Newsletter #5

iToBOS

Intelligent Total Body Scanner for Early Detection of Melanoma

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 965221.

2023

Content

New partner in iToBoS consortium: Canfield Scientific GMBH

From December 1st, 2022, a new partner officially joined to the iToBoS consortium: Canfield Scientific GMBH. Due the termination of Barco NV's activities in the project on M18 (September 2022), it was necessary to include a new partner to replace it.

In the framework of the iToBoS project, Canfield will integrate different software components, develop an intelligent human-computer interface, and evaluate the design and concept of the new total body photography scanner for its clinical use. Canfield is the leader of the WP9 Integration and Technical Validation, and also participates in WP1 Project Coordination and Management, WP4 Implementation of AI privacy and anonymization, WP5 Development of the Total Body Scanner, WP6 Algorithms for real-time 3D full-body mapping and pigmented lesion processing, WP11 Patient engagement and education and WP12 Communication, dissemination & exploitation activities.

Canfield Scientific is a global leader in imaging systems, services and products for scientific research and healthcare applications, including the pharmaceutical, biotechnology, cosmetics, medical and skin care industries.

Canfield Scientific continues to be the premier worldwide supplier of digital photographic systems, imaging software, and associated support services to aid healthcare professionals in improving patient communications and managing treatment outcomes.

As a technology company, Canfield Scientific creates leading edge technology assets on our own and in partnership with industry, academia, and research centres to solve complex imaging problems. Moreover, for three decades Canfield Scientific has been developing both hardware and software for medical imaging products.

Canfield is equipped will all the necessary equipment and infrastructure for developing medical products. This includes electronic laboratories, mechanical workshops etc.

As one of the world's leading clinical services imaging providers, Canfield also maintains a secure data managing centre to securely handle extensive customer medical imaging data.

Reveal to revise: an explainable AI life cycle for iterative bias correction of deep models

Deep neural networks (DNNs) are powerful tools for accurate predictions in various applications and have even shown to be superior to human experts in some domains, for instance for Melanoma detection.

However, they are vulnerable to data artifacts, such as band-aids, rulers or skin markers in the Melanoma detection task. In our previous blog posts, we have presented various approaches, both to reveal and correct model (mis-)behaviour.

Reveal to Revise Framework

In this blog post, we want to introduce Reveal to Revise (R2R), a framework entailing the entire Explainable AI (XAI) life cycle, enabling practitioners to iteratively identify, mitigate, and (re-)evaluate spurious model behaviour with a minimal amount of human interaction, as shown in Figure 1.

Overall, R2R consists of four steps: First (1), the potential misbehaviour is identified either using Spectral Relevance Analysis[1] to automatically detect outlier behaviour in large sets of local explanations, or by inspecting human-understandable concepts employed by the model using Concept Relevance Propagation (CRP)[2]. In a second step (2), the data artifact to be unlearned is modelled in latent space and localized in input space using Concept Activation

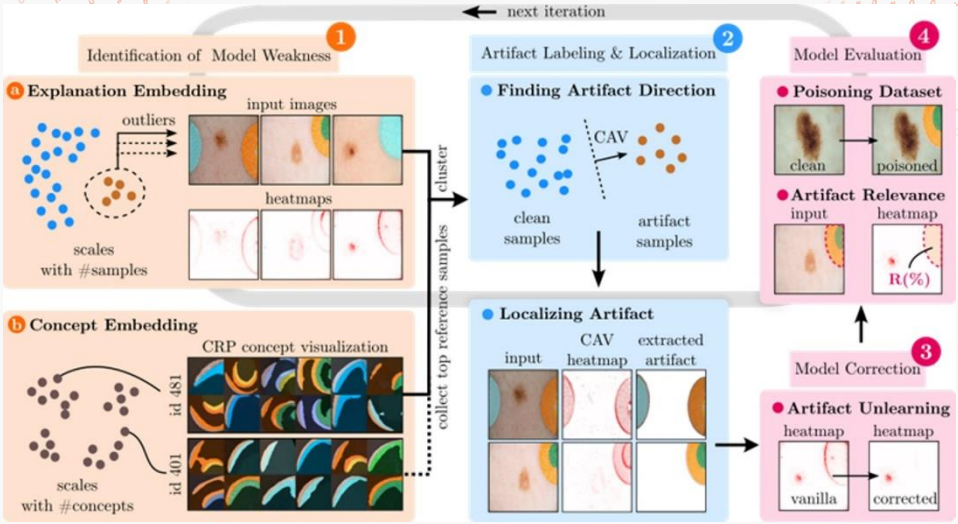

Figure 1: Reveal to Revise framework entailing the entire XAI life cycle to (1) identify model weaknesses, (2) label and localize artifacts, (3) correct the model, and (4) re-evaluate the model. The entire process can be repeated in an iterative fashion.

