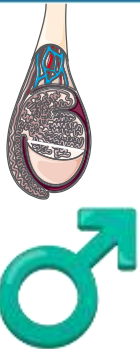


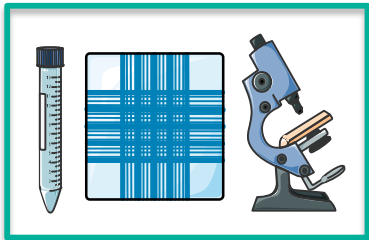


Intelligence Artificielle & Assistance Médicale à la Procréation

Dr. E. Saïs (M.D.)




Spermogramme



Paramètres spermatozoaires	Valeur normale
Nombre d'échantillons	3-7 jours
Volumen total	1.5 ml
Concentration spermatozoaire	15 millions/ml
Nombre par éjaculat	39 millions
Mobilité progressive des spermatozoaires	>32%
Mobilité totale des spermatozoaires	>40%
Vitalité	>10%
Pourcentage de formes normales	>4%
Créatine sérique	<27%
Classification de World Health Organization de la fertilité	1-2 million

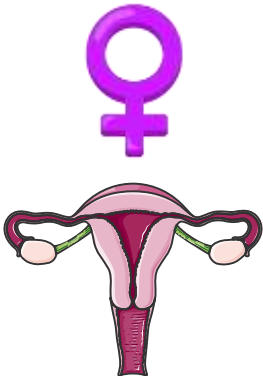
Consultation
Prélèvement chirurgical testiculaire
Bilan Génétique
Échographie testiculaire
BH

