Breast cancer CAD tools

António Polónia, MD, PhD

Ipatimup Diagnostics

@PoloniaAntonio

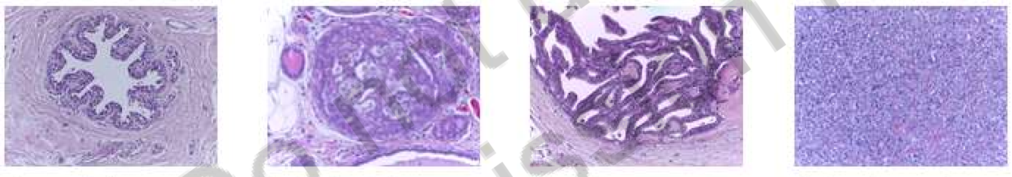
Disclosure

None

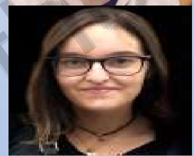
@PoloniaAntonio

25 ANOS A DESCOBRIR O CANCRO ipatimup

Breast cancer CAD tools



a) normal tissue b) benign lesion c) carcinoma *in situ* d) invasive carcinoma


INEB Instituto de Engenharia Biomédica

25 ANOS A DESCOBRIR O CANCRO ipatimup

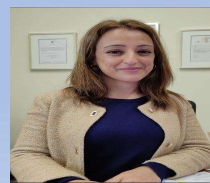
INESCTEC ASSOCIATE LABORATORY PORTUGAL | C-BER BIOMEDICAL ENGINEERING

BIOMEDICAL IMAGING LAB

ICIAR

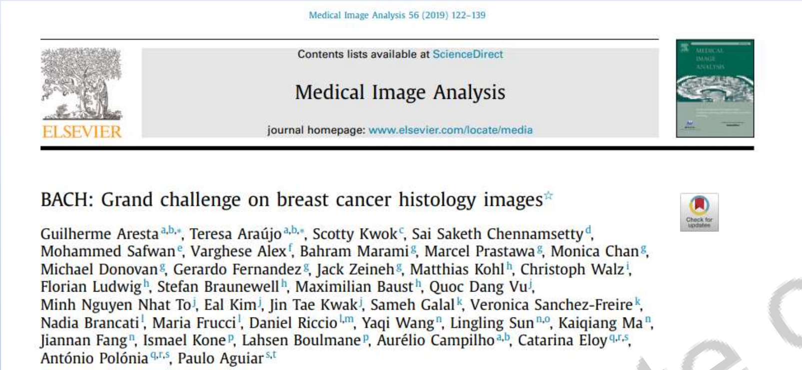
U.PORTO FEUP FACULDADE DE ENGENHARIA UNIVERSIDADE DO PORTO





@PoloniaAntonio

Breast cancer CAD tools


Medical Image Analysis 56 (2019) 122–139

Contents lists available at ScienceDirect

Medical Image Analysis

journal homepage: www.elsevier.com/locate/media

ELSEVIER

BACH: Grand challenge on breast cancer histology images

Guilherme Aresta[a,b,*], Teresa Araújo[a,b,*], Scotty Kwok[c], Sai Saketh Chennamsetty[d], Mohammed Safwan[e], Varghese Alex[f], Bahram Marami[g], Marcel Prastawa[g], Monica Chan[g], Michael Donovan[g], Gerardo Fernandez[g], Jack Zeineh[g], Matthias Kohl[h], Christoph Walz[i], Florian Ludwig[h], Stefan Braunewell[h], Maximilian Baust[h], Quoc Dang Vu[j], Minh Nguyen Nhat To[j], Eal Kim[j], Jin Tae Kwak[j], Sameh Galal[k], Veronica Sanchez-Freire[k], Nadia Brancati[l], Maria Frucci[l], Daniel Riccio[l,m], Yaqi Wang[n], Lingling Sun[n,o], Kaiqiang Ma[n], Jiannan Fang[n], Ismael Kone[p], Lahsen Boulmane[p], Aurélio Campilho[a,b], Catarina Eloy[q,r,s], António Polónia[q,r,s], Paulo Aguiar[s,t]

B

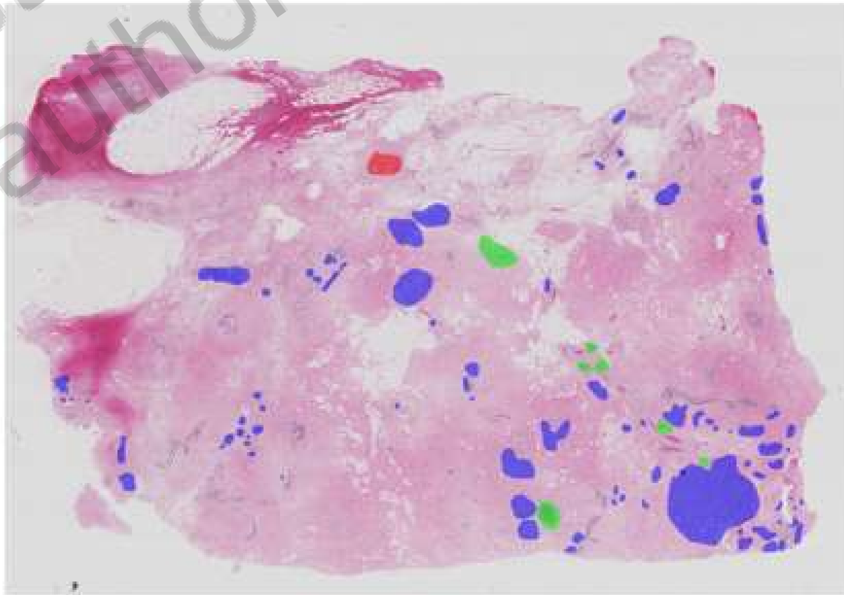
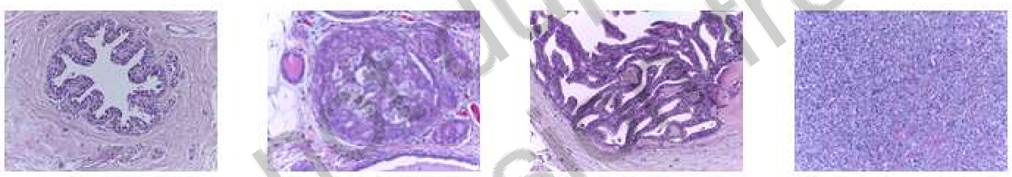


Fig. 3. Example of a pixel-wise annotated whole-slide image from the training set. ■ benign; ■ *in situ*; ■ invasive.

A



a) normal tissue b) benign lesion c) carcinoma *in situ* d) invasive carcinoma

@PoloniaAntonio

Breast cancer CAD tools

25 ANOS A DESCOBRIR O CANCRO ipatimup

BACH ICIAR 2018 Grand Challenge on BreAst Cancer Histology images

Table 2
Summary of the methods submitted for Part **A**. [A]detailed description in Section 3.2; [AB]detailed description in Section 3.4. Pre-training is performed on ImageNet (Krizhevsky et al., 2012). **Acc.** is the overall prediction success for the four classes; **Approach** lists the main methods to label the images; **Ensemble** (Ens.) indicates if the approach uses a single or multiple models (and their number, when available); **External sets** indicates if the method was trained using datasets other than from Part **A; Context (area ratio)** is the ratio between the original size and the size of the patch used for training the network (prior to rescaling); **Input size (pixels)** is the size of the image to be analyzed by the model; **Color normalization** (color norm.) indicates if any histology-inspired normalization was used. N/A: information not available. [1]Pre-trained on CAMELYON (https://camelyon17.grand-challenge.org/). M1: (Bejnordi et al., 2016); M2: (Krishnan and Shah, 2012); M3: (Macenko et al., 2009); M4: (Reinhard et al., 2001).

Team	Acc.	Approach	Pre-trained	Ens.	External sets	Context (area ratio)	Input size (pixels)	Color norm.
(Chennamsetty et al., 2018) (216)[A]	0.87	Resnet-101; Densenet-161	√	3	✗	1	224 × 224	✗
(Kwok, 2018) (248)[AB]	0.87	Inception-Resnet-v2	√	✗	Part **B**	0.71	299 × 299	✗
(Brancati et al., 2018) (1)[A]	0.86	Resnet-34, 50, 101	√	3	✗	1	308 × 308 615 × 615	✗
(Marami et al., 2018) (16)[AB]	0.84	Inception-v3	√	4	Part **B** BreakHis	0.33	512 × 512	M1
(Kohl et al., 2018) (54)[AB]	0.83	Densenet-161	√[1]	✗	✗	1	205 × 154	✗
(Wang et al., 2018a) (157)[A]	0.83	VGG16	√	✗	✗	0.765	224 × 224	✗
Steinfeldt *et al.* (186)	0.81	XCeption	√	✗	✗	0.028-0.751	229 × 229	✗
(Koné and Boulmane, 2018) (19)[A]	0.81	ResNeXt50	√	√	BISQUE	1	299 × 299	✗
Nedjar *et al.* (36)	0.81	Inception-v3, Resnet-50, MobileNet	√	√	✗	1	224 × 224	✗
Ravi *et al.* (412)	0.8	Resnet-152	√	✗	✗	0.875	224 × 224	M2
(Wang et al., 2018b) (22)	0.79	VGG16	√	✗	✗	0.255	224 × 224	M3
(Cao et al., 2018) (425)	0.79	PTFAS+GLCM, ResNet-18, ResNeXt, NASNet-A, ResNet-152, VGG16, Random Forest SVM	√	√	✗	1	224 × 224 331 × 331	✗
Seo *et al.* (60)	0.79	ResNet, Inception-V3, Random Forests	√	✗	√	1	299 × 299	✗
Sidhom *et al.* (370)	0.78	ResNet-50	√	✗	✗	0.018 0.289	224 × 224	M4
(Guo et al., 2018) (242)	0.77	GoogLeNet	√	2	✗	1 0.083	224 × 224	M4
Ranjan *et al.* (61)	0.77	AlexNet	√	2	✗	1	224 × 224	✗
(Mahbod et al., 2018) (73)	0.77	ResNet-50, ResNet-101	√	2	✗	1	224 × 224	M3
(Ferreira et al., 2018) (18)	0.76	Inception-ResNet-v2	√	✗	✗	1	224 × 224	✗
(Pimkin et al., 2018) (256)	0.76	ResNet34, Densenet169, Densenet201 XGBoost	√	12	Part **B** BreakHis	1	300 × 300	✗
Sarker *et al.* (358)	0.75	Inception-v4	√	✗	✗	0.083	299 × 299	✗
(Rakhlin et al., 2018) (98)	0.74	VGG16, ResNet-50, IcenptionV3, LightGBM	√	√	✗	0.20 0.54	400 × 400 600 × 600	M3
(Iesmantas and Alzbutas, 2018) (164)	0.72	Custom CNN (Capsule Network)	✗	✗	✗	0.029	512 × 512	M4
Xie *et al.* (253)	0.72	CNN	✗	✗	✗	0.083	512 × 512	✗
(Weiss et al., 2018) (268)	0.72	Xception, Logistic Regression	√	✗	✗	1	1024 × 768	M3
(Awan et al., 2018) (6)	0.71	ResNet50, SVM	√	✗	✗	0.33	512 × 512	M4
Liang (62)	0.7	VGG16, VGG19, ResNet50, InceptionV3, Inception-Resnet, k-NN	√	5	✗	0.083	N/A	✗

