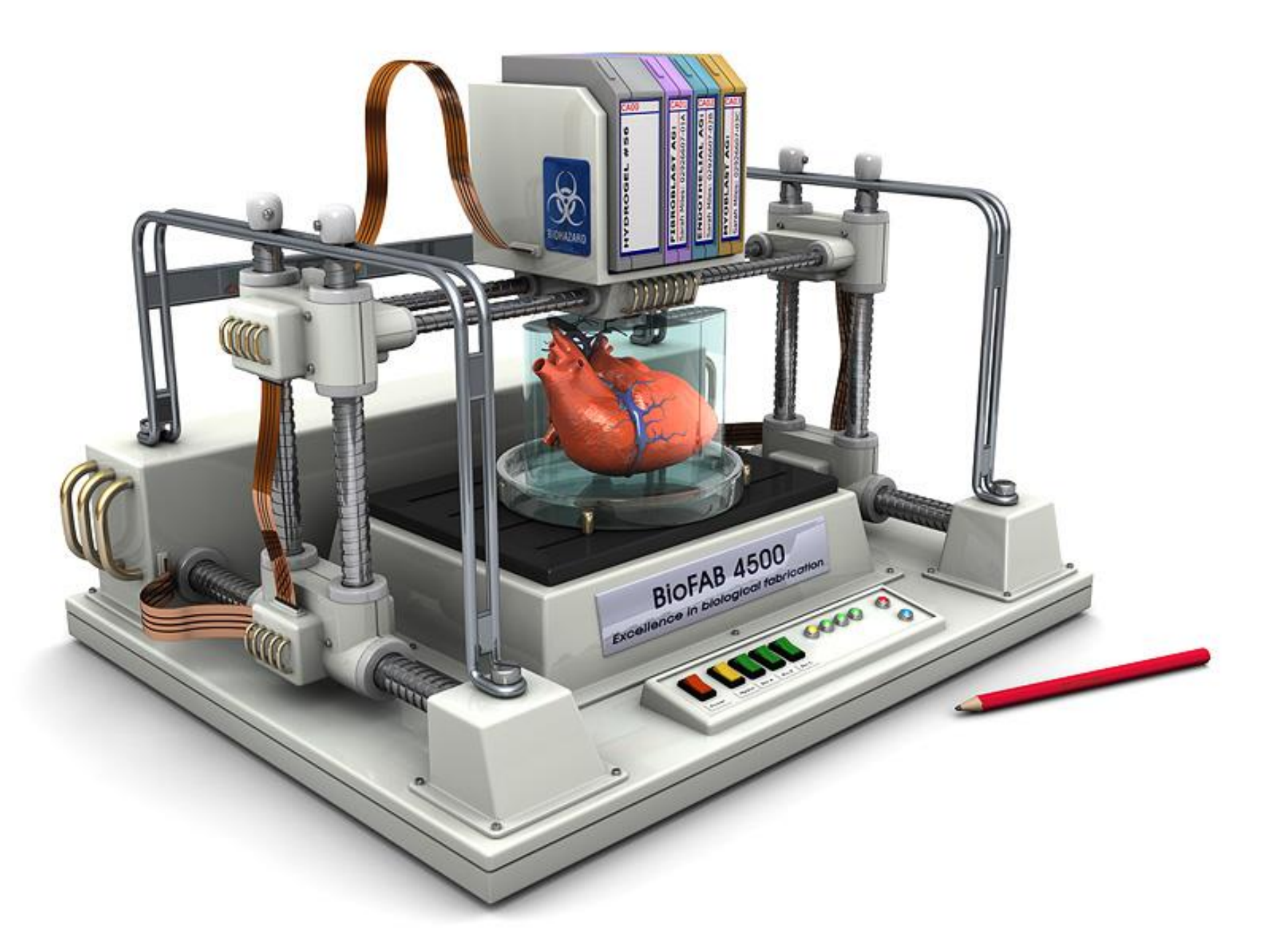
Pan-cancer computational histopathology reveals mutations, tumor composition and prognosis