[1] Lapuschkin, S., Wäldchen, S., Binder, A., Montavon, G., Samek, W., & Müller, K. R. (2019). Unmasking Clever Hans predictors and assessing what machines really learn. Nature communications, 10(1), 1096.

[2] Achtibat, R., Dreyer, M., Eisenbraun, I., Bosse, S., Wiegand, T., Samek, W., & Lapuschkin, S. (2022). From" Where" to" What": Towards Human-Understandable Explanations through Concept Relevance Propagation. arXiv preprint arXiv:2206.03208.

Vectors. Then (3), the undesired behaviour can be unlearned using various model correction methods (see previous blog post) and the model is re-evaluated by measuring the relevance left on the artifact regions and the sensitivity of its output scores to the artifact by artificially inserting the artifact into test samples. If required, the entire process can be repeated in an iterative fashion.

R2R for Melanoma Detection

We apply the R2R framework to a VGG-16 model trained on ISIC2019 data by iteratively unlearning the usage if skin marker, band-aid and ruler artifacts using the correction method Right for the Right Reason[3]. The heatmaps after each correction step for artifactual samples are shown in Figure 2. After three iterations, the model's attention is mainly focusing on the mole itself and artifactual regions of the input image are ignored.

Conclusions

We introduced R2R, an XAI life cycle to reveal and revise spurious model behaviour requiring minimal human interaction via high automation and demonstrated its applicability to the task of Melanoma detection. We corrected the model behaviour with respect to three data artifacts, namely skin marker, band-aids and rulers. If you are interested in our work, please check out our paper[4].

Relevance to iToBoS

In iToBoS, many different AI systems will be trained for specific tasks, which in combination will culminate in an "AI Cognitive Assistant". All those systems will need to be explained with suitable XAI approaches to elucidate all possible and required aspects of the systems' decision making. Throughout the iToBoS project, we must detect and avoid the usage of data artifacts for model predictions.

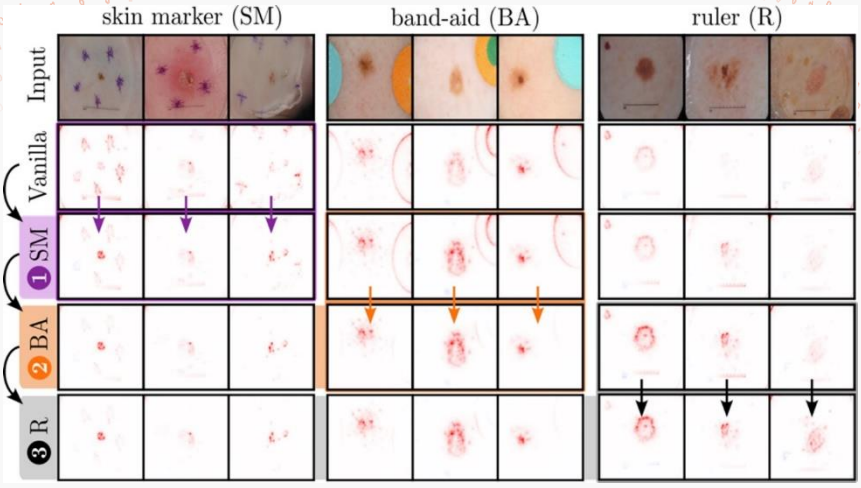

Figure 2: Application of R2R to a VGG-16 model trained on ISIC2019. In three iterations, the usages of skin marker (SM), band-aid (BA) and ruler (R) features are unlearned.

[3] Ross, A. S., Hughes, M. C., & Doshi-Velez, F. (2017). Right for the right reasons: Training differentiable models by constraining their explanations. arXiv preprint arXiv:1703.03717.

[4] Frederik Pahde, Maximilian Dreyer, Wojciech Samek, Sebastian Lapuschkin. (2023). Reveal to Revise: An Explainable AI Life Cycle for Iterative Bias Correction of Deep Models arXiv preprint arXiv:2303.12641.