Consultation

STIMULATION OVARIENNE

Fécondation FIV/ICSI Zygote J1 J2 J3 J4 Blastocyte J5/6

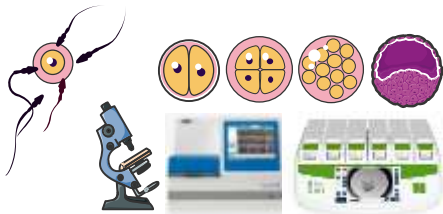
TEF
TEC

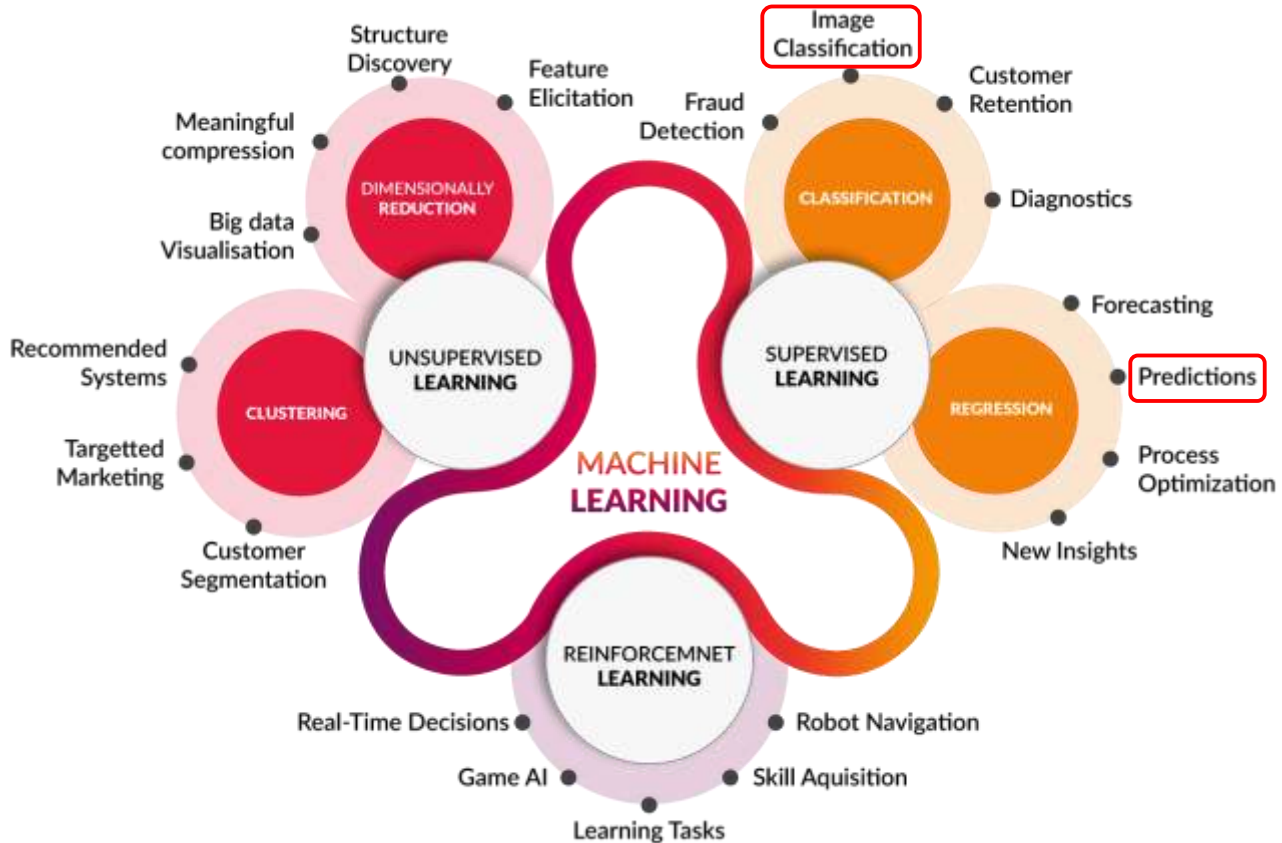


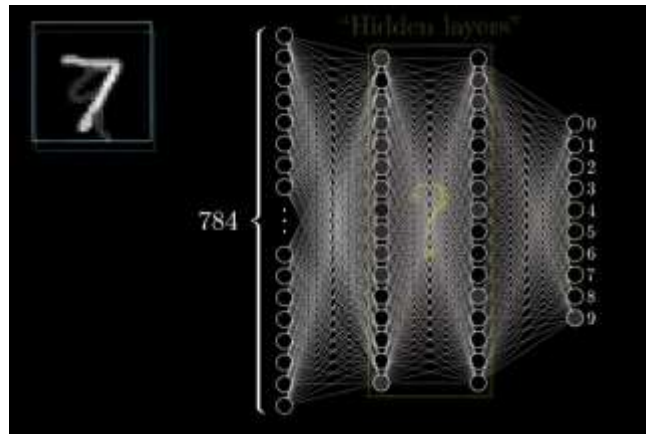
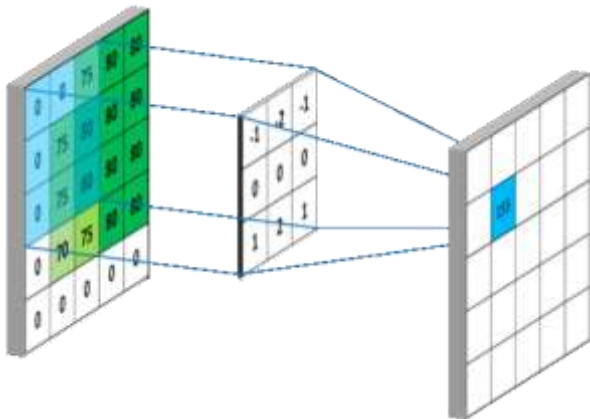
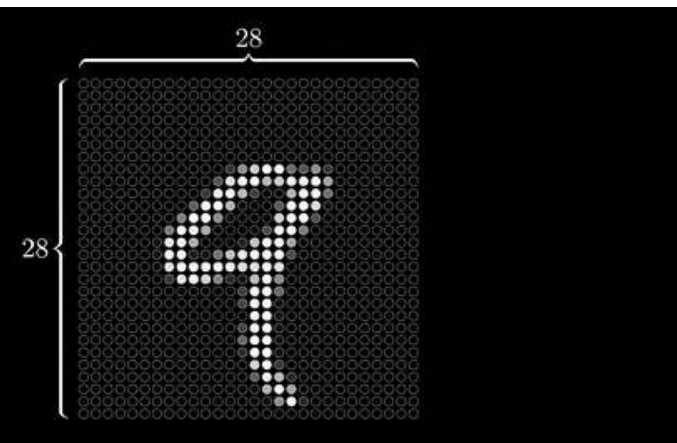
Echographie pelvienne (CFA)
BH (AMH, FSH, LH, E2, Pg)
Hystérosonographie (cavité utérine)
Hystérosalpingographie (trompes)

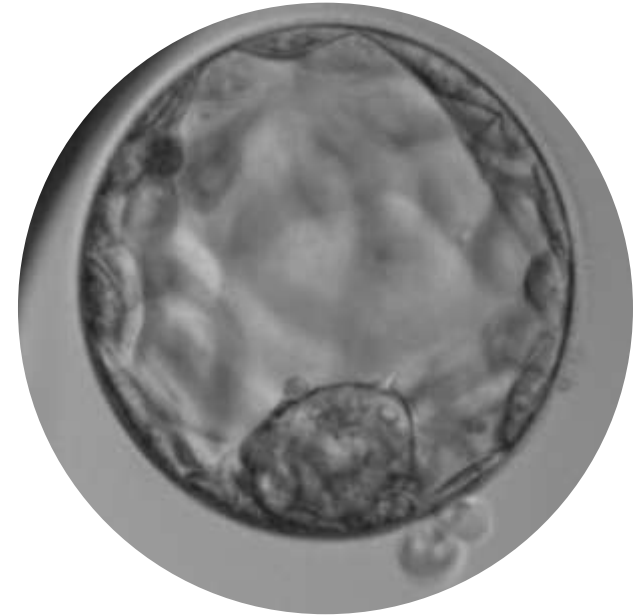
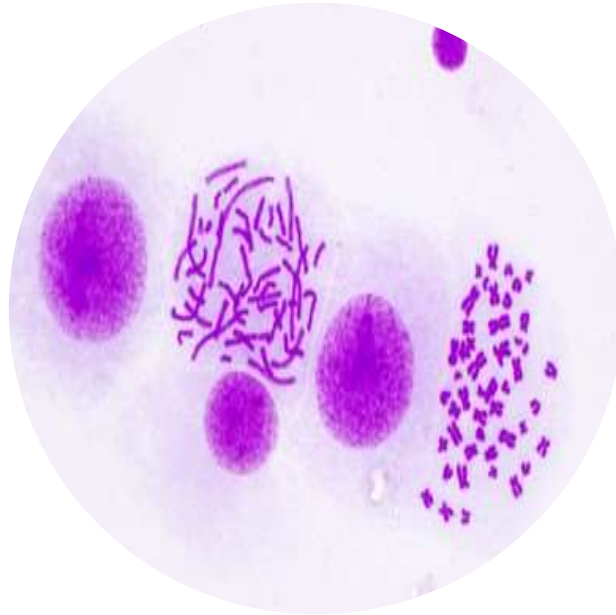
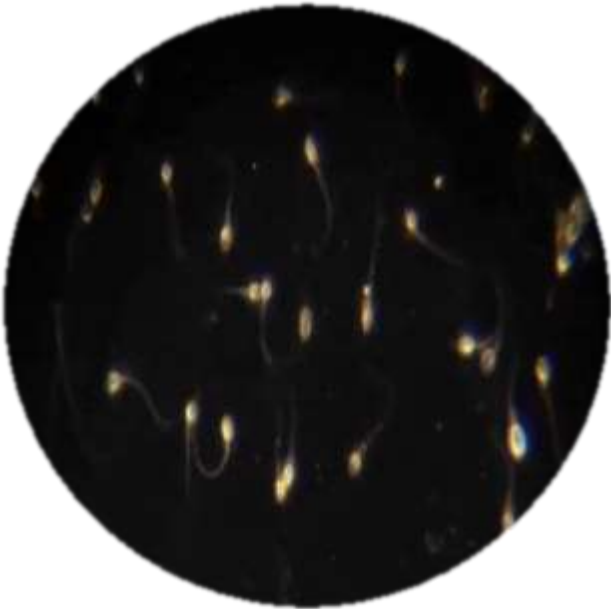


Biopsie d'endomètre
Bilan Génétique











NETFLIX

Who's watching?



Emine S.



H.



S.