Article | Full-text available | Aug 2020

Yu Fu · Alexander W. Jung · Ramon Viñas Torné · [...] · Moritz Gerstung

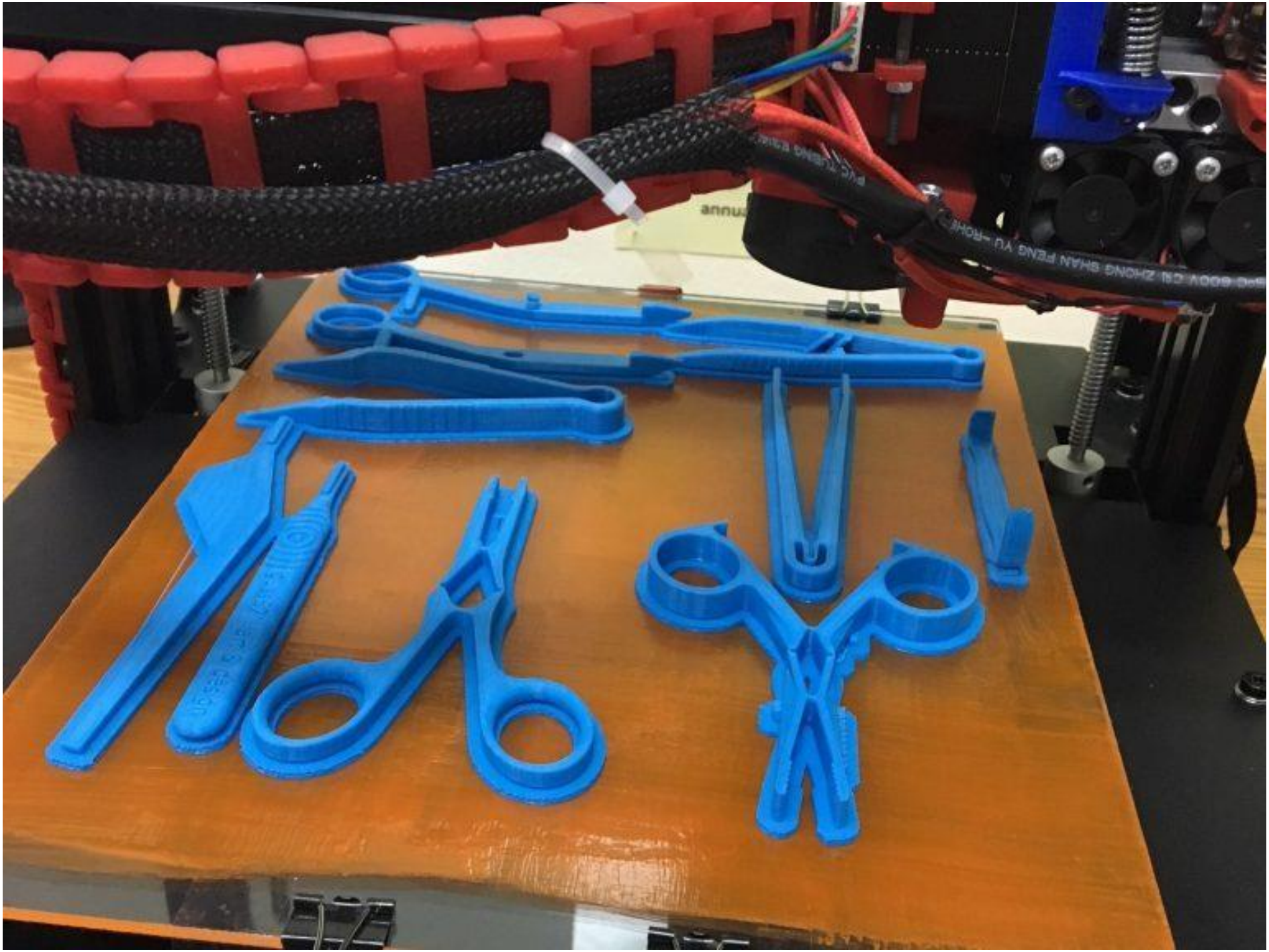
3D εκτυπωτές

- BIO- εκτυπωτές


HYDROGEL #56
FIBROBLAST AGI
ENDOTHELIAL AGI
MYOBLAST AGI
BIOHAZARD
BioFAB 4500
Excellence in biological fabrication

3D εκτυπωτές

- BIO- εκτυπωτές
- Εκπαίδευση ιατρών- ομοιώματα οργάνων ασθενών
- Τεχνητές Αρθρώσεις- άκρα
- Χειρουργικά εργαλεία



JMAI JOURNAL OF MEDICAL ARTIFICIAL INTELLIGENCE
AN OPEN ACCESS JOURNAL FOCUS ON MEDICAL ARTIFICIAL INTELLIGENCE

- The immediate past president of the Australasian College of Dermatologists, Dr Andrew Miller, said it was true that there is a global shortage of dermatologists worldwide, making it difficult for people with concerns to see a specialist.

- “Around the world there are about 100,000 dermatologists, and considering there are almost eight billion people in the world that’s an amazing **shortage**,” he said. “We also have **maldistribution** of more in city and well-off areas and less in rural and disadvantaged areas. So I definitely understand that issues of access are front of mind.”

- 1500 (;;!!) Δερματολόγοι
- 10.000.000

Computer learns to detect skin cancer more accurately than doctors

Artificial intelligence machine found 95% of melanomas in study compared to 86.6% for dermatologists

▲ An computer that was taught to distinguish malignant moles from benign ones outperformed dermatologists. Photograph: Dan Himbrechts/AAP

Andre Esteva

@AndreEsteva

Stanford AI PhD, advised by Sebastian Thrun.

Brett Kuprel

@kuprel

Humanitarian

Stanford, CA

stanford.edu/~kuprel


nature
THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE
LESIONS LEARNT
Artificial intelligence powers detection of skin cancer from images PAGES 36 & 115
NATURE.COM/NATURE
2 February 2017 £10
Vol. 542, No. 7639

2017

Dermatologist-level classification of skin cancer

An artificial intelligence trained to classify images of skin lesions as benign lesions or malignant skin cancers achieves the accuracy of board-certified dermatologists.