Spotting the difference: how do you tell melanomas apart from healthy moles?

The earlier you find a skin cancer, the easier and more effective the treatment is. However, it's not always easy to tell apart harmless, healthy moles and those that need excision and histopathology analysis. iToBoS aims to incorporate total body imaging and a holistic risk assessment, enabled by an AI clinical assistant, to help clinicians make that decision.

The easiest way of all to spot a melanoma is if you notice a new mole, or an existing mole that is changing. In fact, in Australia more than half of all melanomas are detected by patients or their partners when they notice these changes. However, for clinicians seeing a patient for the first time, or seeing them more than once but without total body photography, individual moles have to be assessed. One of the common guidelines for assessing whether a mole is suspicious for melanoma is the ABCDEFG rule[5]:

- Asymmetry.
- Border irregularity.
- Colour variation.
- Diameter larger than five millimetres.
- Elevated.
- Firm.
- Growing for more than a month.

Clinicians have used this rule for more than 35 years to identify suspicious moles, but because border irregularity is a feature of many benign moles, and there are melanomas smaller than 5mm, these features are not always good predictors of whether a lesion is really a melanoma or not.

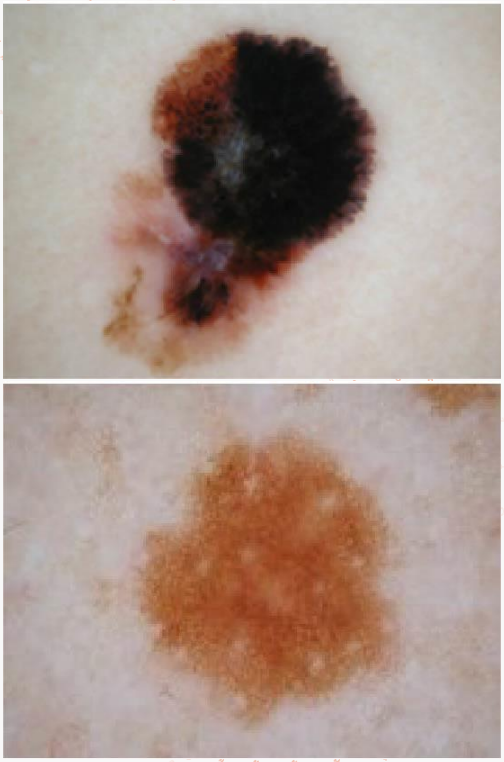

Figure 3: A melanoma showing asymmetry and multiple colours, and a benign mole with a broadly symmetrical shape and consistent colour. Photos by Peter Soyer.

The iToBoS clinical assistant aims to fold in more information, including information about the distribution of the patient's moles, signs of local or total body sun damage and other signs of melanoma risk, to give a risk score to each mole examined. There are many visible signs of increased melanoma risk, including:

[5] https://dermnetnz.org/topics/abcdes-of-melanoma

- Older age.
- A large number of moles.
- Multiple moles larger than five millimetres in diameter.
- Skin colour.
- Skin response to strong sun exposure, especially if you always burn and never tan.
- Freckles.
- Red or light hair.

Backed by an AI model trained on hundreds of patients and thousands of moles, iToBoS aims to use all these signs to detect real melanomas earlier and reduce the number of healthy moles being excised.

Some project events and activities

In the fifth semester of the project, which covers from April 2023 to September 2023, iToBoS organized and participated in different events for communication, dissemination and outreach purposes.

iToBoS project representatives presented the project and shared experiences with a wide range of stakeholders, including relevant players from the fields of ICT, innovation, research, opto-electronics, healthcare, and business, highlighting the following events and activities:

- Rome, 20-22/04/2023. 19th EADO Congress.
- Budapest, 25/04/2023. Semmelweis University to engage upcoming medical professionals.
- Brussels, 28-30/04/2023. MPNE Conference 2023.
- Sevilla, 18-20/05/2023. EADV Symposium 2023.
- Torino, 12-15/06/2023. European Association of Cancer Research 2023 Congress.
- Sevilla, 15-17/06/2023. International Course for Aesthetic and Cosmetic Dermatology.
- Vancouver, 18-22/06/2023. Safe Artificial Intelligence for All Domains - CVPR2023 conference.
- Firenze, 29-30/06/2023. 3rd International Symposium on Microgenomics 2023.
- Stockholm, 31/07-04/08/2023. 14th European Biophysics Congress.
- Santiago de Chile, 07-09/09/2023. 5th Latino-americano Dermoscopy Congress.
- Online, 14-27/09/2023. Meet iToBoS members workshop series.