Kids



Add Profile

Manage Profiles



NETFLIX

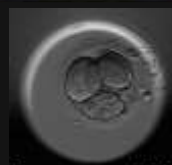
Home TV Shows Movies New & Popular My List Browse by Languages



Kids



Continue Watching for Emine



Trending Now



European Movies & TV





NETFLIX

Home TV Shows Movies New & Popular My List Browse by Languages



Kids



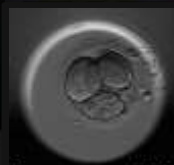
Continue Watching for Emine



TOP 10



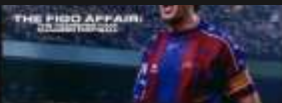
I like this



Trending Now

96% Match 16+ 8 Episodes HD

Violent - Dark - Action

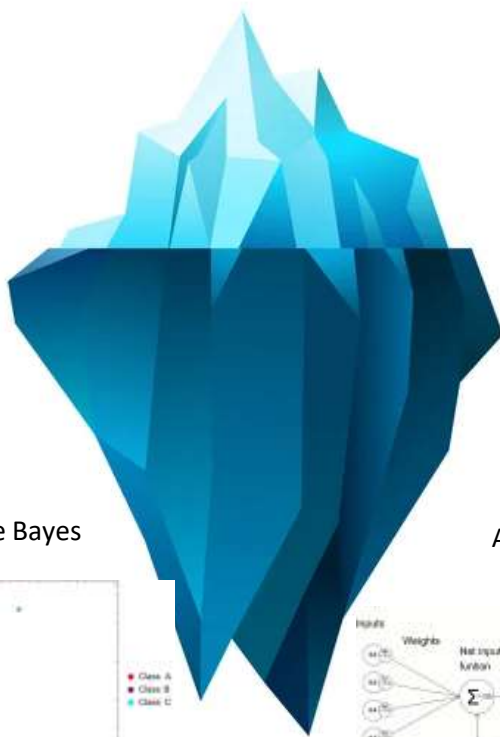


European Movies & TV

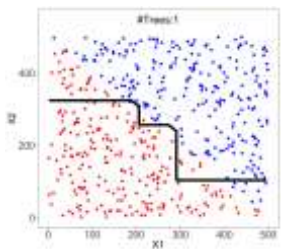




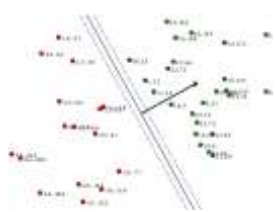




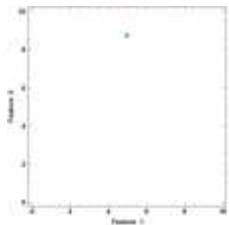
Random forest



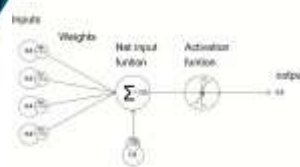
Support Vector Machine



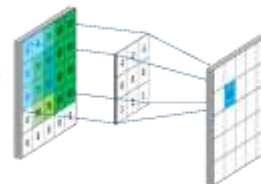
Naïve Bayes



ANN

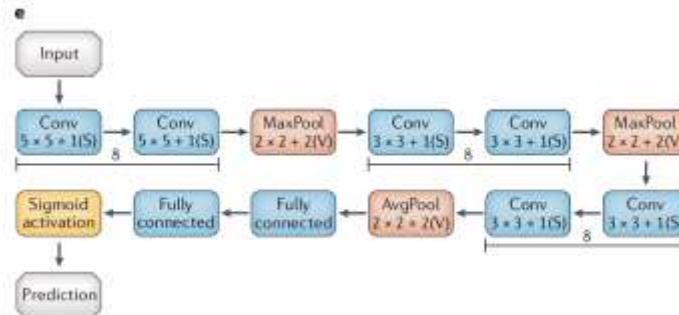
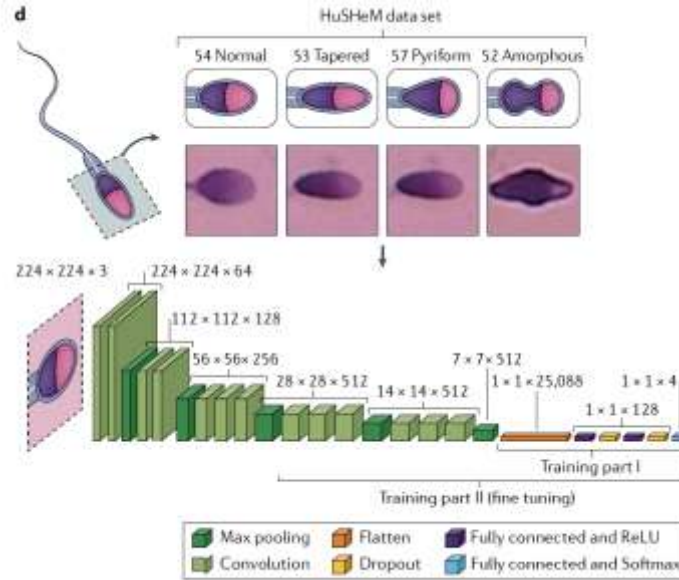
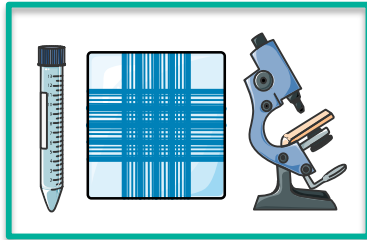


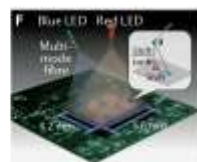
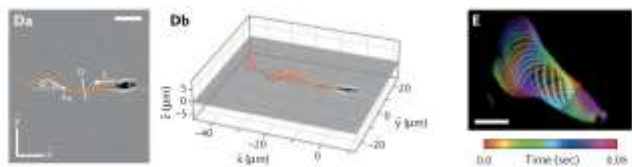
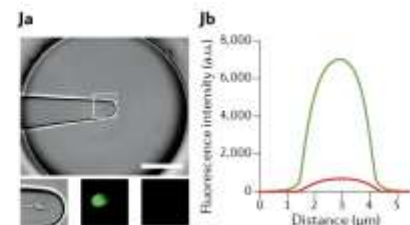
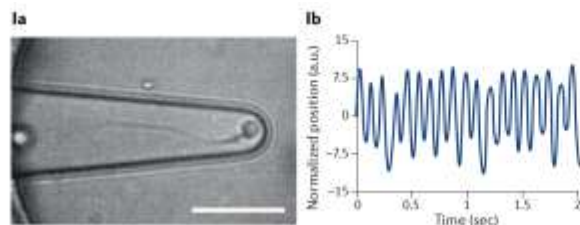
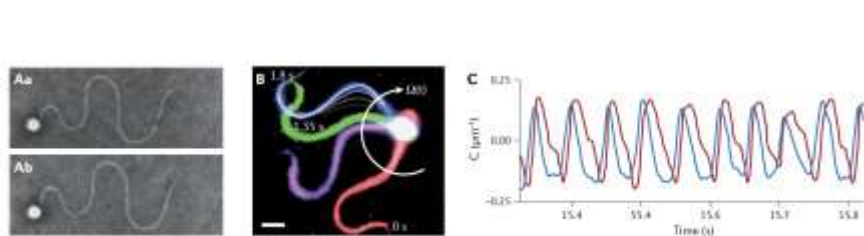
CNN