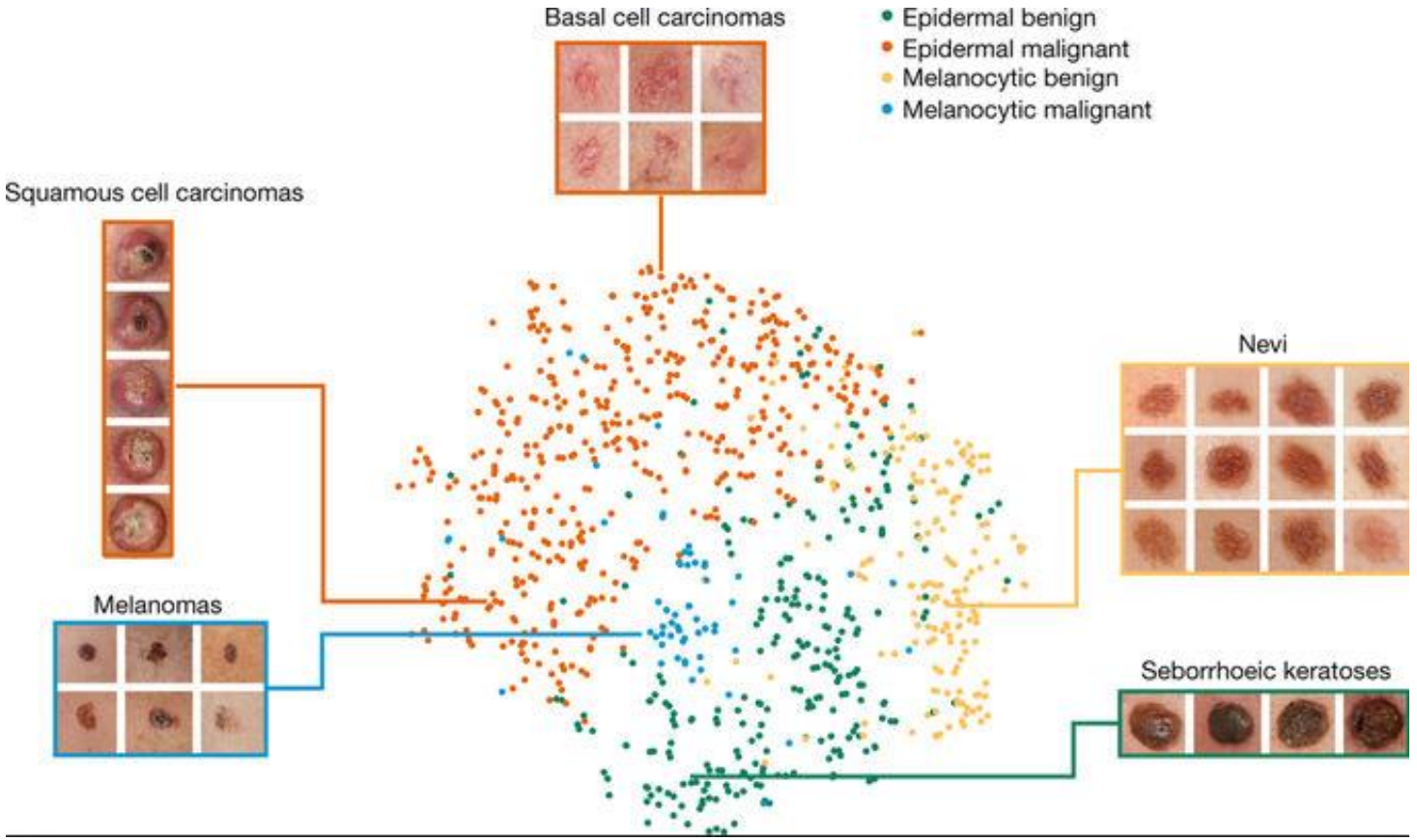
Υπερβολές!!!

BBC

Health

Artificial intelligence 'as good as cancer doctors'

By James Gallagher


Basal cell carcinomas
Epidermal benign
Epidermal malignant
Melanocytic benign
Melanocytic malignant
Squamous cell carcinomas
Nevi
Melanomas
Seborrhoeic keratoses

Skin Image Search™

First Derm Skin Image Search™ searches our image database for matches and returns the skin condition's name.

Instructions

Upload or take two photos of your skin condition, one showing the whole area, and one closeup photo.

☑ Check this box to indicate you have read and agree with our Terms & Conditions (tap here to view)

Skin Image Search™

First Derm Skin Image Search™ searches our image database for matches and returns the skin condition's name.

Your Images

Start Over?

Searching

Skin Image Search™

First Derm Skin Image Search™ searches our image database for matches and returns the skin condition's name.

Your Images
Start Over?


Results

b08.1: Molluscum Contagiosum

40% Probability

b08.1: Molluscum Contagiosum		40 %
l73.9: Folliculitis		25 %
t63.4: Insect Bite		14 %

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or ask a real dermatologist

Ask our board certified dermatologists today


12:45
08:16
07:06
11:00
06:23
2:00
01:10

Int J Biomed Comput. 1984 Jul-Aug;15(4):271-84.

Computer diagnosis of skin disease: system design and preliminary results.

Evans SJ, Norwich KH, Cobbold RS, Diehl DL, Haberman H, Harvey BJ, O'Beirne H, Zingg W.

Abstract

A system for computer-assisted diagnosis of dermatological disease is described. This is an 'expert system' whose knowledge base has been prepared with the aid of a dermatological specialist. The user enters the key elements of the patient's disease history and physical examination into the computer. The computer then returns a summary of the patient's medical record, and a differential diagnosis. The rules of operation by which a given diagnosis was included or rejected is accessible to the user. The system is currently being evaluated in a large dermatology clinic. Preliminary evaluation of the accuracy of diagnosis by the computer indicates that while it nearly always includes the correct diagnosis in its differential diagnosis (94% of cases), it frequently also includes diseases thought to be inappropriate (34% of diseases listed).

J Fam Pract. 1990 Feb;30(2):201-10.

Computer diagnosis of skin disease.

Potter B[1], Ronan SG.

Author information

Abstract

A transferable computer program for the differential diagnosis of diseases of the skin, CLINDERM, has been produced for use by physicians on standard IBM and compatible personal microcomputers. This program lists the differential diagnosis and definitive diagnosis of any presented disease of the skin, except single tumors. The physician operator indicates the distribution and detailed description of lesions, which the interactive system integrates with a comprehensive knowledge base. The computer diagnosis in 129 cases was compared with independent interpretation of the same information by an academic dermatologist. Results were synonymous in 66.7% of all diseases and similar in an additional 4.7%. A common differential diagnosis was obtained in 24%, for a 95.3% rate of synonymous, similar, or common differential diagnoses. Diagnosis was different in 3.9% and description was inadequate for diagnosis in 0.8%. The variation in diagnosis showed that some descriptive terms are prejudicial of certain diagnoses; that diagnostic terms are not all completely standardized; that some diagnoses are variants of another disease; and that drug-induced eruptions simulate many other diseases. A skin disease can usually be diagnosed by specific description. Most lesions that are not diagnostic from inspection are nodular. A computer can be programmed to list diagnoses according to morphologic description.