@PoloniaAntonio

25 ANOS A DESCOBRIR O CANCRO
ipatimup

Breast cancer CAD tools

BACH
ICIAR 2018 Grand Challenge on BreAst Cancer Histology images

Table 3
Summary of the methods submitted for whole-slide image analysis (Part **B**). [B]detailed description in Section 3.3; [AB]detailed description in Section 3.4. Pre-training is performed on ImageNet (Krizhevsky et al., 2012) unless stated otherwise. **Score** is the custom metric from Eq. (1); **Approach** lists the main methods to label the images; **Ensemble** (Ens.) indicates if the approach uses a single or multiple models (and their number, when available); **External sets** indicates if the method was trained using datasets other than from Part **A**; **Context (area ratio)** is the ratio between the average original size and the size of the patch that is used for training the network (prior to rescaling); **Input size (pixels)** is the size of the image to be analyzed by the model; **Color normalization** (Color norm.) indicates if any histology-inspired normalization was used. [1] trained on ImageNet, [2] trained on VOC2012.

Team	Score	Approach	Pretrained	Ens.	External sets	Context (area ratio)	Input size (pixels)	Color norm.
(Kwok, 2018) (248)[AB]	0.69	Inception-Resnet-v2	√	✗	Part **A**	8.5e−4	299 × 299	✗
(Marami et al., 2018) (16)[AB]	0.55	Inception-v3 + adaptive pooling	√	4	Part **A** BreakHis	9.9e−5	512 × 512	✗
Jia *et al.* (296)	0.52	ResNet-50 + multiscale atrous convolution	√	✗	✗	9.9e−5	512 × 512	✗
Li *et al.* (137)	0.52	VGG16[1], DeepLabV2[1], Resnet50[2]	√	√	✗	9.9e−5	512 × 512	✗
Murata *et al.* (91)	0.50	U-Net	✗	✗	✗	1.6e−2	256 × 256	✗
(Galal and Sanchez-Freire, 2018) (264)[B]	0.50	DenseNet	✗	✗	✗	1.6e−3	2048 × 2048	✗
(Vu et al., 2018) (166)[AB]	0.49	DenseNet, SENet, ResNext	√	✗	✗	1.5e−4	630 × 630	✗
(Kohl et al., 2018) (54)[AB]	0.42	Densenet-161	√	✗	Part **B** non-annotated	9.3e−6	157 × 157	✗

@PoloniaAntonio

Breast cancer CAD tools

ICIAR 2018 Grand Challenge on BreAst Cancer Histology images

Multiclass Classification of Breast Cancer in Whole-Slide Images

Scotty Kwok[✉]

Seek AI Limited, Hong Kong, China

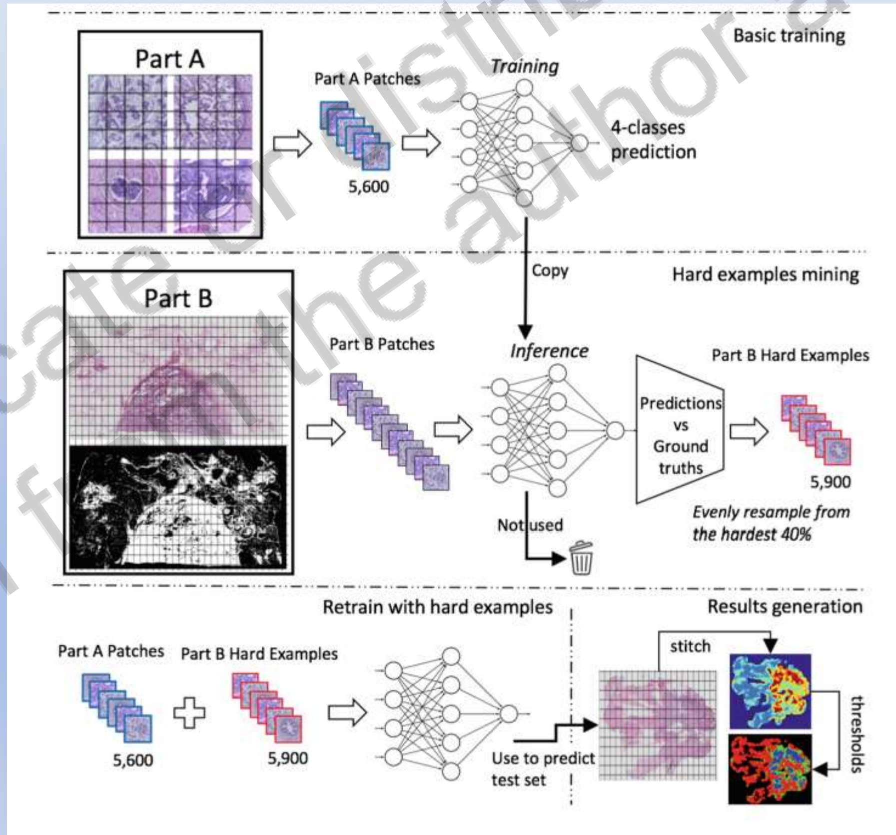


Fig. 1. Overview of the framework

@PoloniaAntonio

Breast cancer CAD tools

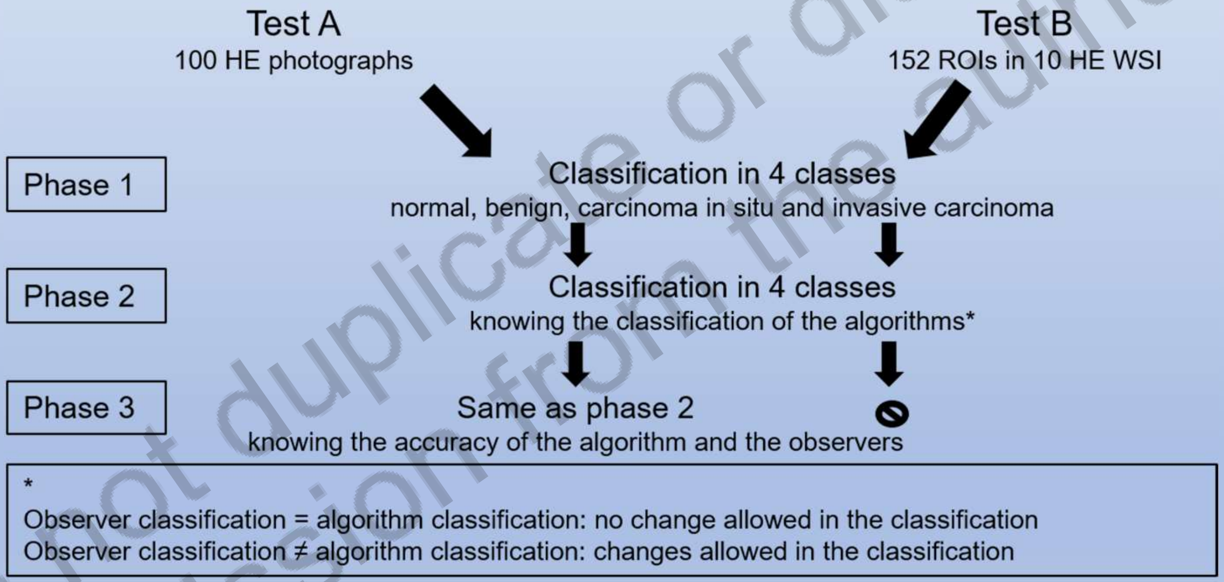
AJCP / Original Article

Artificial Intelligence Improves the Accuracy in Histologic Classification of Breast Lesions

António Polónia, MD, PhD,[1,2,] Sofia Campelos, MD,[1,2] Ana Ribeiro, MD,[3] Ierece Aymore, MD,[1,2] Daniel Pinto, MD,[4] Magdalena Biskup-Fruzynska, MD,[5] Ricardo Santana Veiga, MD,[6] Rita Canas-Marques, MD,[7] Guilherme Aresta, MEng,[8,9] Teresa Araújo, MEng,[8,9] Aurélio Campilho, PhD,[8,9] Scotty Kwok, MSc,[10] Paulo Aguiar, PhD,[2,11] and Catarina Eloy, MD, PhD[1,2,12]*