Work presented

During the fifth semester of the project the following deliverables have been produced and submitted:

Deliverable submitted	Month	Leader	Diss. level
D11.4-Second dedicated training modules for Melanoma Patient Advocates	25	MPNE	PU
D4.2-Image anonymisation tools	26	UDG	CO
D7.6-XAI Software and methods for verifying multi-class classification of lesions	26	FHHI	CO
D5.2-Prototype of the liquid lens system for optimal image quality	27	OPT	CO
D7.1-Ground truth annotated dataset-initial release	27	FCRB	CO
D4.5-Second Data management plan aligned with FAIR principles and other initiatives including RDA and EOSC	28	SZTAKI	PU
D6.4-Software for detection of individual moles	28	TA	CO
D5.1-System specifications, scanner components and final technical design	29	BOSCH	CO
D11.2-Workshop for Melanoma Advocates	30	MPNE	PU

Publications

During the fifth semester of the project the following scientific works have been published in the iToBoS context.

- "*Revealing Hidden Context Bias in Segmentation and Object Detection through Concept-specific Explanations*". 2023. Maximilian Dreyer, Reduan Achtibat, Thomas Wiegand, Wojciech Samek & Sebastian Lapuschkin.
- "*Shortcomings of Top-Down Randomization-Based Sanity Checks for Evaluations of Deep Neural Network Explanations*". 2023. Alexander Binder, Leander Weber, Sebastian Lapuschkin, Grégoire Montavon, Klaus-Robert Müller & Wojciech Samek.
- "*Optimizing Explanations by Network Canonization and Hyperparameter Search*". 2023. Frederik Pahde, Galip Ümit Yolcu, Alexander Binder, Wojciech Samek & Sebastian Lapuschkin.
- "*The Meta-Evaluation Problem in Explainable AI: Identifying Reliable Estimators with MetaQuantus*". 2023. Anna Hedström, Philine Lou Bommer, Kristoffer Knutsen Wickstrøm, Wojciech Samek, Sebastian Lapuschkin & Marina MC Höhne.
- "*A group of three miRNAs can act as candidate circulating biomarkers in liquid biopsies from melanoma patients*". 2023. Eleonora De Martino, Ilaria Gandin, Eros Azzalini, Cesare Massone, Maria Antonietta Pizzichetta, Erika Giulioni, Sanja Javor, Caterina Pinzani, Claudio Conforti, Iris Zalaudek & Serena Bonin.
- *"Association of germline variants in telomere maintenance genes (POT1, TERF2IP, ACD, and TERT) with spitzoid morphology in familial melanoma: A multi-center case series"*. 2023. Alisa M. Goldstein PhD, Richard Qin BS, Emily Y. Chu MD, PhD b, David E. Elder MBChB c, Daniela Massi MD, PhD, David J. Adams PhD, Paul W. Harms MD, PhD, Carla Daniela Robles-Espinoza PhD, Julia A. Newton-Bishop MD, PhD, D. Timothy Bishop PhD, Mark Harland PhD, Elizabeth A. Holland BS, Anne E. Cust PhD, Helen Schmid MPH, Graham J. Mann MBBS, PhD, Susana Puig MD, PhD, Miriam Potrony PhD, Llucia Alos MD, PhD, Eduardo Nagore MD, PhD, David Millán-Esteban PhD & Michael R. Sargen MD.

In addition, different articles aimed at broader audiences have been developed and published on the project website, presenting the project from different perspectives, considering the different profiles of all the project partners.

iToBoS team

The consortium with 20 partner organizations is led by the University of Girona (Spain). This international consortium brings together **leading research / academic institutions** (5 research centres), **industries** (4 large companies and 7 SMEs) and **end-user entities** (3 hospitals and 1 patients' NPO).

The University of Queensland has received funding from the Australia's NHMRC under grant number APP2007014.

Let's stay in contact!

iToBoS has deployed some **digital channels to keep in touch with you and bring you the latest news** about the project. They are also a way to receive your ideas and comments as well as learn more about your needs.

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This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 965221.
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