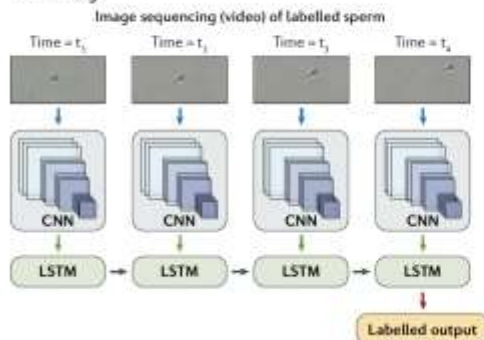
rNN



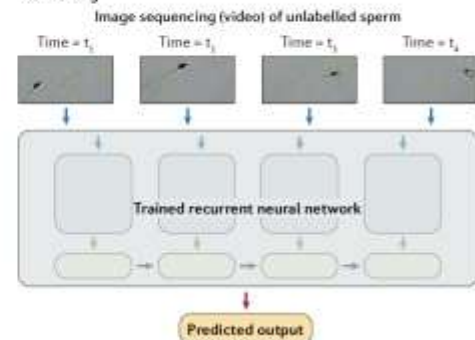


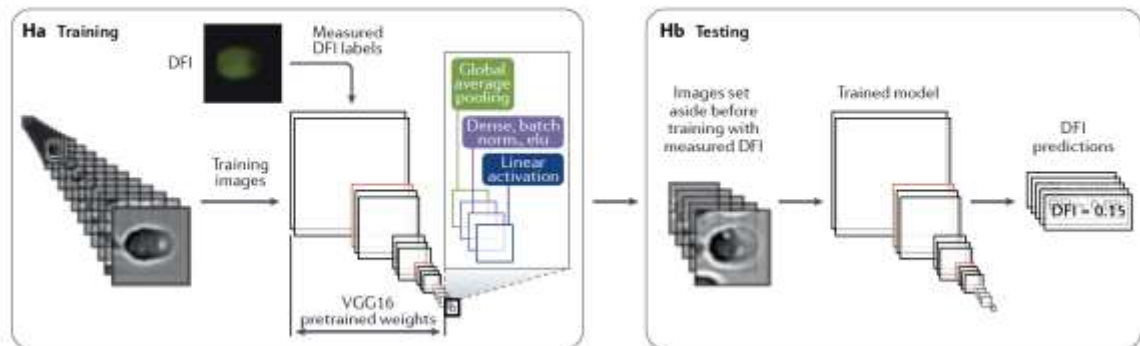
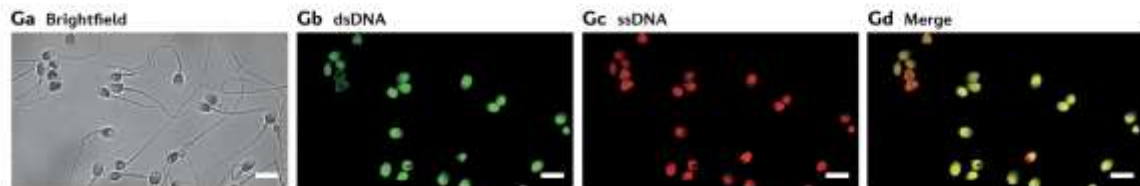
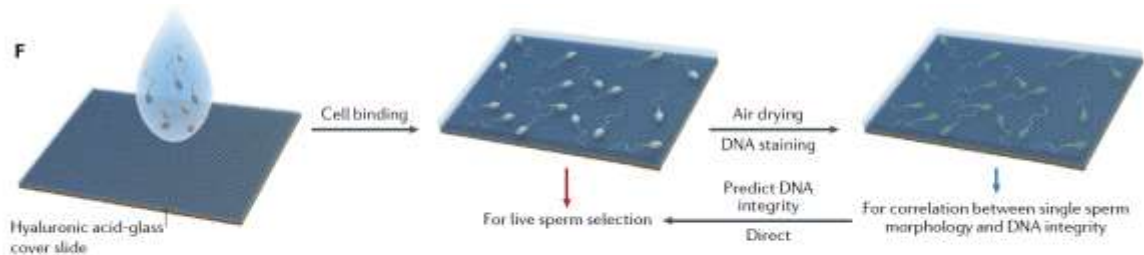


Ka Training



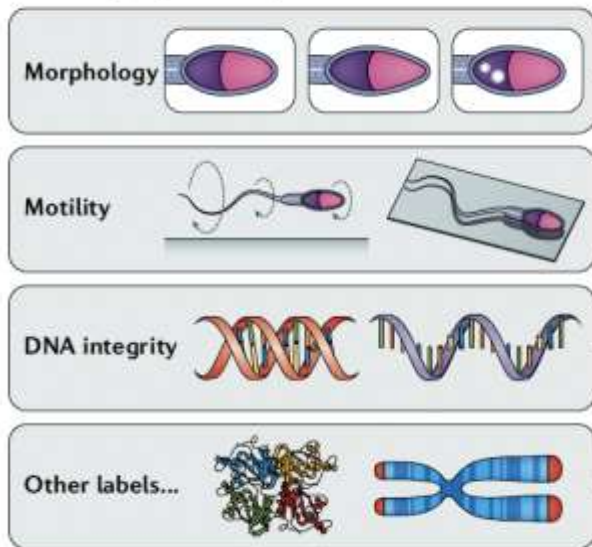
Kb Testing



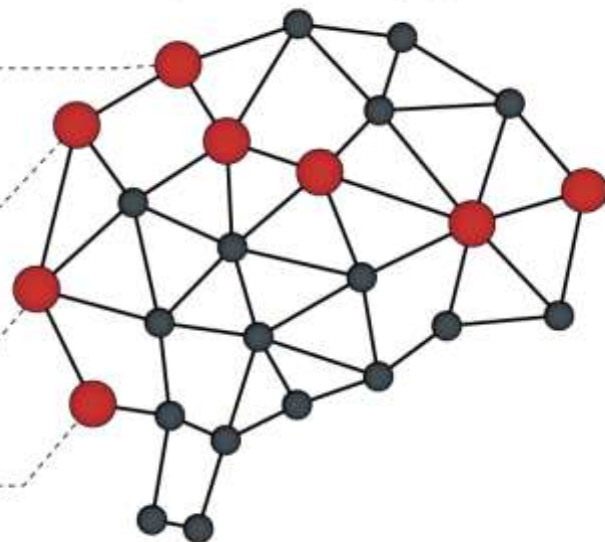




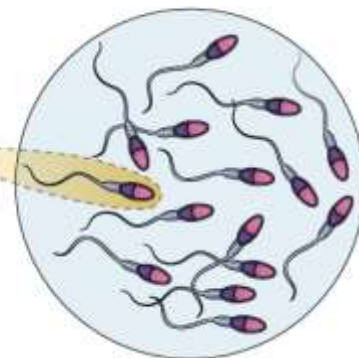
Single sperm analysis and data collection