@PoloniaAntonio

Breast cancer CAD tools



@PoloniaAntonio

Breast cancer CAD tools

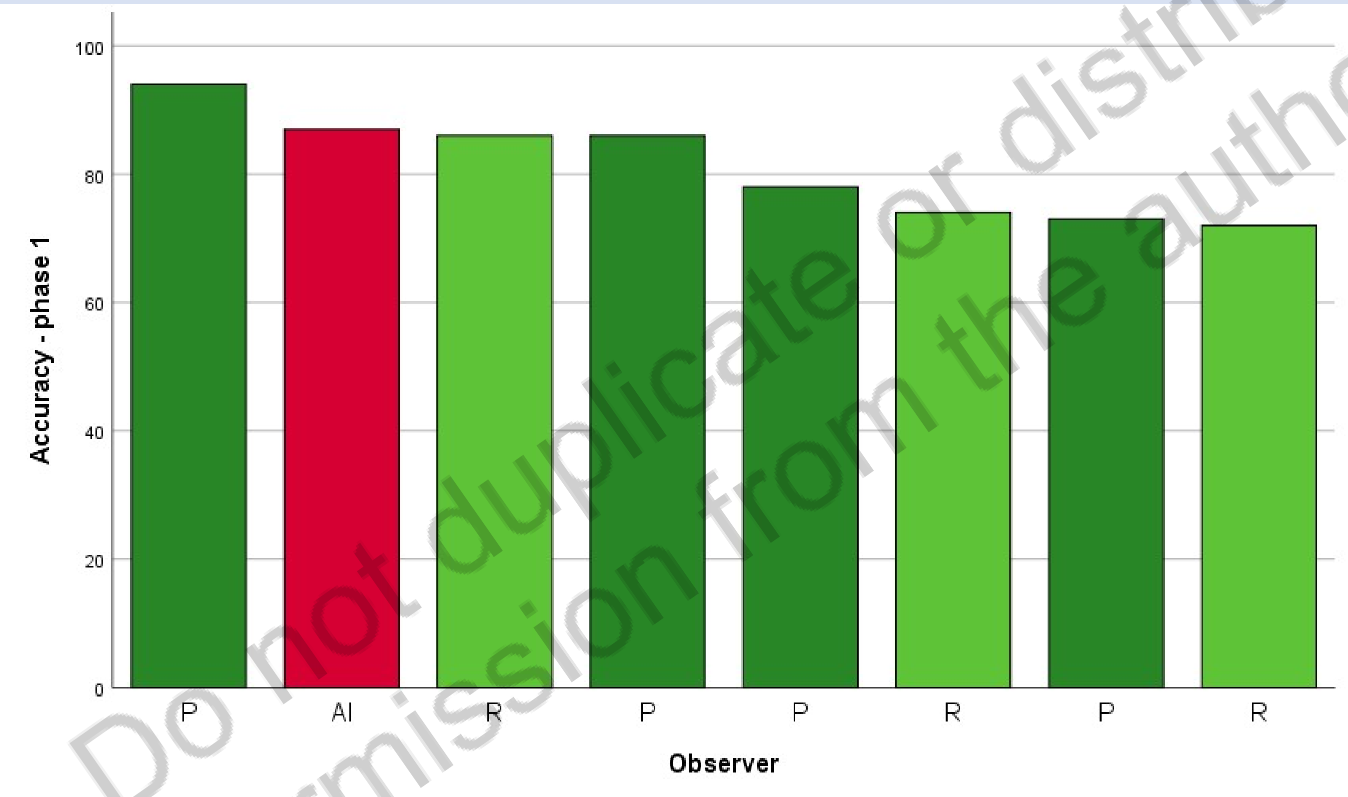


Table 3
Diagnostic Accuracy in Test A and B

	Phase	Test A	Test B
Algorithm A	1	0.87	NA
Algorithm B	1	NA	0.49
Pathologists (average)	1	0.83	0.83
	2	0.87	0.82
	3	0.90	NA
Residents (average)	1	0.77	0.89
	2	0.82	0.88
	3	0.87	NA
All observers (average)	1	0.80[a]	0.86
	2	0.85[a,b]	0.85
	3	0.88[b]	NA

NA, not applicable.
[a]Wilcoxon, $P < .001$
[b]Wilcoxon, $P = .001$.

@PoloniaAntonio

Breast cancer CAD tools

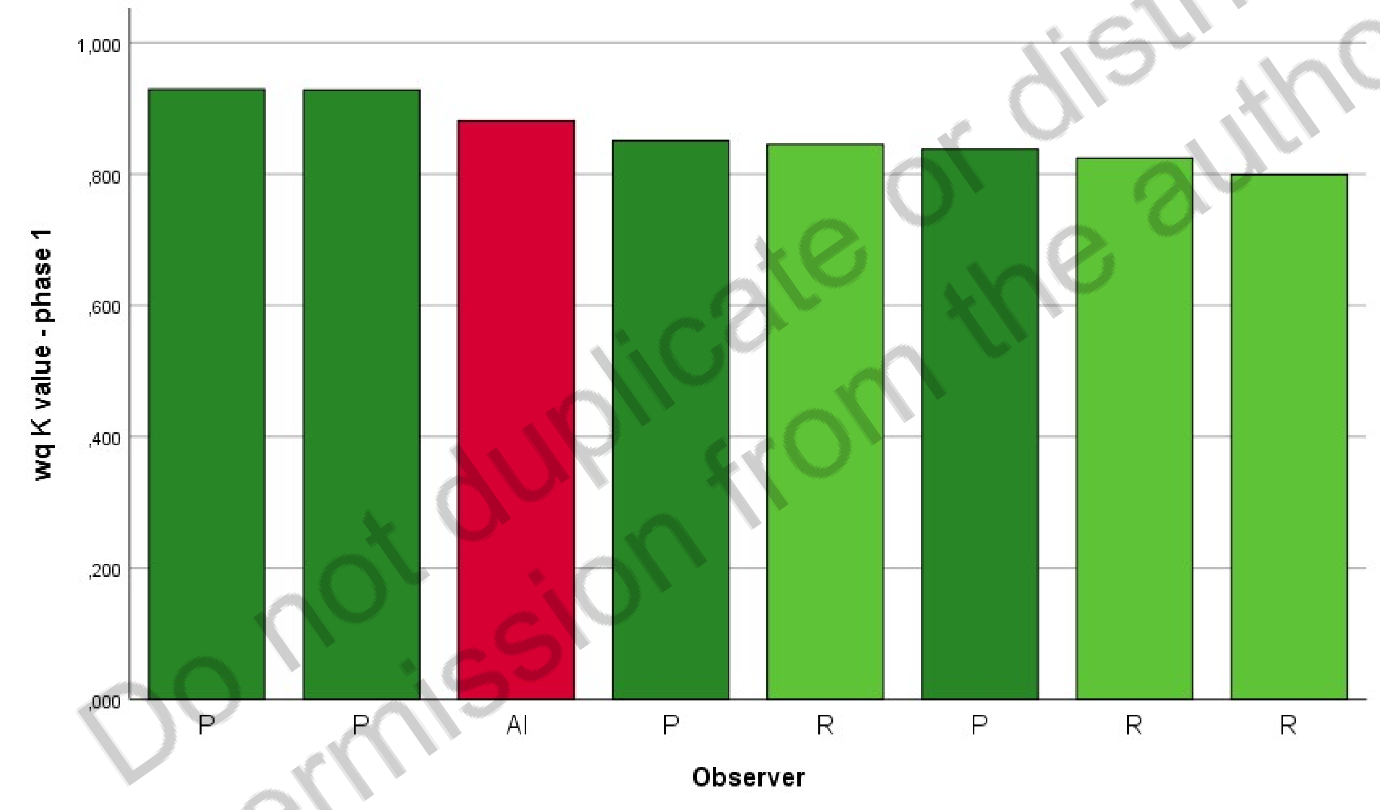


Table 3
Diagnostic Accuracy in Test A and B

	Phase	Test A	Test B
Algorithm A	1	0.87	NA
Algorithm B	1	NA	0.49
Pathologists (average)	1	0.83	0.83
	2	0.87	0.82
	3	0.90	NA
Residents (average)	1	0.77	0.89
	2	0.82	0.88
	3	0.87	NA
All observers (average)	1	0.80[a]	0.86
	2	0.85[a,b]	0.85
	3	0.88[b]	NA

NA, not applicable.
[a]Wilcoxon, $P < .001$
[b]Wilcoxon, $P = .001$.

@PoloniaAntonio

ipatimup 25 ANOS A DESCOBRIR O CANCRO

Breast cancer CAD tools

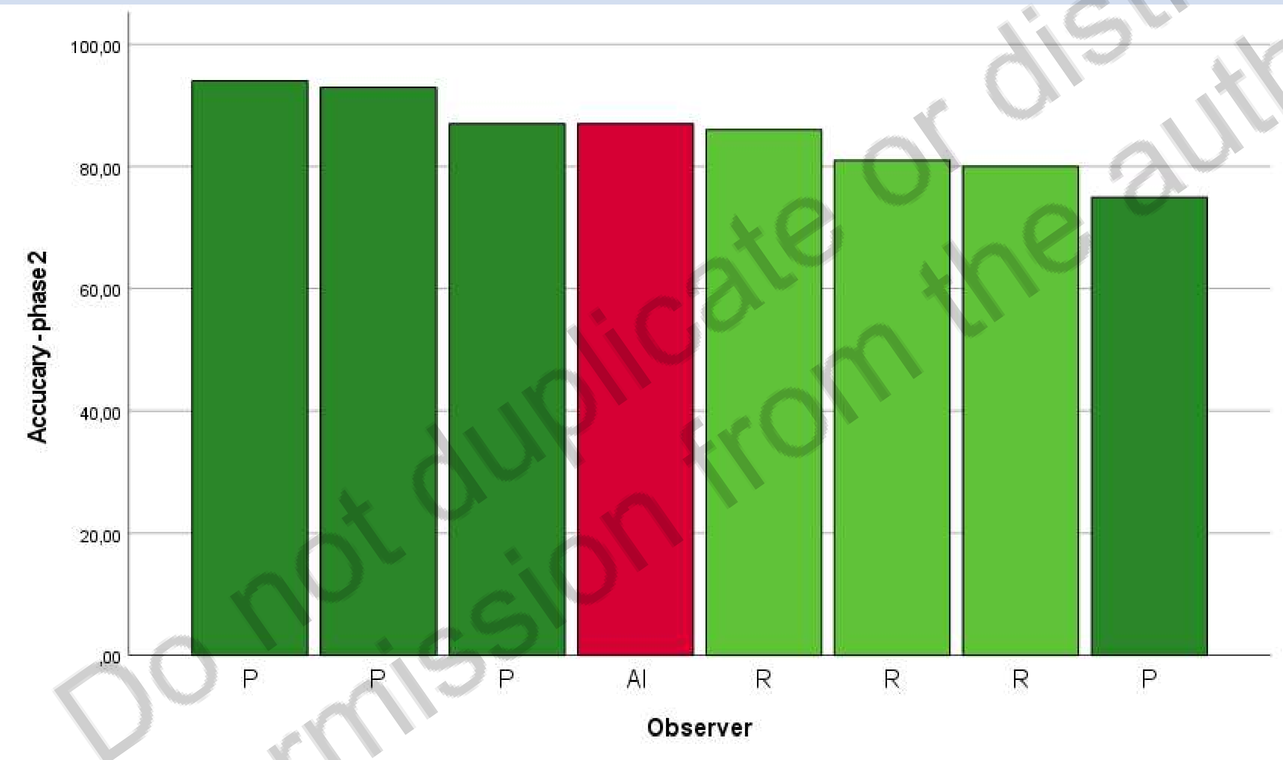


Table 3
Diagnostic Accuracy in Test A and B

	Phase	Test A	Test B
Algorithm A	1	0.87	NA
Algorithm B	1	NA	0.49
Pathologists (average)	1	0.83	0.83
	2	0.87	0.82
	3	0.90	NA
Residents (average)	1	0.77	0.89
	2	0.82	0.88
	3	0.87	NA
All observers (average)	1	0.80[a]	0.86
	2	0.85[a,b]	0.85
	3	0.88[b]	NA

NA, not applicable.
[a]Wilcoxon, $P < .001$
[b]Wilcoxon, $P = .001$.