Comment in

The computer and clinical decision-support systems in primary care. [J Fam Pract. 1990]

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What makes us different?

We treat you personally — and honestly.

1

Answer questions & snap pictures

2

Get your personal provider

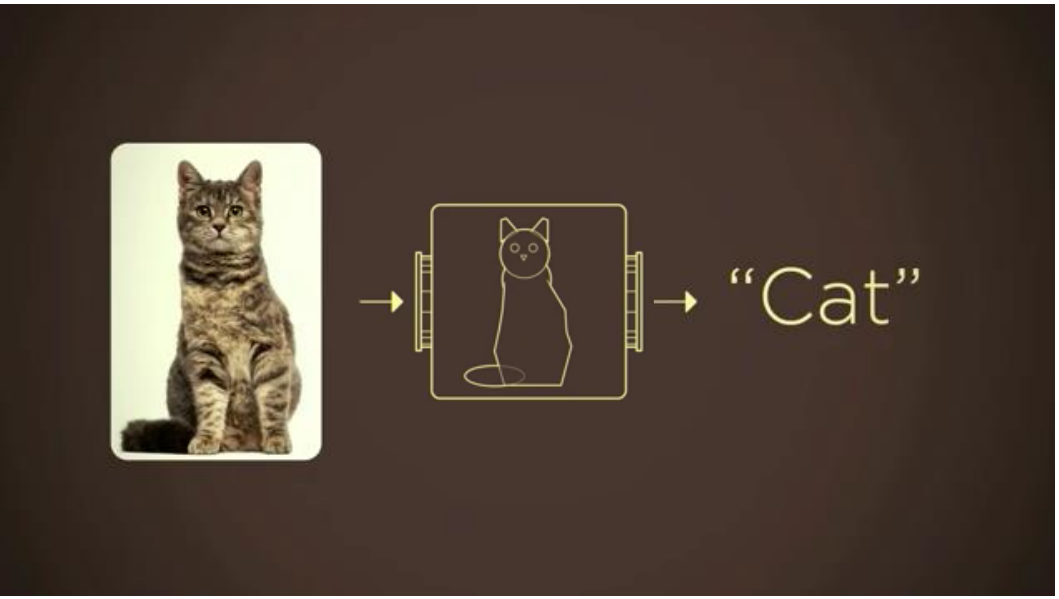
3

Your custom superbottle arrives!

Google Launches a New Medical App—Outside the US

The dermatology AI app won approval for use in the EU but not with the FDA, an odd twist on Europe's reputation for tough rules on tech.

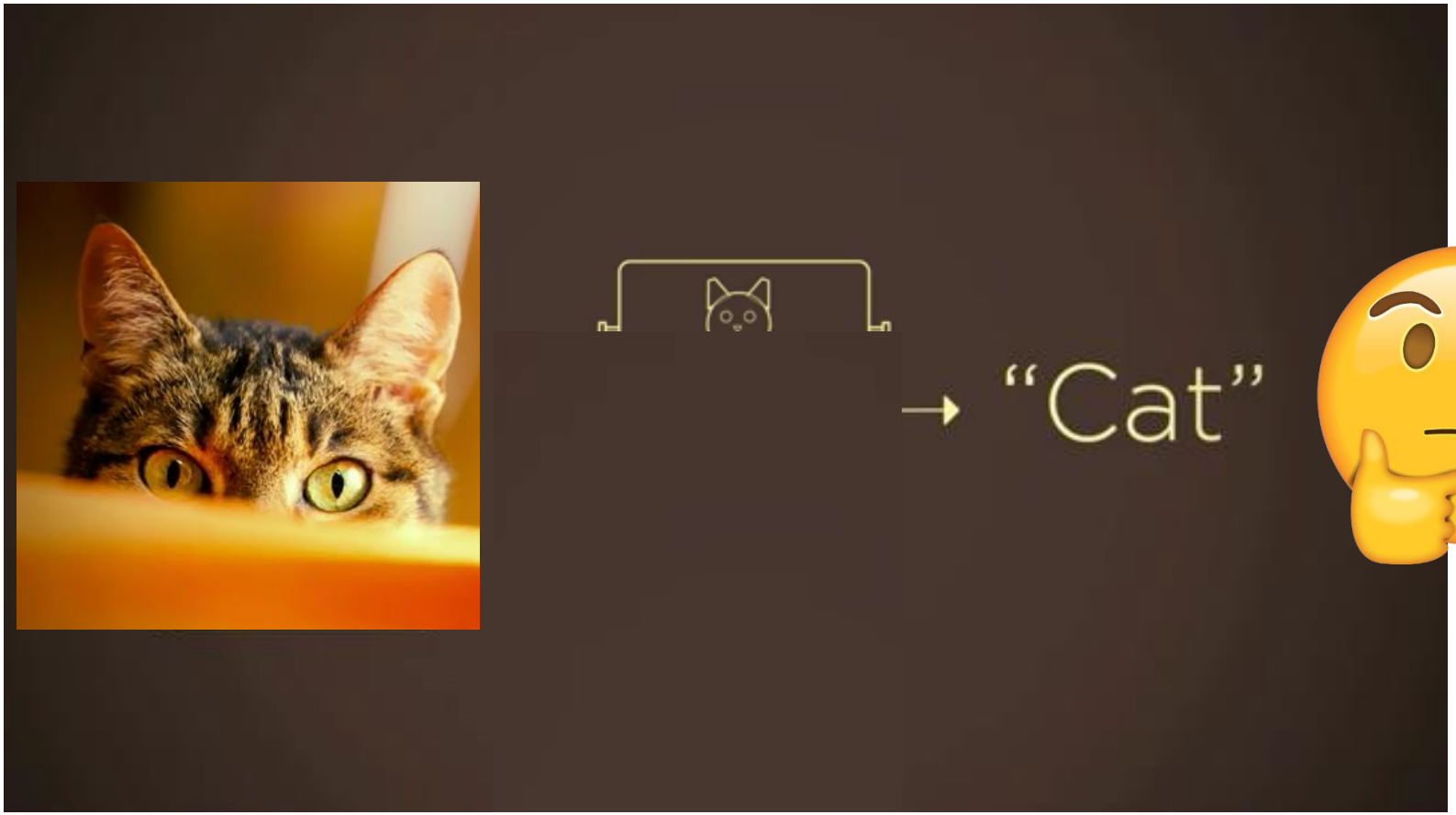
Παραδοσιακή προσέγγιση του AI: Προγραμματισμός ενός υπολογιστή να αναγνωρίζει μια γάτα