Training of machine learning algorithm



Machine learning algorithm-based sperm selection





Sharma & al. 2017

Segmentation

IEEE TRANSACTIONS ON PATTERN ANALYSIS AND MACHINE INTELLIGENCE, VOL. 39, NO. 12, DECEMBER 2017

2481

SegNet: A Deep Convolutional Encoder-Decoder Architecture for Image Segmentation

Vijay Badrinarayanan, Alex Kendall¹, and Roberto Cipolla, Senior Member, IEEE

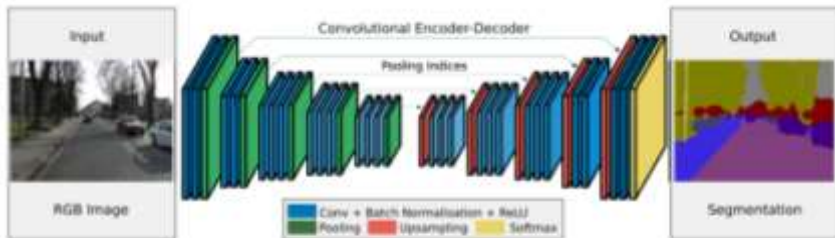


Fig. 2. An illustration of the SegNet architecture. There are no fully connected layers and hence it is only convolutional. A decoder upsamples its input using the transferred pool indices from its encoder to produce a sparse feature map(s). It then performs convolution with a trainable filter bank to densify the feature map. The final decoder output feature maps are fed to a soft-max classifier for pixel-wise classification.

Xie & al. 2019

Classification

Received September 23, 2018; accepted October 5, 2018; date of publication November 5, 2018; date of current version December 23, 2018.

Digital Object Identifier 10.1109/TPAMI.2018.2851292

Statistical Karyotype Analysis Using CNN and Geometric Optimization

NING XIE¹, XU LI², KANG LI¹, YANG YANG¹, AND HENG TAO SHEN¹

¹Center for Future Media, School of Computer Science and Engineering, University of Electronic Science and Technology of China, Chengdu 611731, China

²Shengze College, University of Electronic Science and Technology of China, Chengdu 611731, China

Corresponding author: Ning Xie (xianing@ipmail.com)

SegNet 2015 -> Segmentation -> Classification

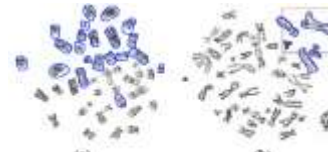
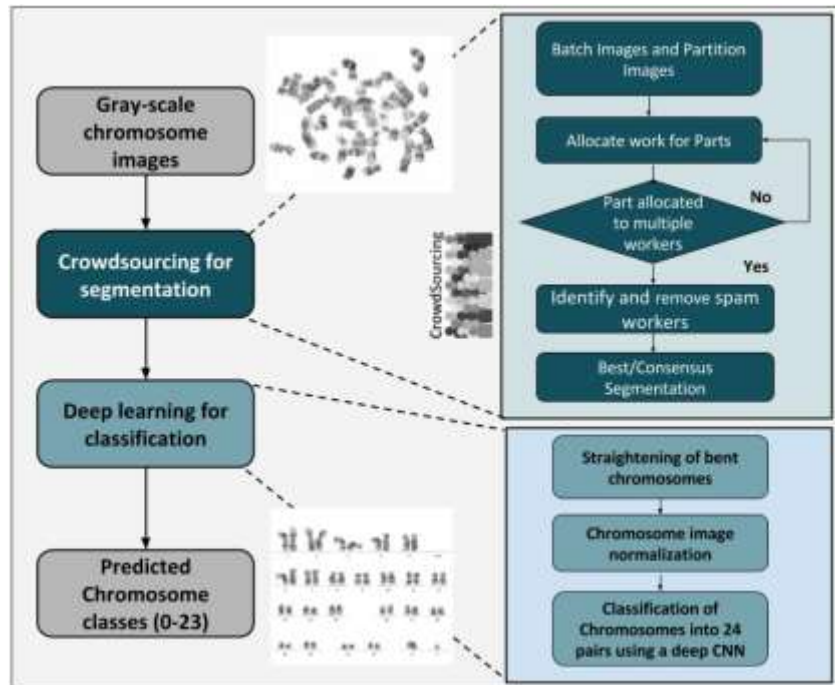


Figure 3. Examples of crowd marking in Phase 1 and Phase 2.

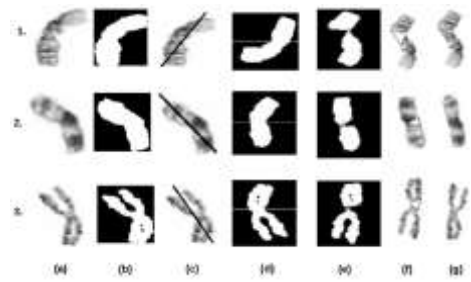
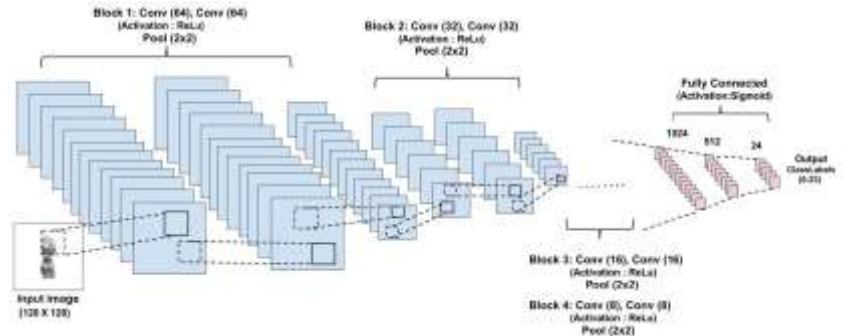


Figure 4. Examples of erroneous crowd responses.