@PoloniaAntonio

Breast cancer CAD tools

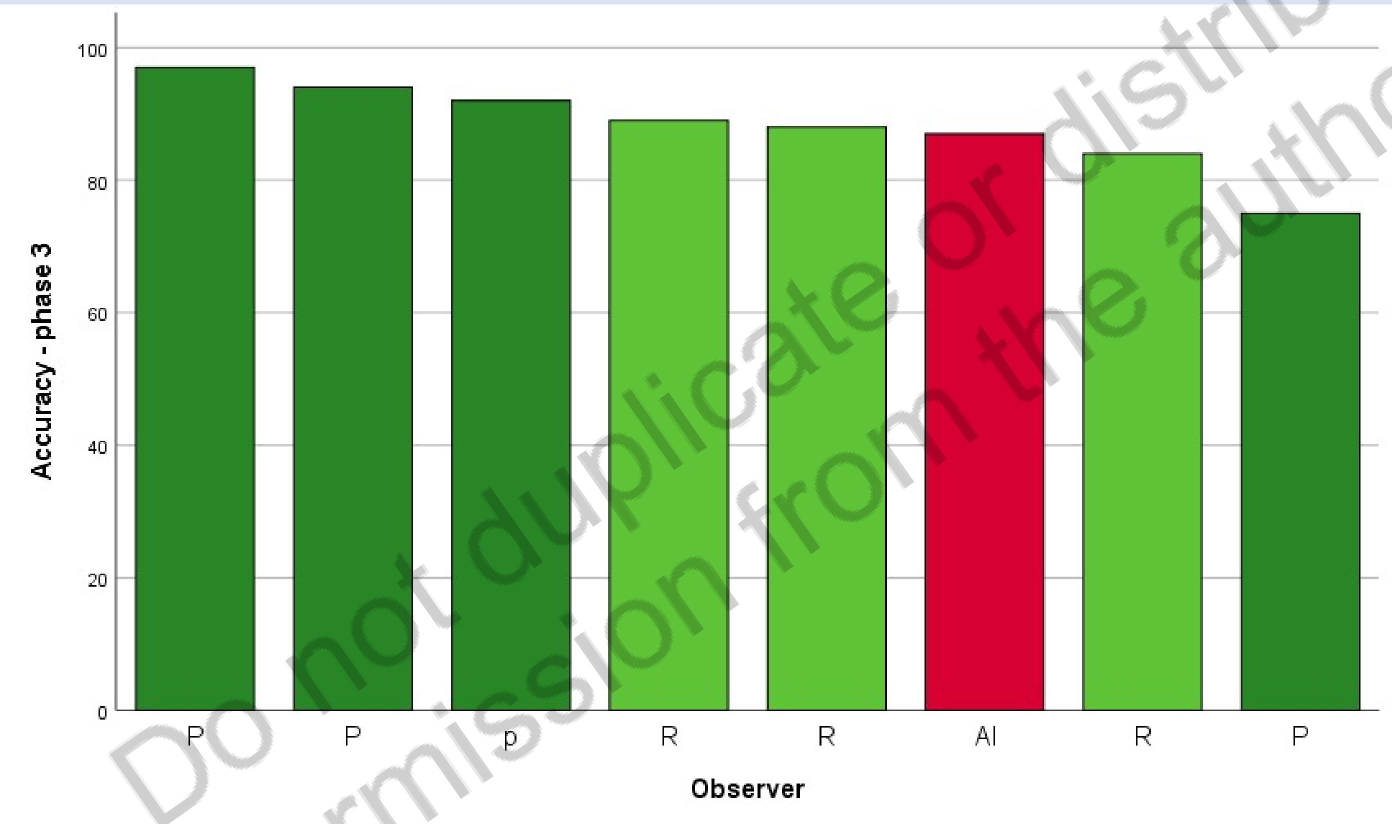


Table 3
Diagnostic Accuracy in Test A and B

	Phase	Test A	Test B
Algorithm A	1	0.87	NA
Algorithm B	1	NA	0.49
Pathologists (average)	1	0.83	0.83
	2	0.87	0.82
	3	0.90	NA
Residents (average)	1	0.77	0.89
	2	0.82	0.88
	3	0.87	NA
All observers (average)	1	0.80[a]	0.86
	2	0.85[a,b]	0.85
	3	0.88[b]	NA

NA, not applicable.
[a]Wilcoxon, $P < .001$
[b]Wilcoxon, $P = .001$.

@PoloniaAntonio

Breast cancer CAD tools

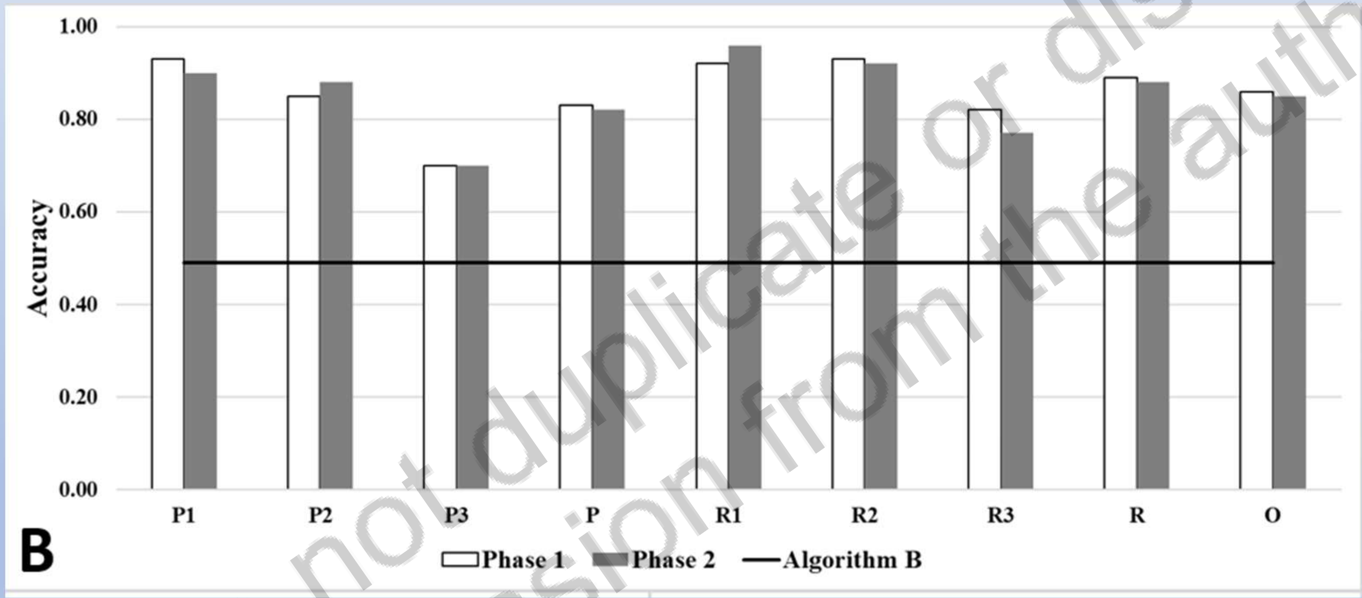
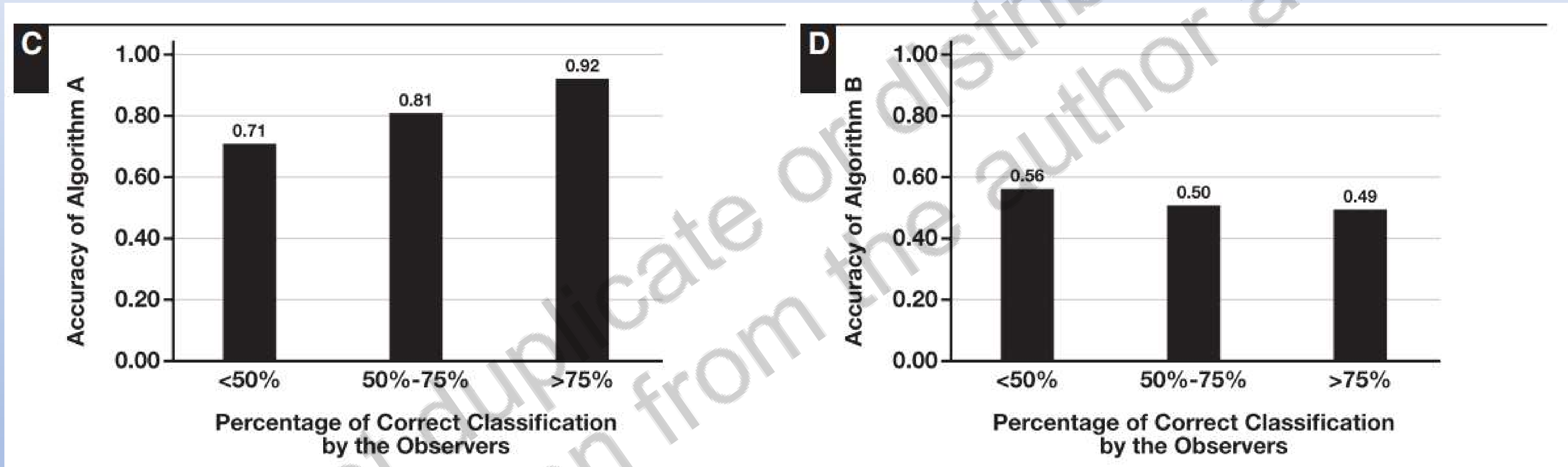


Table 3
Diagnostic Accuracy in Test A and B

	Phase	Test A	Test B
Algorithm A	1	0.87	NA
Algorithm B	1	NA	0.49
Pathologists (average)	1	0.83	0.83
	2	0.87	0.82
	3	0.90	NA
Residents (average)	1	0.77	0.89
	2	0.82	0.88
	3	0.87	NA
All observers (average)	1	0.80[a]	0.86
	2	0.85[a,b]	0.85
	3	0.88[b]	NA

NA, not applicable.
[a]Wilcoxon, $P < .001$
[b]Wilcoxon, $P = .001$.