- Στρογγυλό πρόσωπο
- 2 τριγωνικά αυτιά = 'ΓΑΤΑ'
- 2 μάτια
- Ουρά

Το πρόβλημα : Δύσκολες εικόνες…

Ημιστρόγγυλο πρόσωπο, Τριγωνικά αυτιά… And, that’s it.

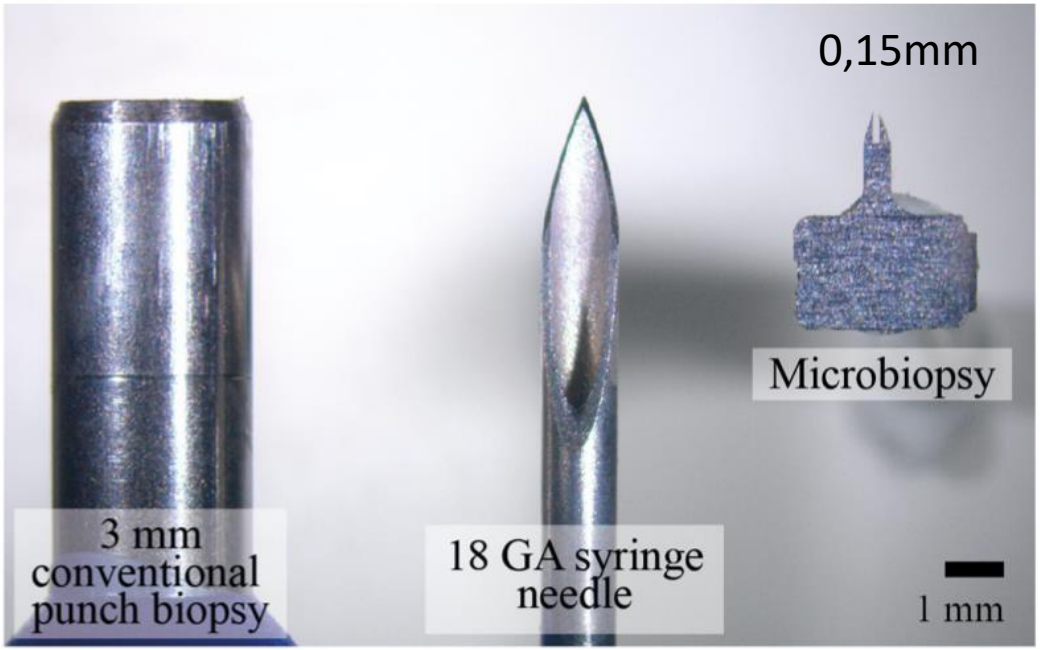


METHOD ARTICLE

UPDATED Microbiopsy engineered for minimally invasive and suture-free sub-millimetre skin sampling [v2; ref status: indexed, http://f1000r.es/1h7]

Lynlee L Lin, Tarl W Prow, Anthony P Raphael, Robert L Harrold III, Clare A Primiero, Alexander B Ansaldo, H Peter Soyer

Dermatology Research Centre, The University of Queensland, School of Medicine, Translational Research Institute, Brisbane, QLD 4012, Australia



Application of the relatively small microbiopsy device **does not require local anaesthesia** or **sutures** and therefore no set up for a minor clinical procedure is necessary.