Segmentation manuelle "crowdsourcing" mais classification automatique

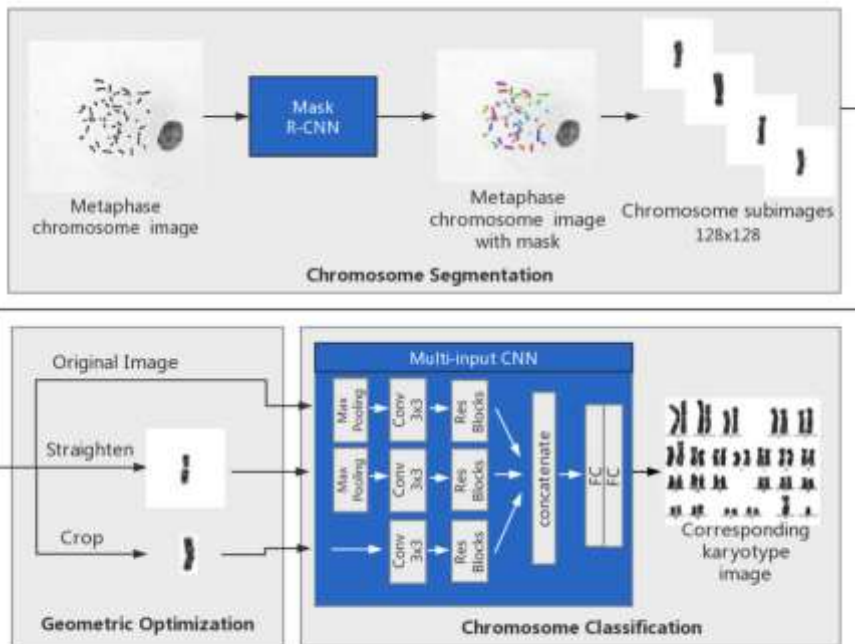
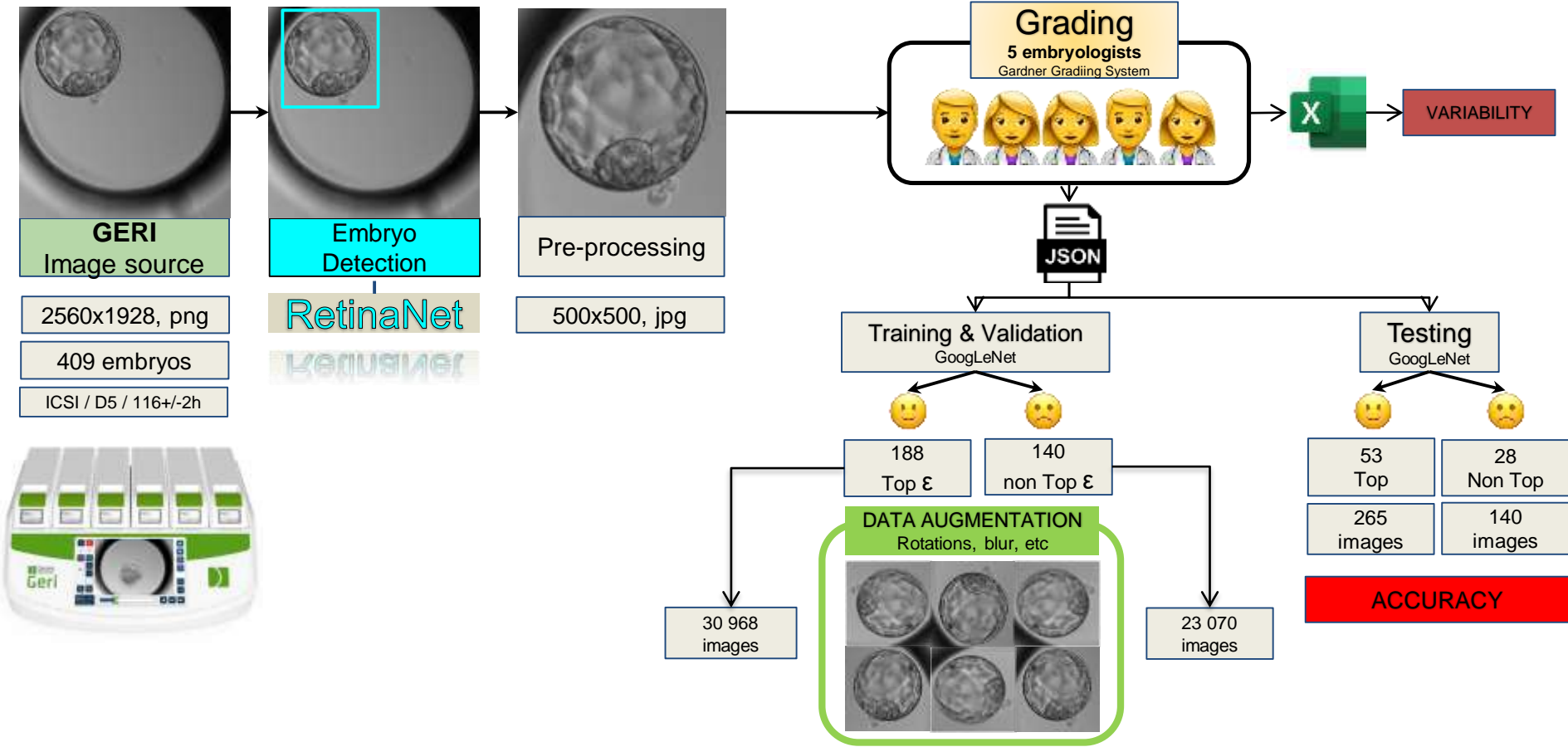


FIGURE 1. The pipeline of our system, includes: 1) Chromosome Segmentation 2) Geometric Optimization and 3) Chromosomes Classification.

Method	Accuracy
AlexNet [27]	0.8975
VGG-16 [28]	0.9023
ResNet-50 [29]	0.9445
DenseNet [30]	0.9414
Sharma <i>et al.</i> [1]	0.8670
Jindal <i>et al.</i> [22]	0.8460
Global-only	0.9445
Local-only	0.9220
Straighten-only	0.8200
Global & Local mCNN_GO (Ours)	0.9570