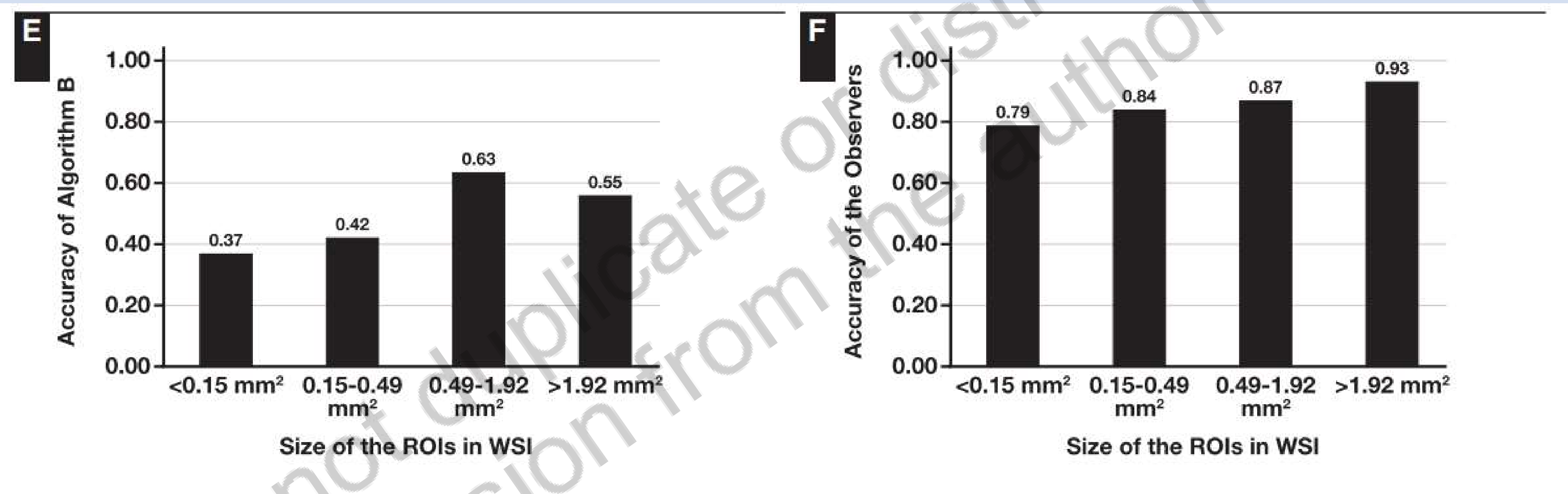
Breast cancer CAD tools



@PoloniaAntonio

25 ANOS A DESCOBRIR O CANCRO ipatimup

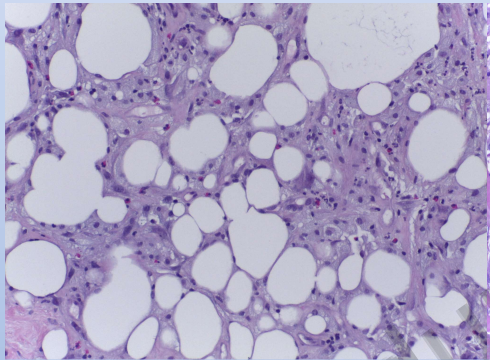
Breast cancer CAD tools



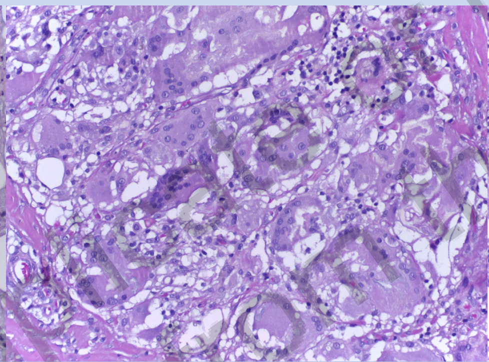
@PoloniaAntonio

25 ANOS A DESCOBRIR O CANCRO
ipatimup

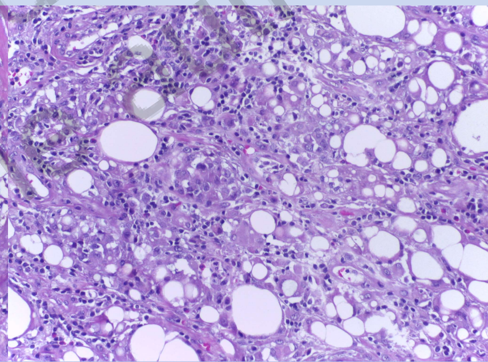
Breast cancer CAD tools



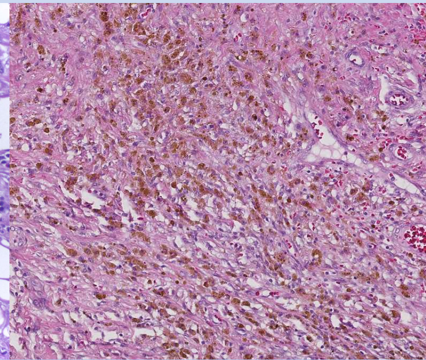
A1 6/7 correct
A3 5/7 correct



A1 5/7 correct
A3 no change



A1 3/7 correct
A3 2/7 correct

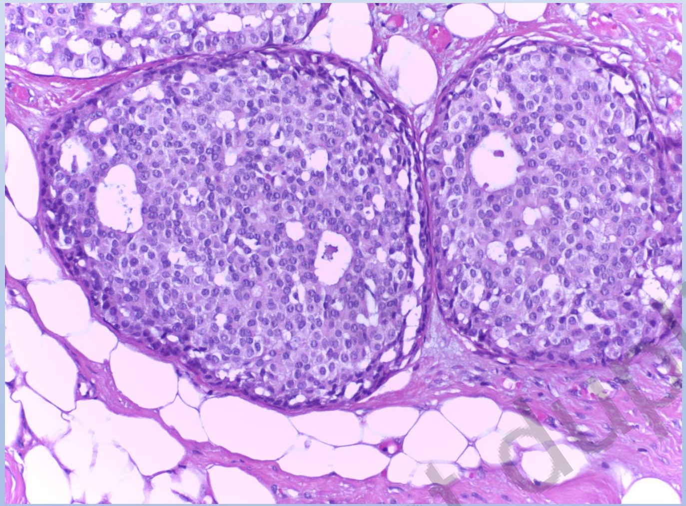


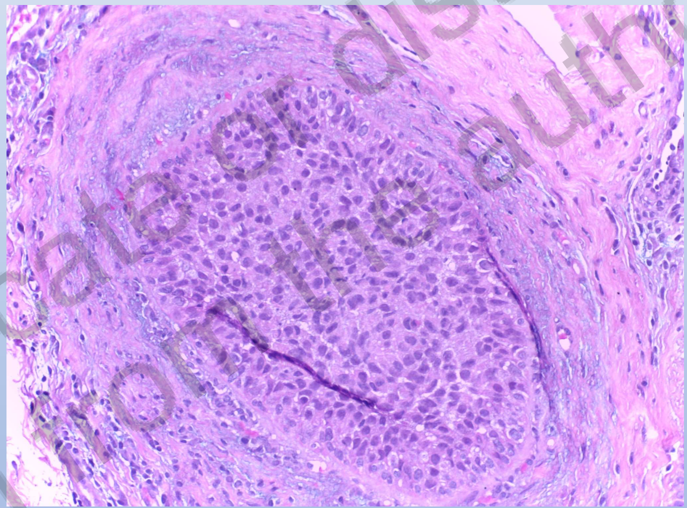
B1 6/6 correct
B2 no change

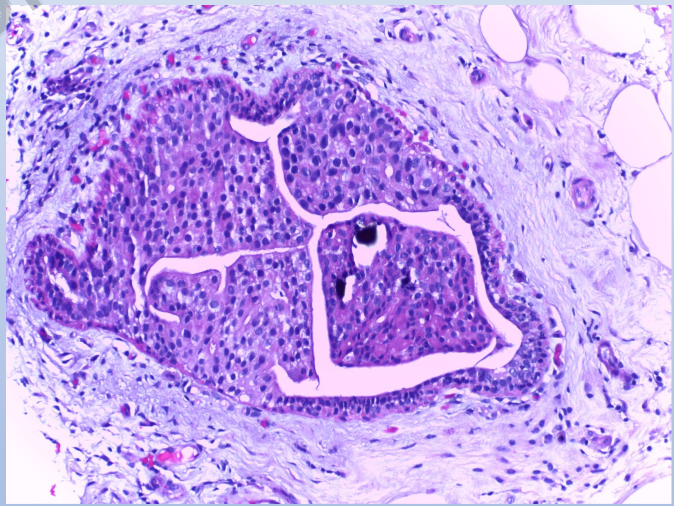
Output of the AI: invasive carcinoma (incorrect)

@PoloniaAntonio

Breast cancer CAD tools







A1 3/7 correct
A3 5/7 correct

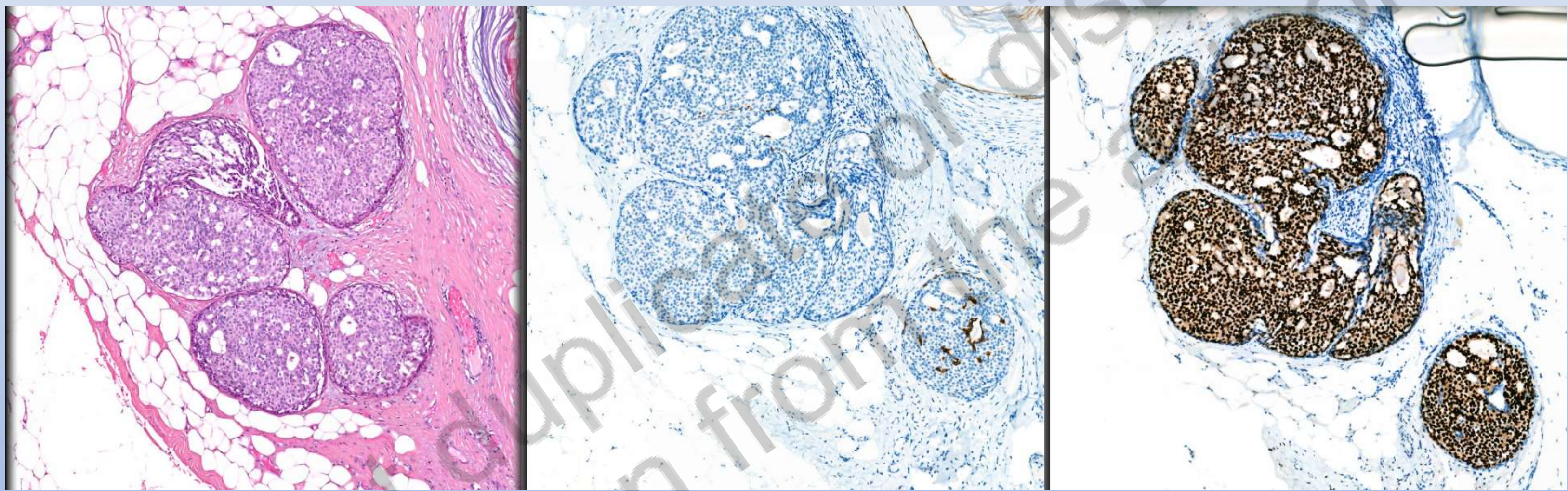
A1 4/7 correct
A3 6/7 correct

A1 3/7 correct
A3 5/7 correct

Output of the AI: carcinoma in situ (correct)