cancers

MDPI

Article

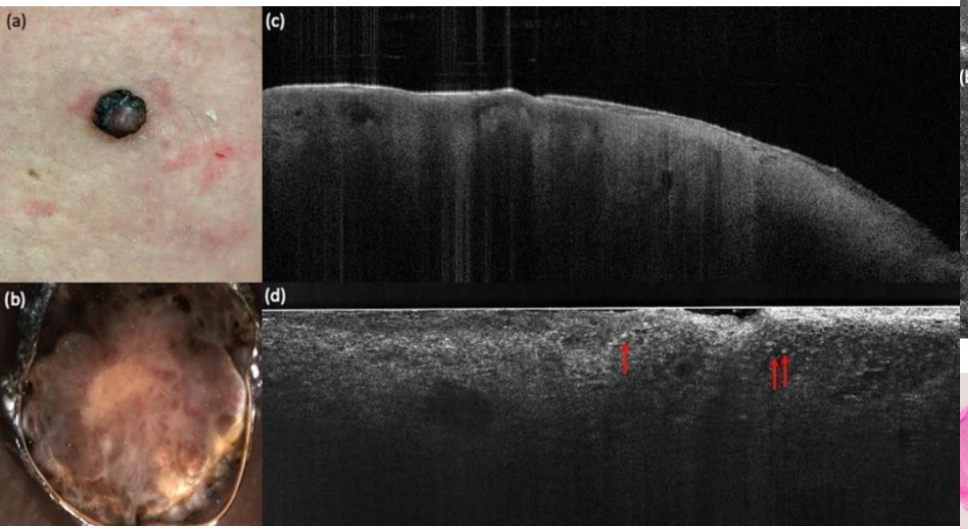
Line-Field Confocal Optical Coherence Tomography: A New Tool for the Differentiation between Nevi and Melanomas?

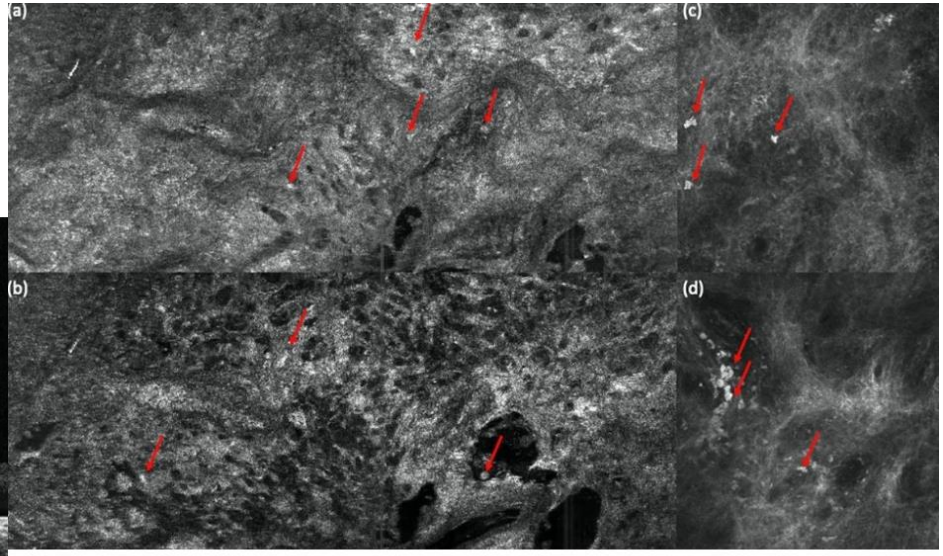
Sandra Schuh [1,*], Cristel Ruini [2], Maria Katharina Elisabeth Perwein [1], Fabia Daxenberger [2], Charlotte Gust [2], Elke Christina Sattler [2,†] and Julia Welzel [1,*,†]

[1] Department of Dermatology and Allergology, University Hospital, 86179 Augsburg, Germany; maria.perwein@web.de
[2] Department of Dermatology and Allergy, University Hospital, LMU Munich, 80337 Munich, Germany; cristel.ruini@med.uni-muenchen.de (C.R.); fabia.daxenberger@gmail.com (F.D.); charlotte.gust@t-online.de (C.G.); elke.sattler@med.uni-muenchen.de (E.C.S.)
* Correspondence: sandra.schuh@uk-augsburg.de (S.S.); julia.welzel@uk-augsburg.de (J.W.)
† These authors contributed equally to this work.

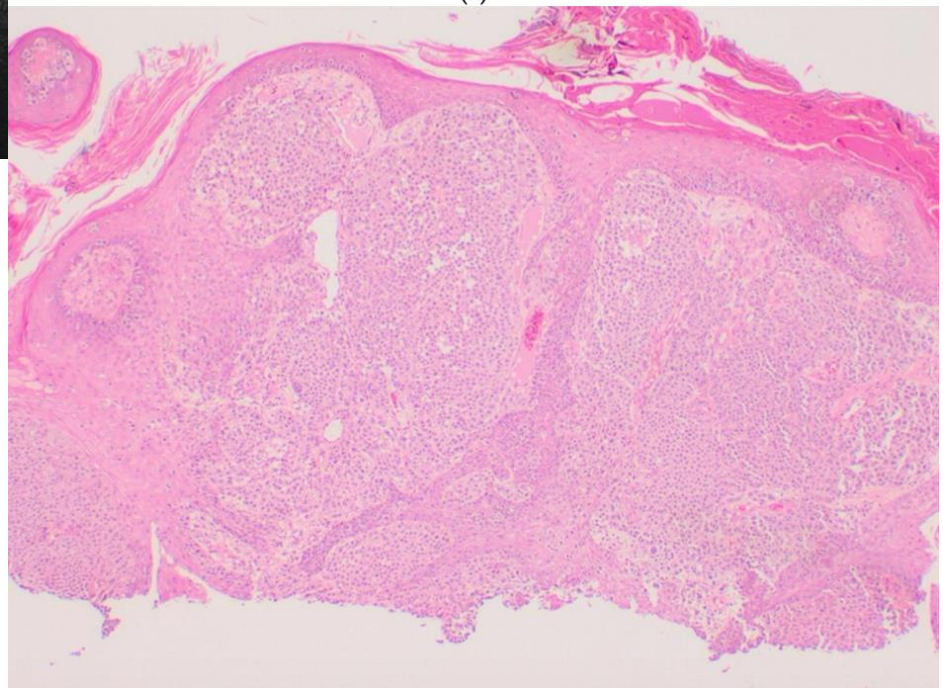
Είναι το τέλος της Βιοψίας;;;