Segmentation & Classification automatiques



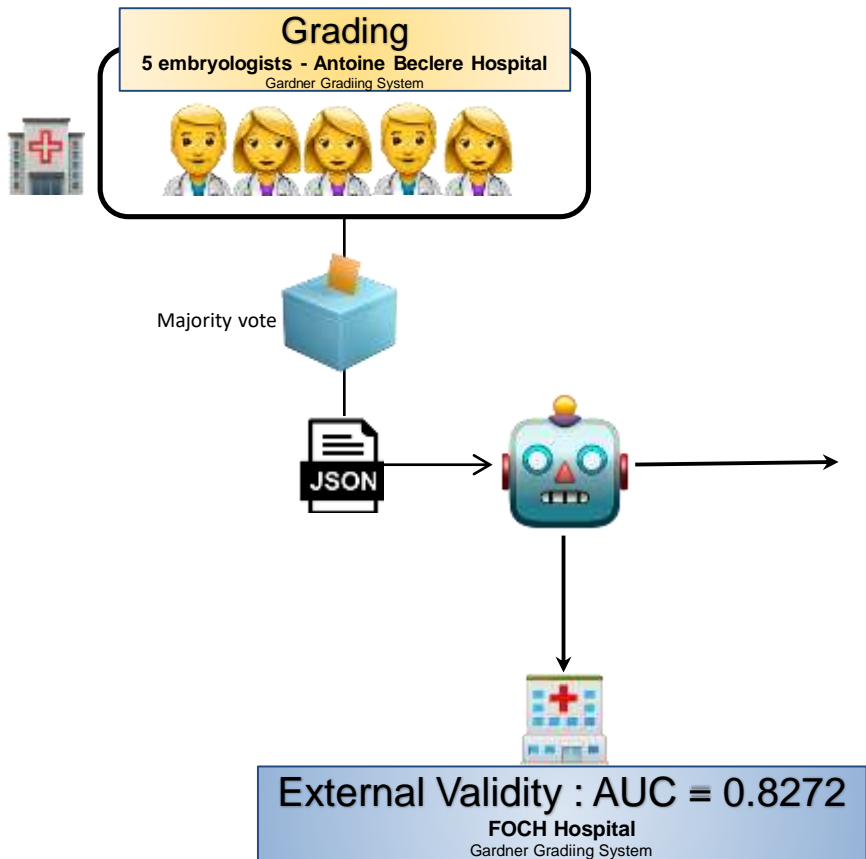
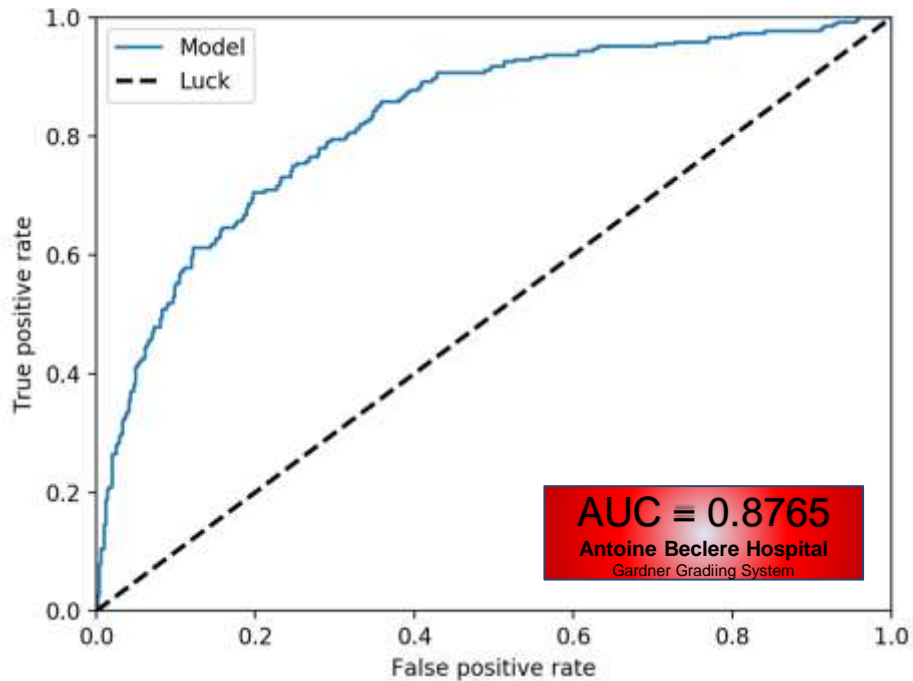


Figure – Accuracy (Top vs Non Top).



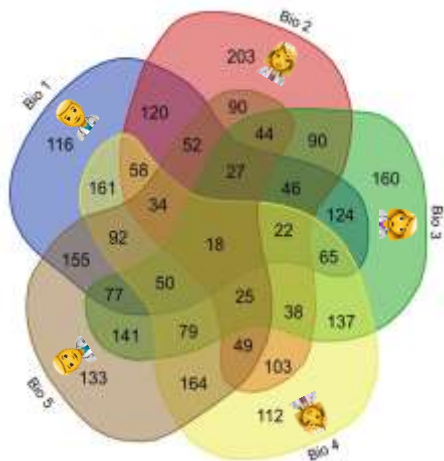
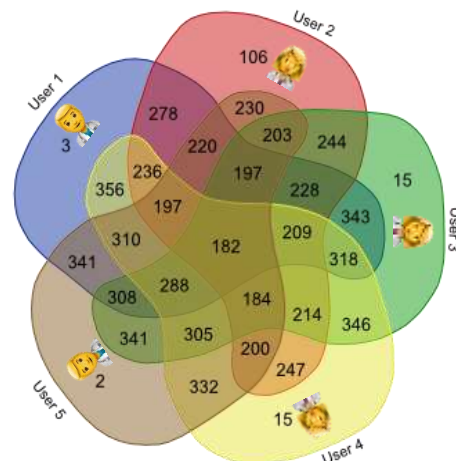


Figure – Venn Diagram (Gardner EXP+ICM+TE).

Figure - Venn Diagram (Top vs Non Top)



	Bio 1	Bio 2	Bio 3	Bio 4	Bio 5
Bio 1		0,29	0,31	0,38	0,38
Bio 2	0,29		0,22	0,25	0,21
Bio 3	0,31	0,22		0,35	0,35
Bio 4	0,38	0,25	0,35		0,39
Bio 5	0,38	0,21	0,35	0,39	

Table – Inter-Observer variability (Gardner EXP+ICM+TE).

Kappa	Interpretation
< 0	Disagreement
0.0 – 0.20	Poor
0.21 – 0.40	Fair
0.41 – 0.60	Moderate
0.61 – 0.80	Good
0.81 – 1.00	Very good

	Bio 1	Bio 2	Bio 3	Bio 4	Bio 5
Bio 1		0,34	0,72	0,77	0,69
Bio 2	0,34		0,33	0,36	0,42
Bio 3	0,72	0,33		0,75	0,70
Bio 4	0,77	0,36	0,74		0,72
Bio 5	0,69	0,42	0,70	0,72	

Table – Inter-Observer variability (Top vs Non Top).