@PoloniaAntonio

Breast cancer CAD tools

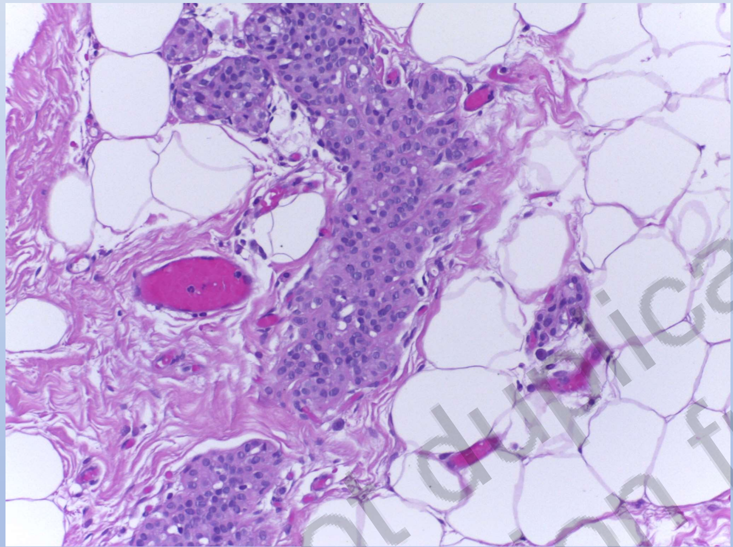


HE CK5/6 ER

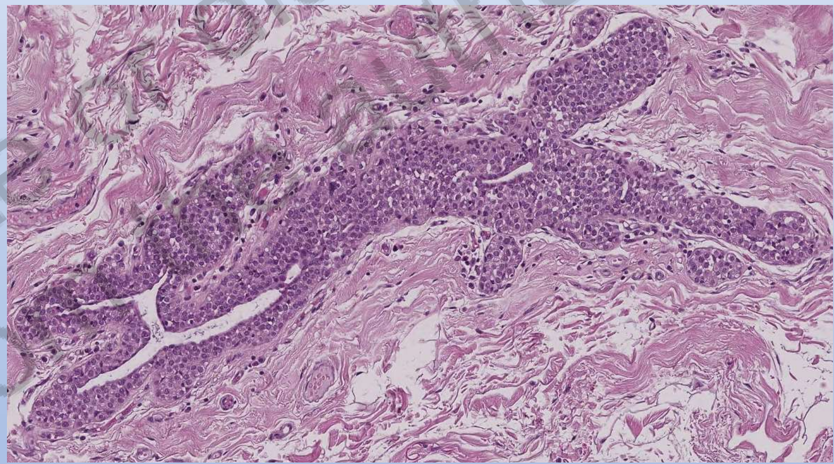
Output of the AI: carcinoma in situ (correct)

@PoloniaAntonio

Breast cancer CAD tools



A1 1/7 correct
A3 1/7 correct

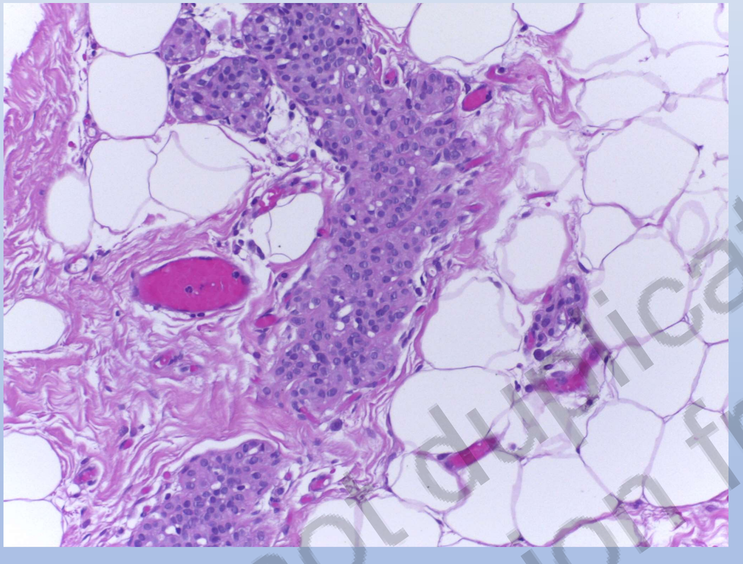


B1 5/6 correct
B2 4/6 correct

Output of the AI: normal (incorrect)

@PoloniaAntonio

Breast cancer CAD tools



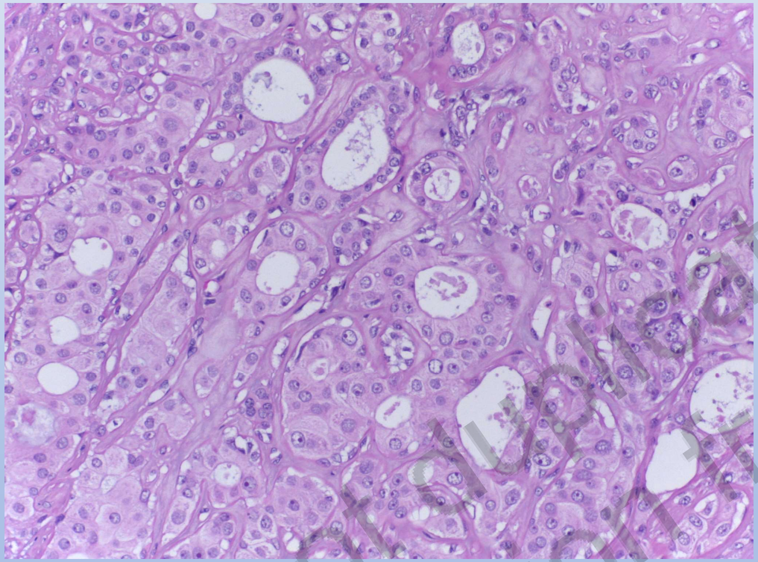
A1 1/7 correct
A3 1/7 correct

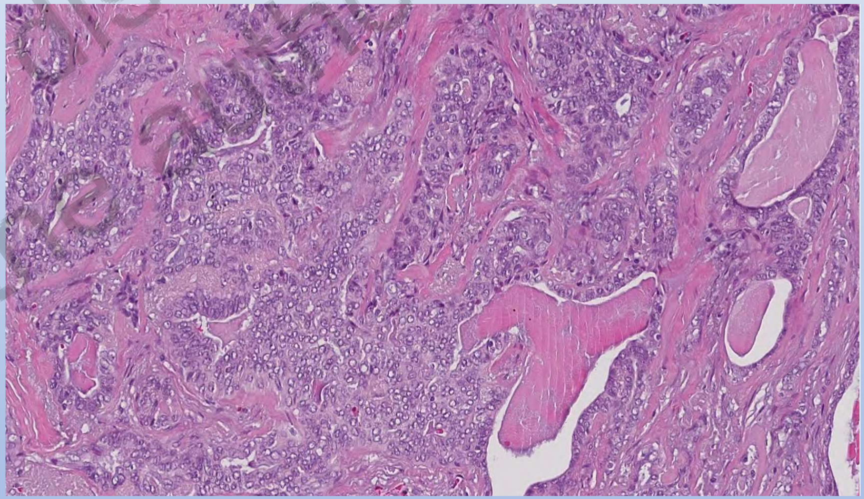
E-cahderin

Output of the AI: normal (incorrect)

@PoloniaAntonio

Breast cancer CAD tools





A1 0/7 correct
A3 1/7 correct

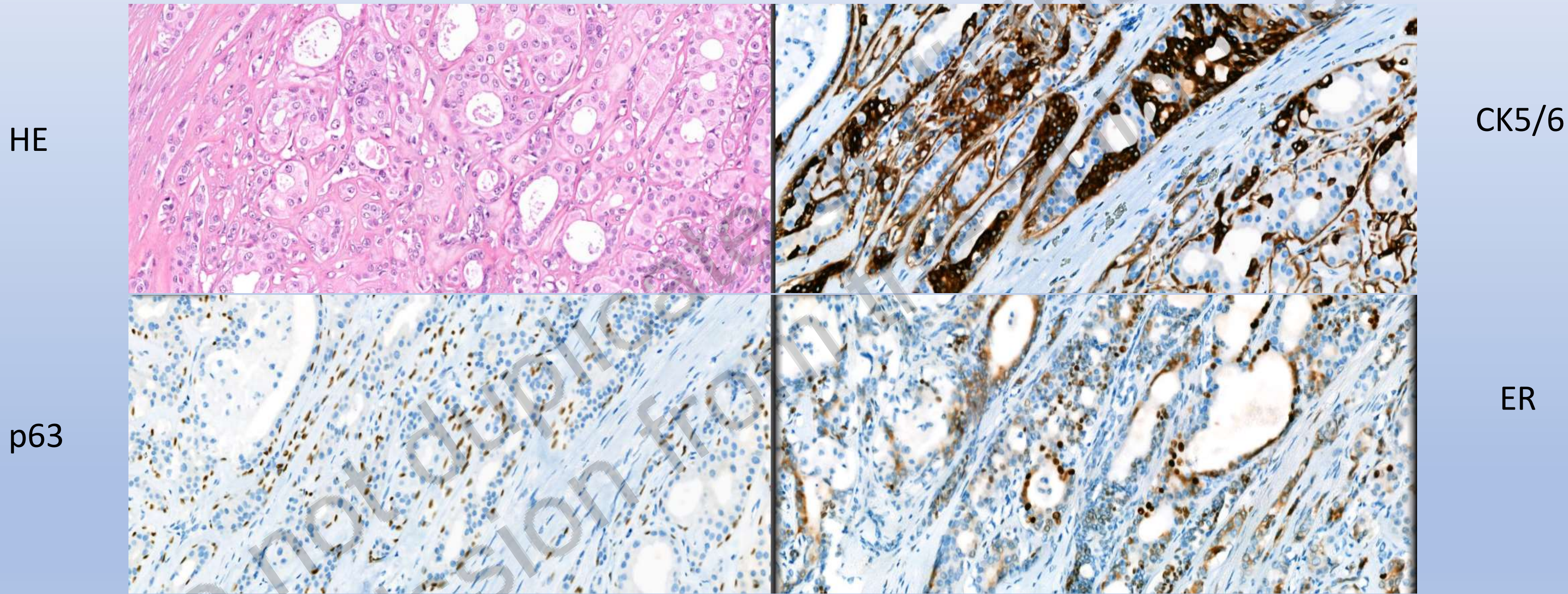
B1 2/6 correct
B2 3/6 correct

Output of the AI: benign (correct)

@PoloniaAntonio

25 ANOS
A DESCOBRIR O CANCRO
ipatimup

Breast cancer CAD tools



Output of the AI: benign (correct)