Cancers **2022**, *14*, 1140. https://doi.org/10.3390/cancers14051140





(2)



Open Access Full Text Article

ORIGINAL RESEARCH

Significant Biomarkers Identification Associated with Cutaneous Squamous Cell Carcinoma Progression

Cheng-Gang Qiu[1], Bin Shen[1], Xiao-Qi Sun[2]

[1]Department of Burn, Affiliated Xiaoshan Hospital, Hangzhou Normal University, Hangzhou, 311200, Zhejiang, People's Republic of China; [2]Department of Plastic Surgery, Affiliated Xiaoshan Hospital, Hangzhou Normal University, Hangzhou, 311200, Zhejiang, People's Republic of China

Correspondence: Xiao-Qi Sun, Department of Plastic Surgery, Affiliated Xiaoshan Hospital, Hangzhou Normal University, 728 Yucai North Road, Chengxiang Town, Xiaoshan District, Hangzhou, Zhejiang, 311200, People's Republic of China, Email xiaoqisun0806@163.com

Background: This study aimed to identify significant genes associated with cutaneous squamous cell carcinoma (CSCC) initiation and development.

Methods: The overlapped differential expressed genes (DEGs) between normal and CSCC samples were firstly screened out, followed by KEGG analysis. The top 10 hub genes were then detected from the whole protein–protein interaction (PPI) network. Further, important biomarkers continuously associated with actinic keratosis (AK), CSCC, and CSCC invasion was successively filtrated. GSEA analysis was finally performed to reveal potential mechanisms associated with biomarkers.

Results: A total of 179 DEGs were identified, which were enriched in pathways in cancer, PI3K-Akt signaling pathway, and human papillomavirus infection. The 10 hub genes were firstly identified from the PPI network, and they were all highly expressed in AK tissues compared with normal tissues. Next, we found that 6 genes were overexpressed in CSCC compared with AK tissues. Further, we identified that the expression of 2 genes (MYBL2 and TK1) was higher in CSCC invasion groups compared with samples without invasion. Through a series of filtrations, we confirmed that MYBL2 and TK1 were the most significant biomarkers associated with CSCC initiation and progression. The pan-cancer analysis further supported their prognostic value in human cancers. GSEA analysis found that they positively correlated with N glycan biosynthesis and p53 signaling pathways.

Conclusion: MYBL2 and TK1 were proved to play a vital role in CSCC tumorigenesis and progression, which may act as promising biomarkers or therapeutic targets for accurate diagnosis and treatment of CSCC.

Keywords: cutaneous squamous cell carcinoma, DEGs, MYBL2, TK1

ΠΡΟΒΛΗΜΑΤΑ-ΕΡΩΤΗΜΑΤΑ

- Αξιολόγηση-Επικύρωση τεχνολογιών που βασίζονται σε τεχνητή νοημοσύνη: Προς μια κρίση αναπαραγωγής;
- Ηθικές Επιπτώσεις της Διαρκούς Παρακολούθησης
- Θα πρέπει να διασφαλισθεί η Αποφυγή της Αποανθρωποίησης από την Τεχνολογία
- Ανάγκη Επαυξημένης Εκπαίδευσης των Ιατρών
- Τελικά Θα αντικατασταθούν οι γιατροί από την τεχνητή νοημοσύνη;

Αντίπαλοι;;;;;

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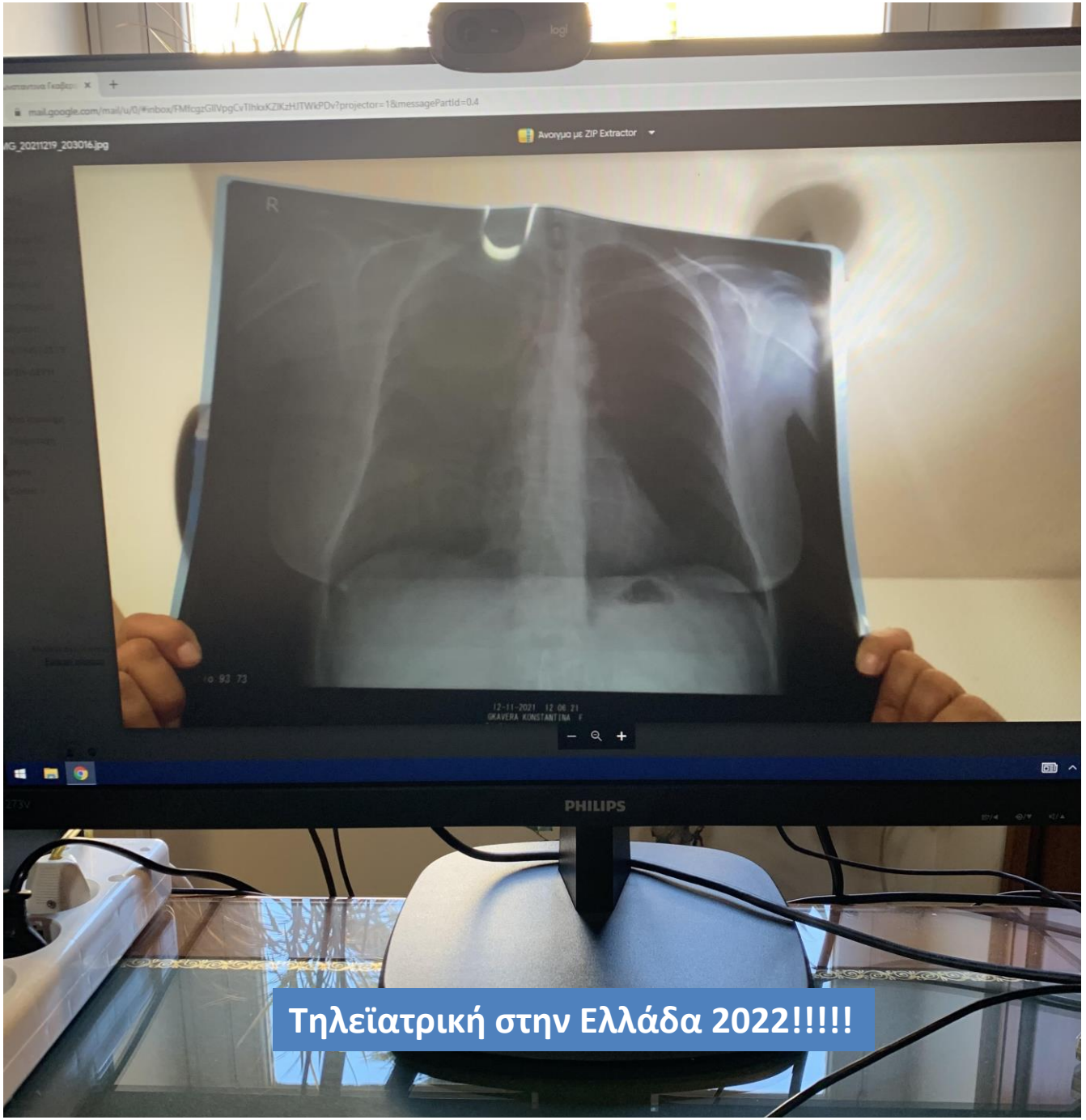
- **Έρχεται λοιπόν το τέλος της Παραδοσιακής Ιατρικής-(Δερματολογίας);**



