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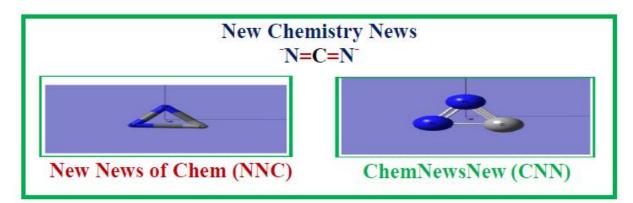
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2023, 12 (4): 553-596 (International Peer Reviewed Journal)





CNN-55--Fit (Figure Image TableScript...) Bases (Bfit) Part 3.xAI. Architectures . Medicine – Part-2

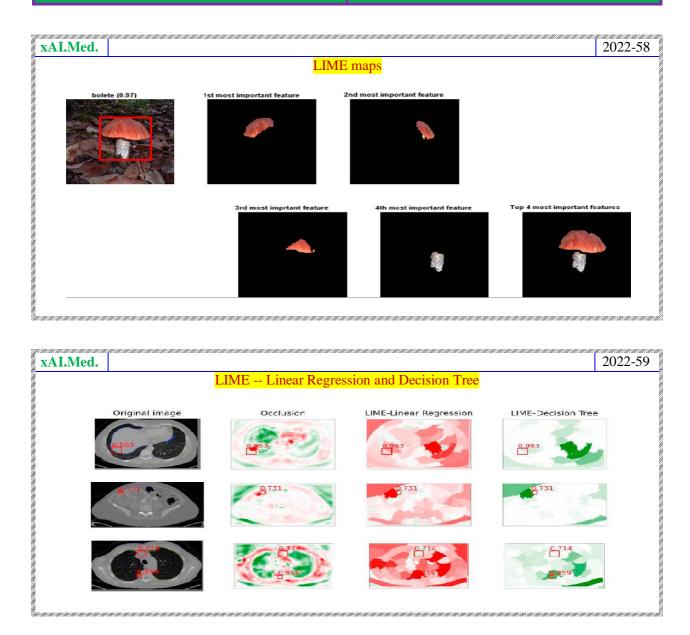
Information Source	sciencedirect.com;						
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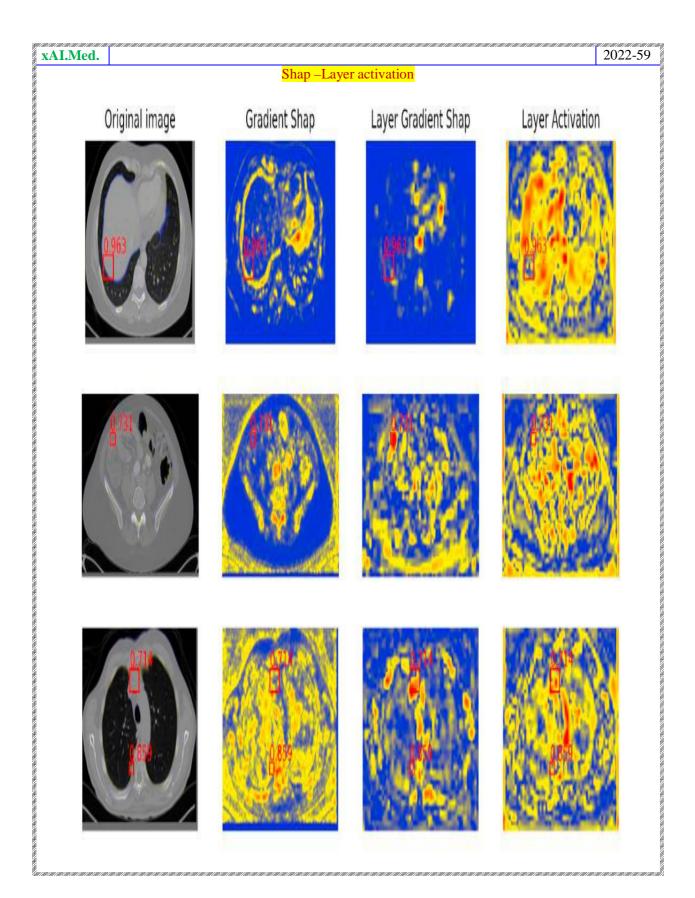
Conspectus: The evolution of scientific Artificial Intelligence (AI) (save consciousness) implementable on computers since mid-nineteen fifties and emergence of eXplainable AI (xAI) during last one decade is briefly described. The extensive application in most of critical research disciplines brought this approach to the fore-front-of state-of-knowledge projects including medicine, defence, industry, commerce etc. The recent trend setting xAI-probes resulted in laying confidence in AI-embedded methods/products/materials. The value and acceptability increased probing more into trust-worthy and