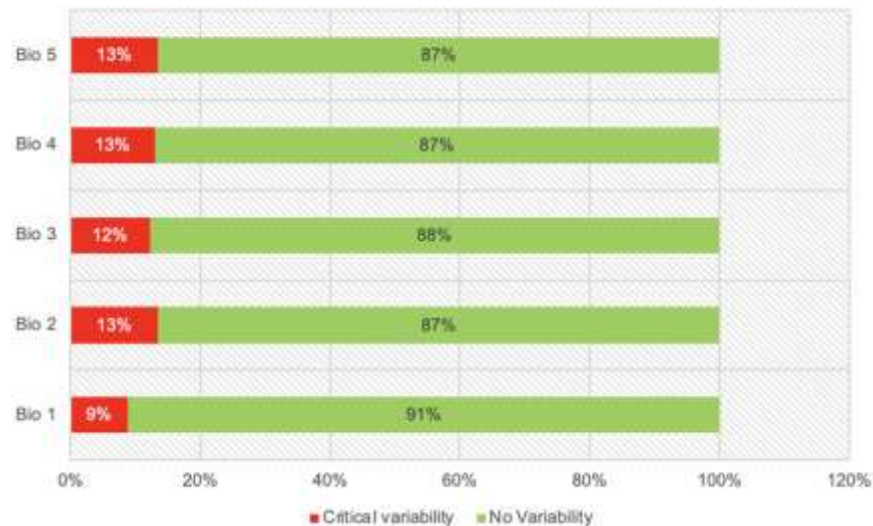


Table : Intra-observer variability

Intra Observer	Bio1	Bio2	Bio3	Bio4	Bio5
Top vs NonTop	0.74	0.74	0.82	0.73	0.70
EXP	0.41	0.76	0.39	0.47	0.37
ICM	0.67	0.75	0.82	0.68	0.74
TE	0.84	0.68	0.84	0.74	0.73
Gardner	0.49	0.50	0.61	0.41	0.45

Kappa	Interpretation
< 0	Disagreement
0.0 – 0.20	Poor
0.21 – 0.40	Fair
0.41 – 0.60	Moderate
0.61 – 0.80	Good
0.81 – 1.00	Very good

Intra-observer Variability : Top vs Non Top





ARTICLE OPEN

Deep learning enables robust assessment and selection of human blastocysts after in vitro fertilization

Pegah Khosravi^{1,2}, Ehsan Kazemi³, Qiansheng Zhan⁴, Jonas E. Malmsten⁵, Marco Toschi⁴, Pantelis Zisimopoulos^{1,2}, Alexandros Sigaras^{1,2}, Stuart Lavery², Lee A. D. Cooper⁶, Cristina Hickman⁵, Marcos Meseguer⁷, Zev Rosenwaks⁴, Olivier Elemento^{1,2,8}, Nikica Zaninovic⁴ and Iman Hajmohammadi^{1,2,9}



human reproduction

ORIGINAL ARTICLE Embryology

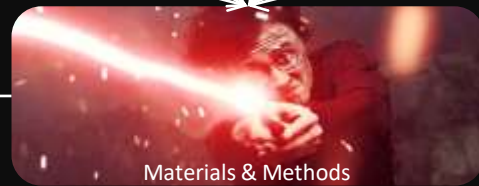
Deep learning as a predictive tool for fetal heart pregnancy following time-lapse incubation and blastocyst transfer

D. Tran^{1,2}, S. Cooke¹, P.J. Illingworth¹, and D.K. Gardner¹

¹Medical AI, Hannon AI, Baragwanath, NSW, Australia; ²Embryology IVF Australia, Goswami, NSW, Australia; ³Embryology Melbourne IVF, East Melbourne, Victoria, Australia



ARTICLE



Results

Conclusion

Améliorer & Automatiser

« Ranking » des embryons

Identification spz

Compter les follicules

Prediction &

Classification

Qualité Spz

Implantation

Grossesse

Naissance vivante

Médecine Personnalisée

Echantillon faible

Transparence faible

Performance variable

Validation externe ?

RCT ?

Grossesse clinique ?

Boite noire !!!



Q183 Reducing inter-observer and intra-observer variability of embryo quality assessment using deep learning
E. Saini¹, A. Meyer¹, O. Binali¹, L. Hassan¹, V. Fay¹, C. Fassarol¹, M. Fiala¹, J. Vandana¹, M. Foukari¹, M. Frydman¹

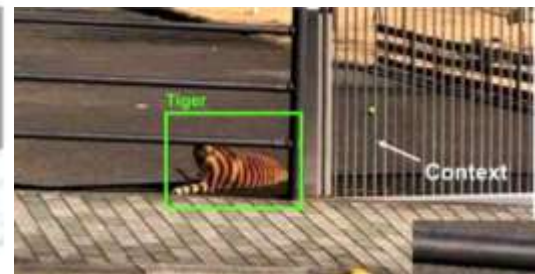
¹Aix Marseille Hospital, Reproductive Biology - Fertility Preservation - CECOC, Campus, France
²York Hospital, Department of Obstetrics and Gynaecology, Surrey, France
Contact: emmanuel.saini@apm.univ-marseille.fr



(a) Husky classified as wolf



(b) Explanation

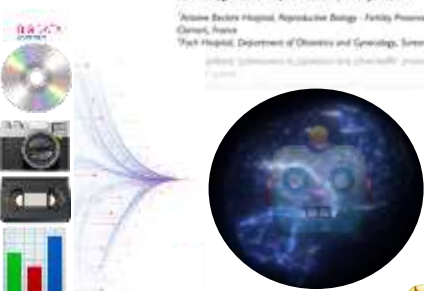


Predictive models of pregnancy based on data from a preconception cohort study

Jennifer J. Yland^{1,2,3}, Taiyao Wang^{1,2,3}, Zahra Zad^{1,4,5}, Sydney K. Willis¹, Tauran R. Wang¹, Amelia K. Wesselink¹, Tammy Jiang¹, Elizabeth E. Hatch¹, Lauren A. Wise^{1,2}, and Joannis Ch. Paschalidis^{1,4,5,2}

Logistic regression

Model	Algorithm	AUC	Weighted F1 score
Logistic regression	L2LR	70.2 (1.6)	61.8 (1.0)
	L1LR	69.8 (1.8)	61.6 (1.0)
Other machine learning	L1SVM	69.8 (1.8)	61.8 (1.0)
	L2SVM	70.0 (1.6)	61.5 (1.1)
	MLP	69.9 (1.8)	62.1 (1.0)
	LightGBM	68.1 (1.4)	61.6 (1.0)



Informations « lives »

Médecine « Personnalisée »

Prédiction grossesse





Dr A. Chargui



Dr H. Assami

**BIOMED-J
2023**