@PoloniaAntonio

Breast cancer CAD tools

Most clinically relevant incorrect classifications

Benign vs Carcinoma in situ

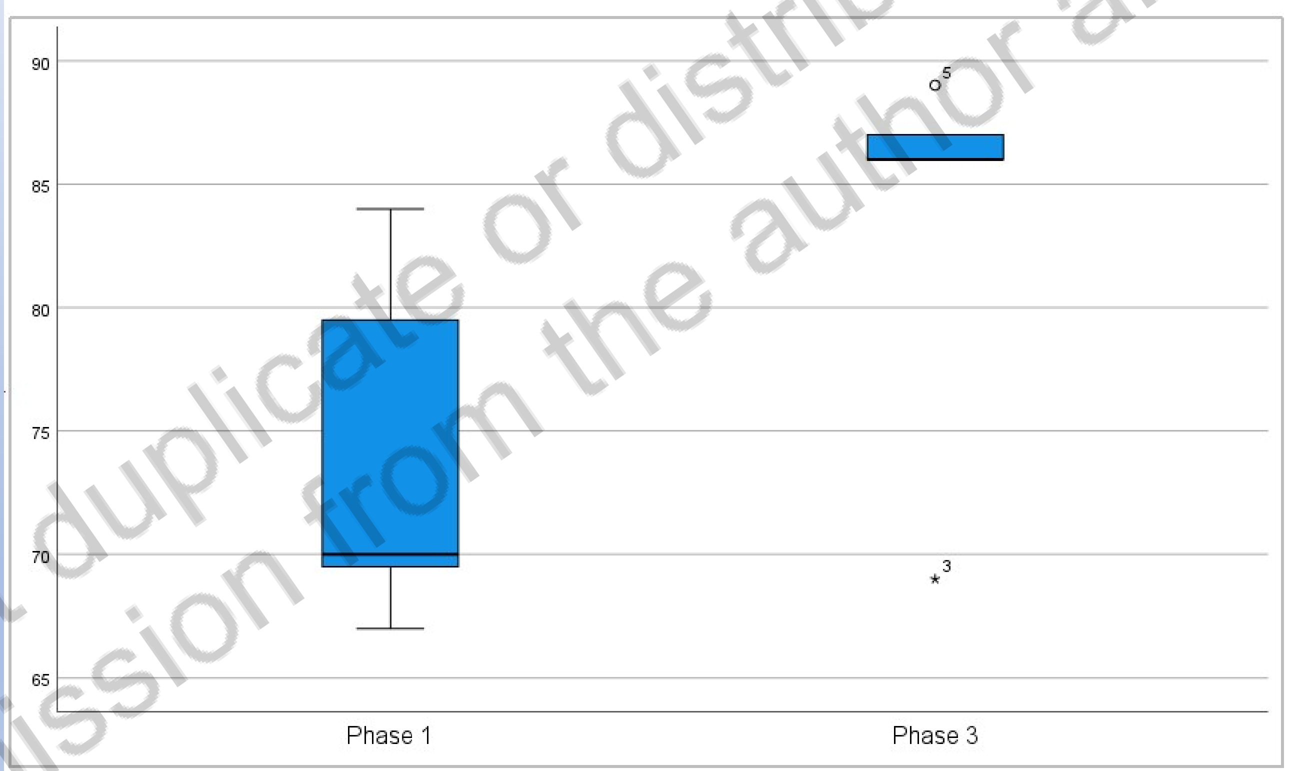
Test A
Phase 1 - 7,1%
Phase 3 - 3,4%

Test B
Phase 1 - 6,3%
Phase 2 - 6,5%

@PoloniaAntonio

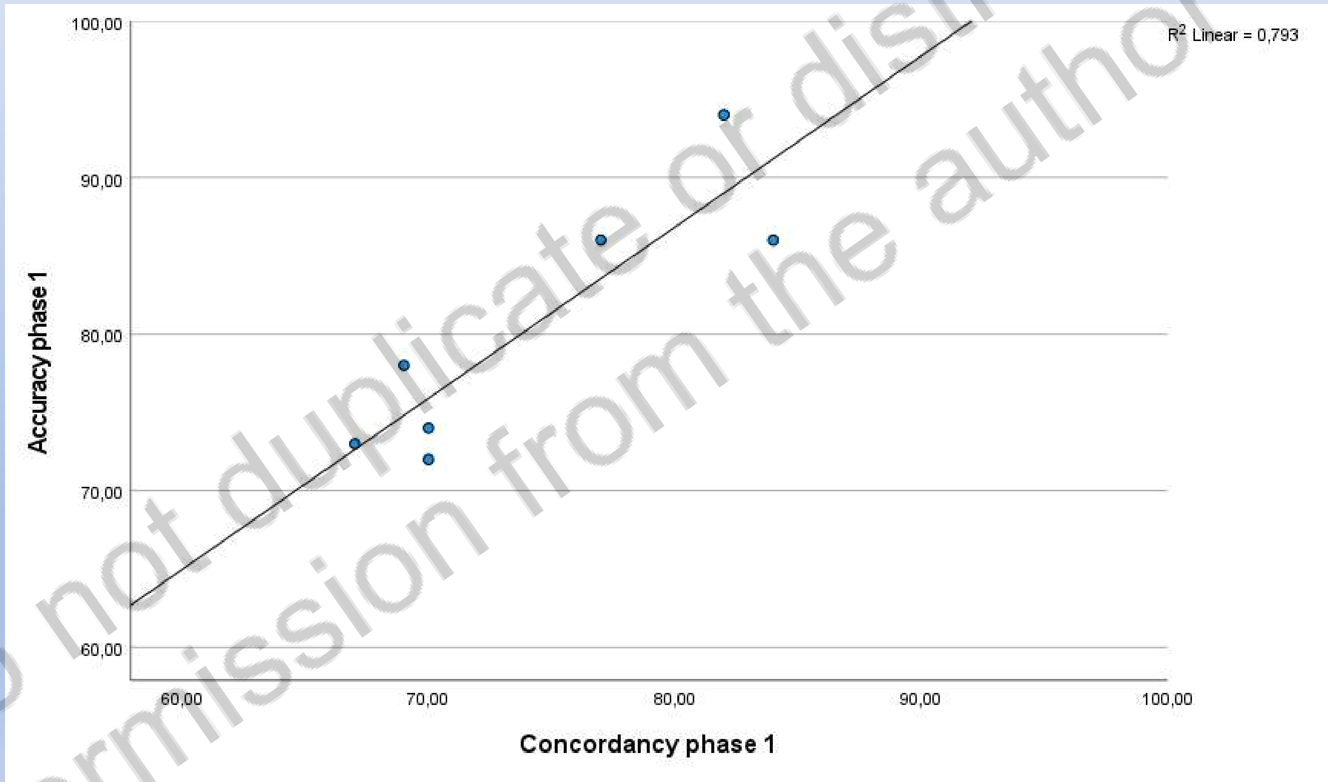
Breast cancer CAD tools

Concordance with AI
P=0.018 (Wilcoxon)