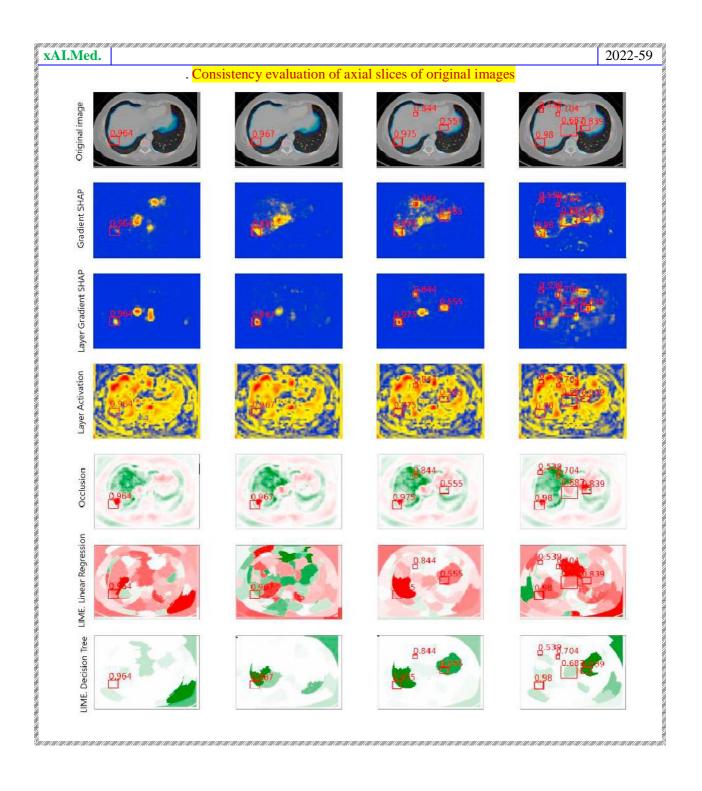
responsible AI to comply with stake-holder's expectations. This indispensable upward trend of more and more AI-integrated technologies is in harmony with safety and security oflife forms and environment. Here, some typical case studies shedding light on benefits of xAI methods in Medical diagnosis and health care are incorporated.

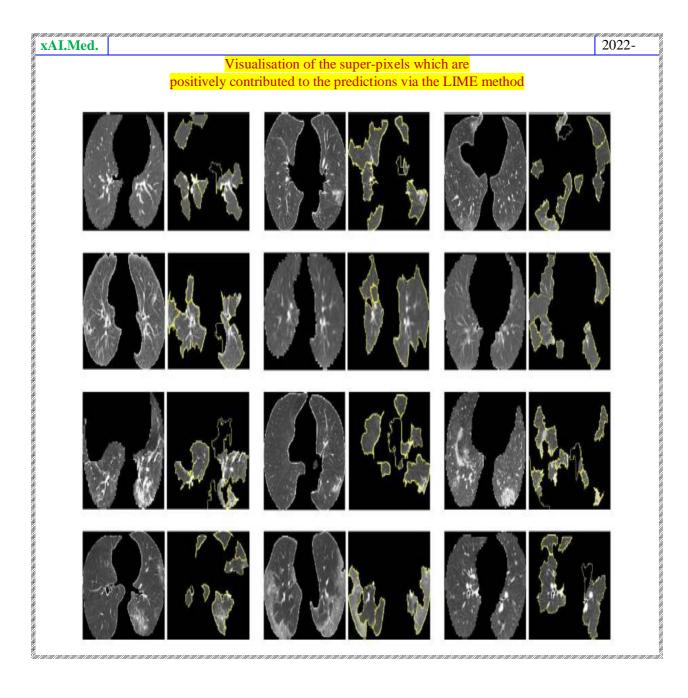
Keywords:AI; evolution (1950-to-2023-Future); eXplainable AI (xAI); interpretable/ Responsible/ Trustworthy AI; DARPA and NSF targets; Industry (Health, Defence, research requirements)-Deep architectures; CNN; Capsule Nets; ALEX; TRANSFORMERS; Machine Learning; Deep Learning— Supervised/unsupervised/Self-supervised data; Figures; Images, Tables, Scripts, Numerical values;