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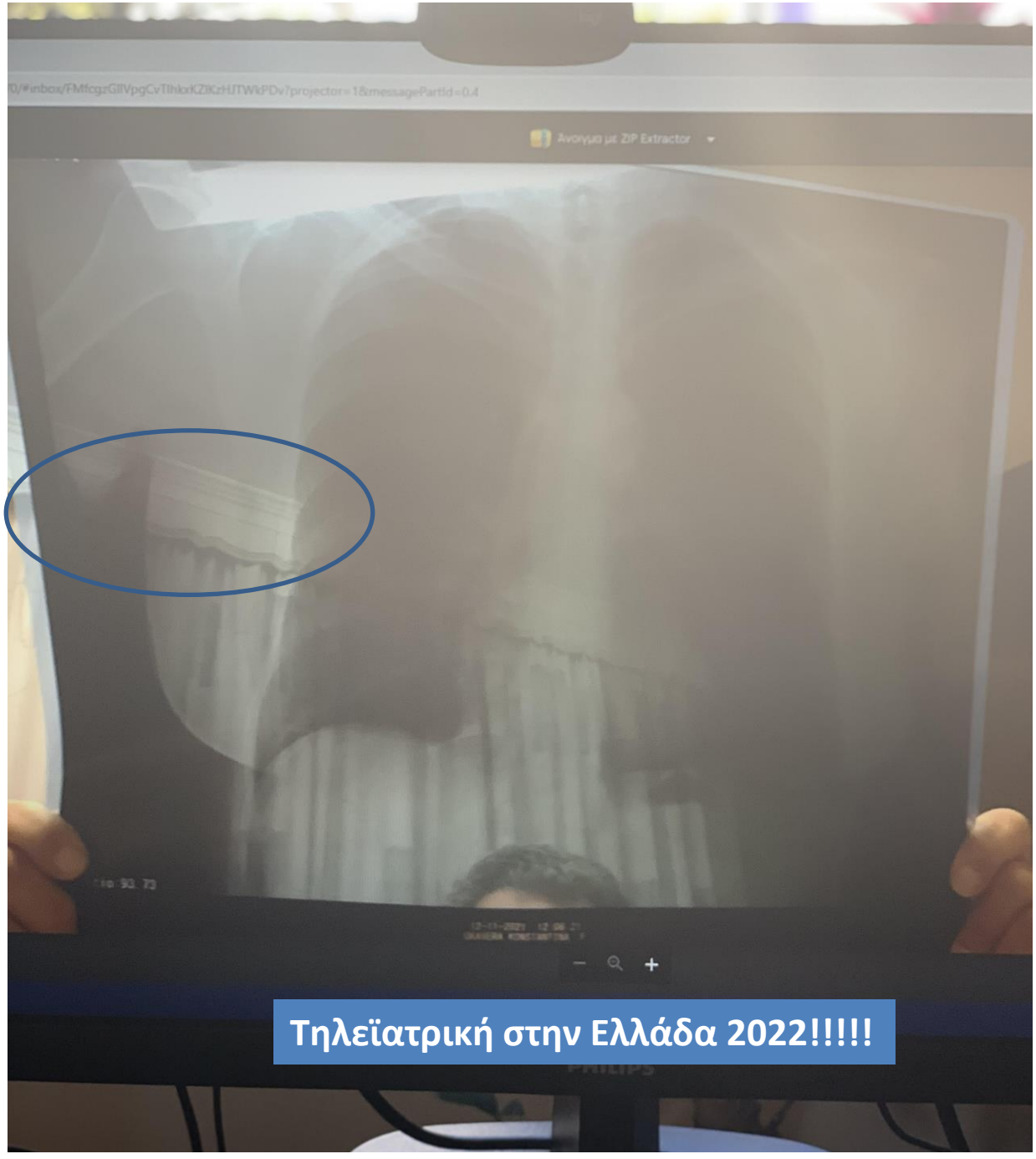
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