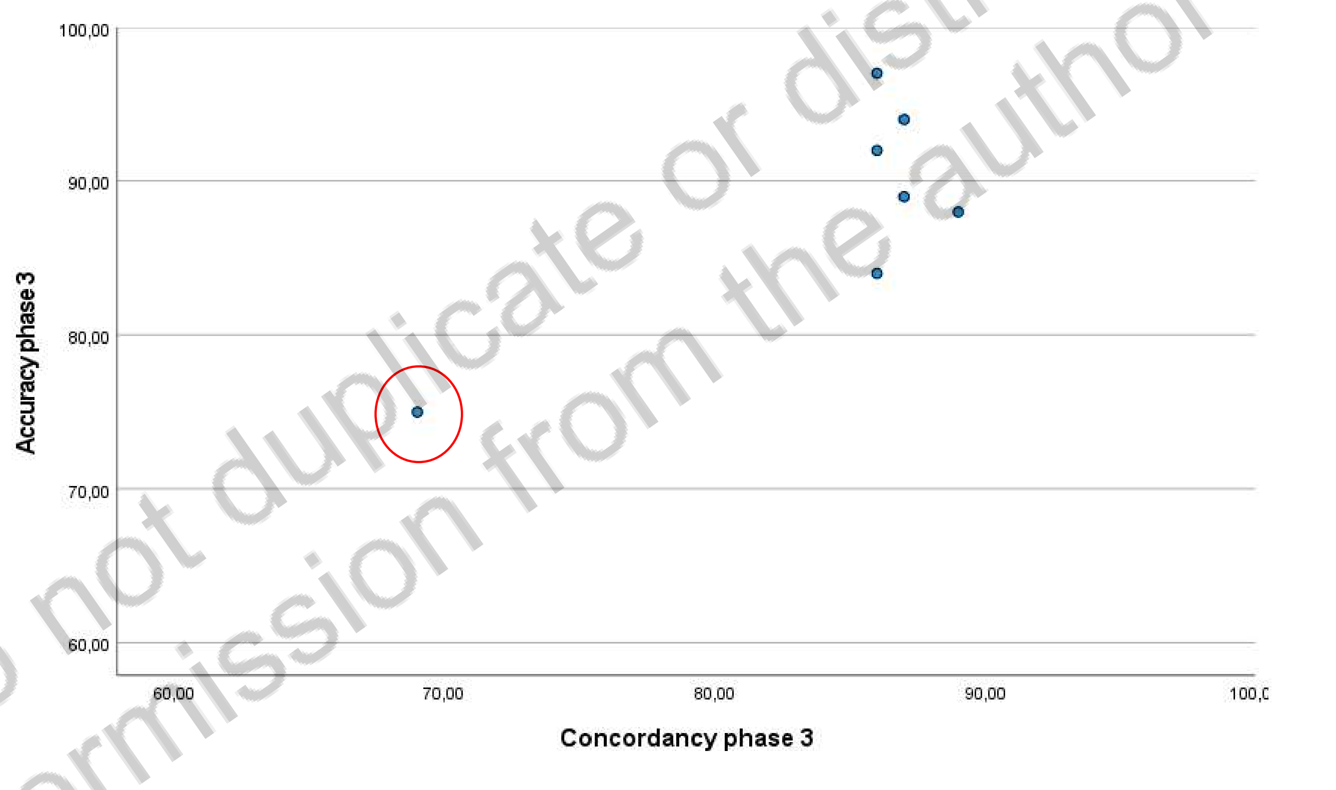


@PoloniaAntonio

Breast cancer CAD tools



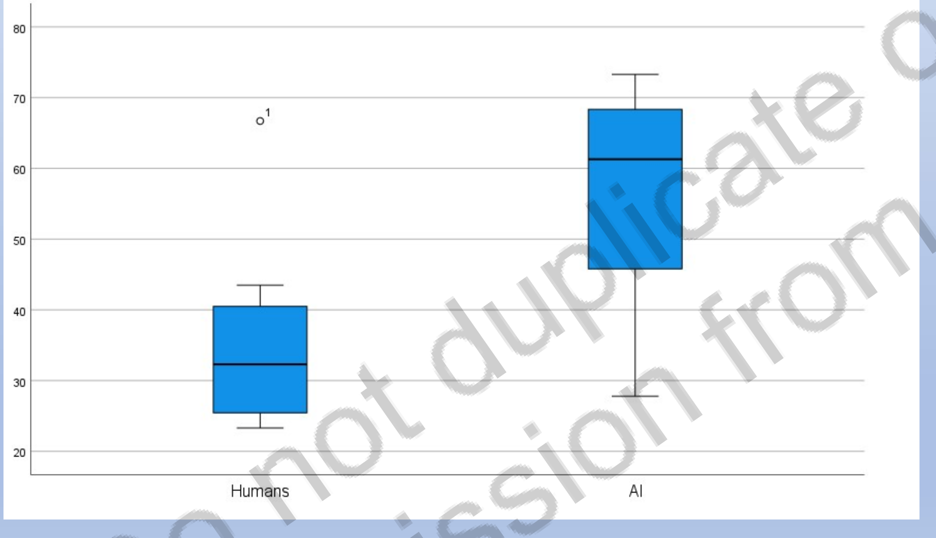
Breast cancer CAD tools

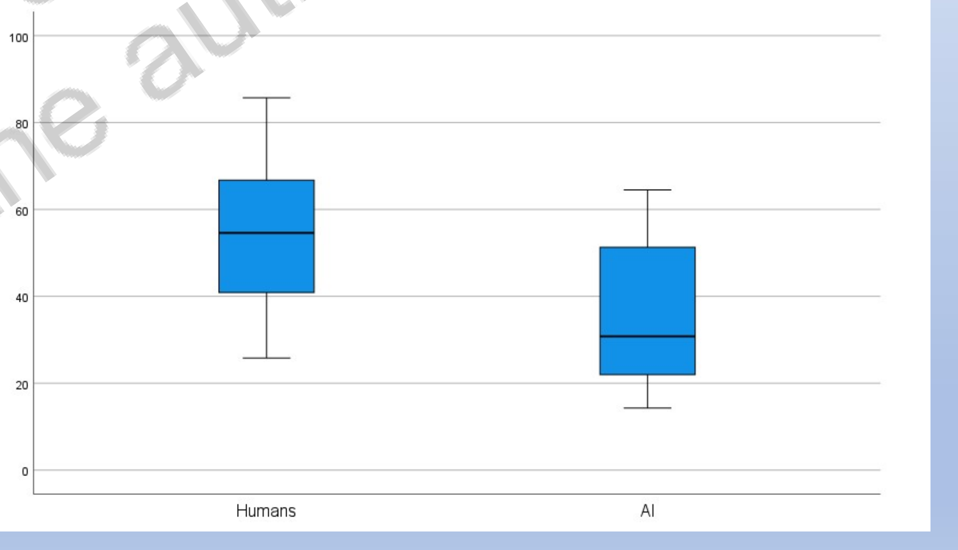


@PoloniaAntonio

Breast cancer CAD tools

Probability of being correct if discordant





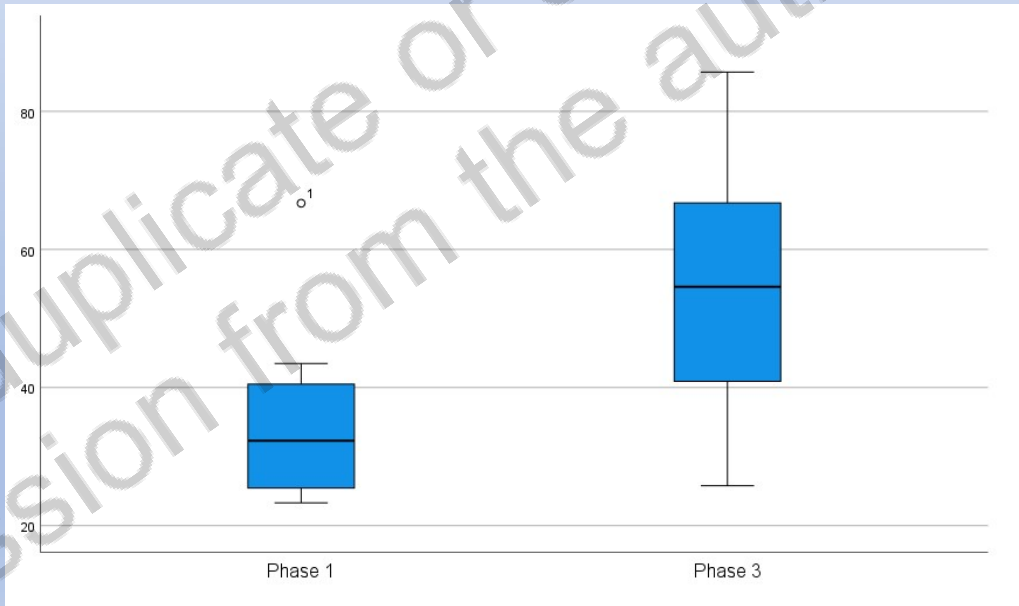
Phase 1
P=0.091 (Wilcoxon)

Phase 3
P=0.310 (Wilcoxon)

@PoloniaAntonio

Breast cancer CAD tools

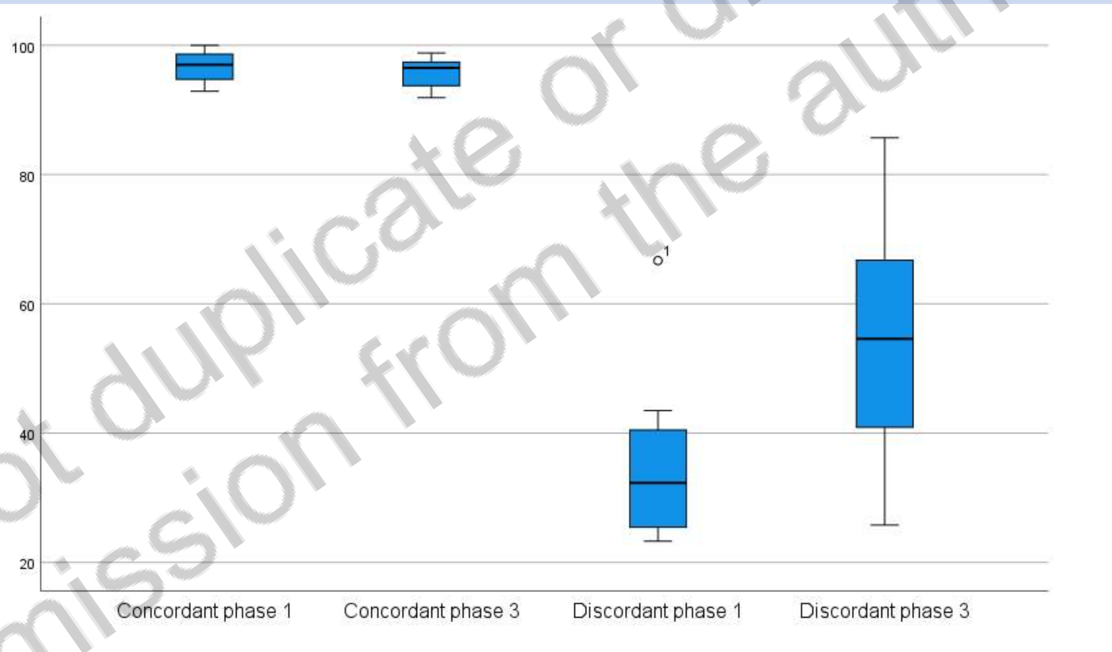
Probability of being correct if discordant (Experts)
P=0.018 (Wilcoxon)



@PoloniaAntonio

Breast cancer CAD tools

Probability of being correct (Experts)
P=0.018 (Wilcoxon)

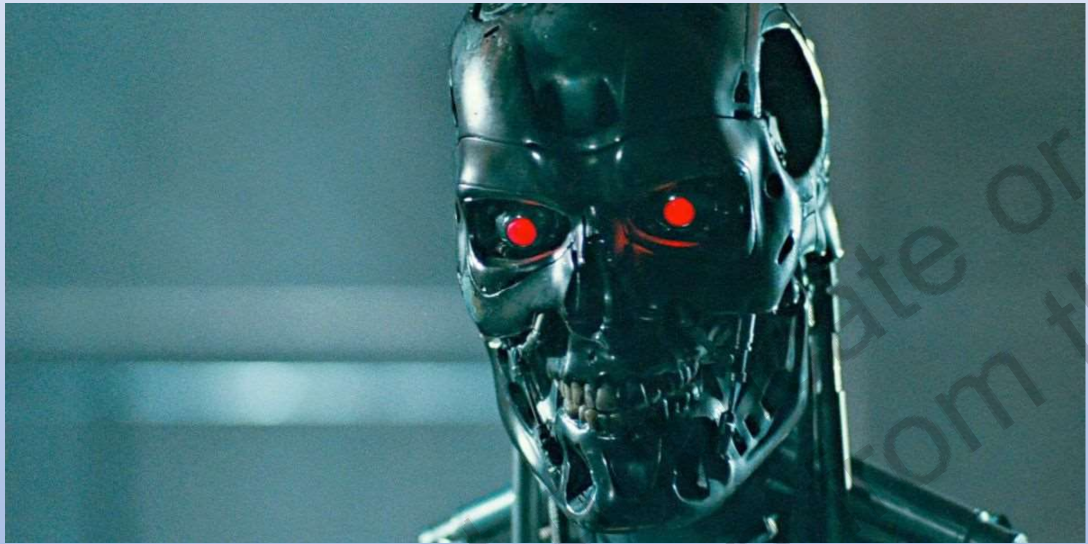


@PoloniaAntonio

25 ANOS
A DESCOBRIR O CANCRO
ipatimup

Breast cancer CAD tools

Will machines replace humans?



Breast cancer CAD tools

Machines need the Holy Grail!!!

The Holy Grail is the Ground Truth!

25 ANOS
A DESCOBRIR O CANCRO
ipatimup

Breast cancer CAD tools

It´s TIME to choose – red pill or blue pill!

Breast cancer CAD tools

ipatimup — 25 ANOS A DESCOBRIR O CANCRO

Maria Sklodowska-Curie Institute – Oncology Center, Gliwice Branch

INEB — Instituto de Engenharia Biomédica

Fundação Champalimaud

INESCTEC | C-BER Biomedical Engineering — BIOMEDICAL IMAGING LAB

Centro Hospitalar de Lisboa Ocidental, E.P.E.

ICIAR — U.PORTO — FEUP Faculdade de Engenharia Universidade do Porto

HOSPITAL DA LUZ LISBOA

@PoloniaAntonio