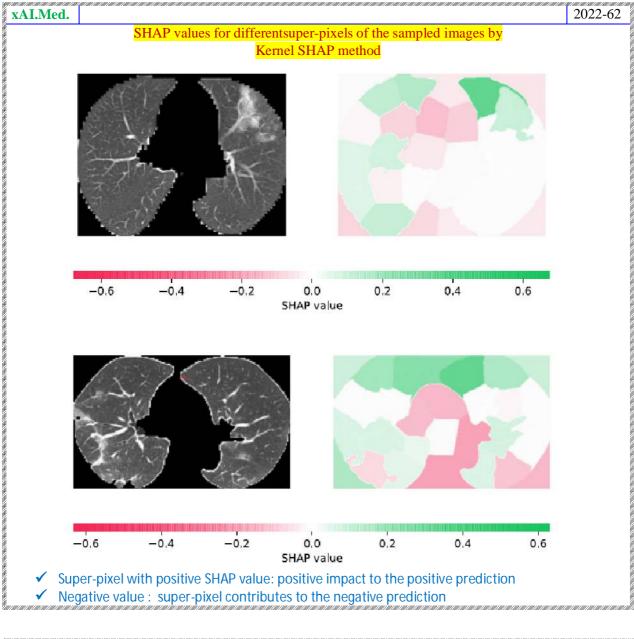
LIME plot



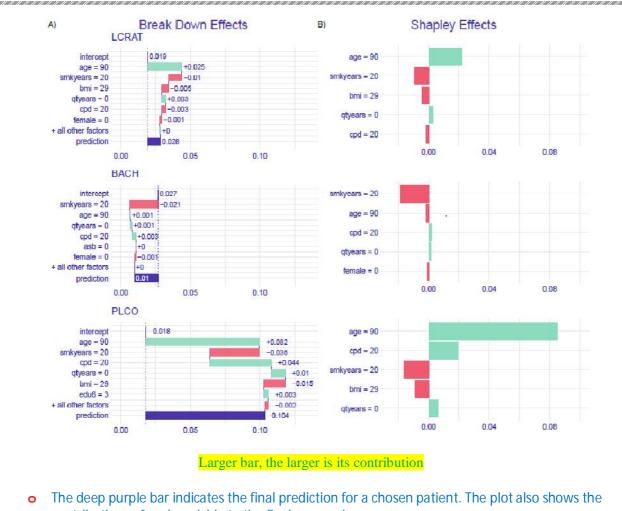




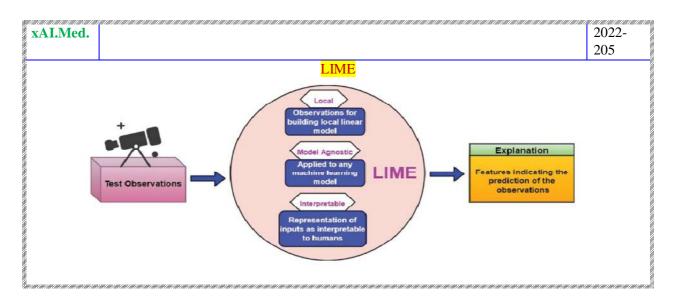


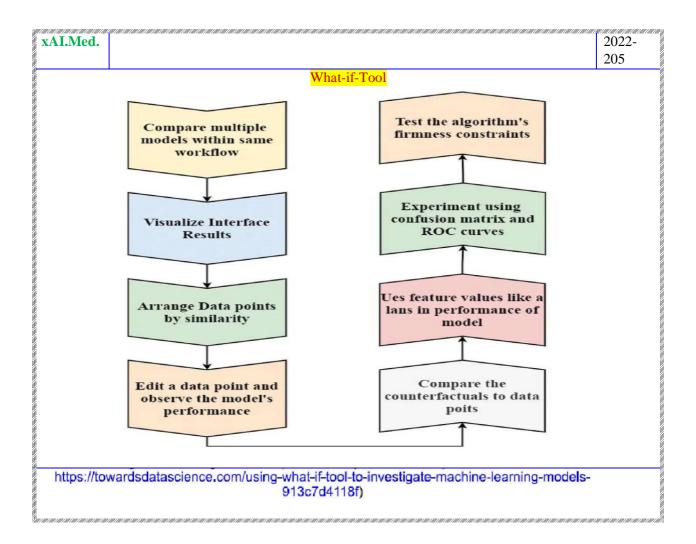


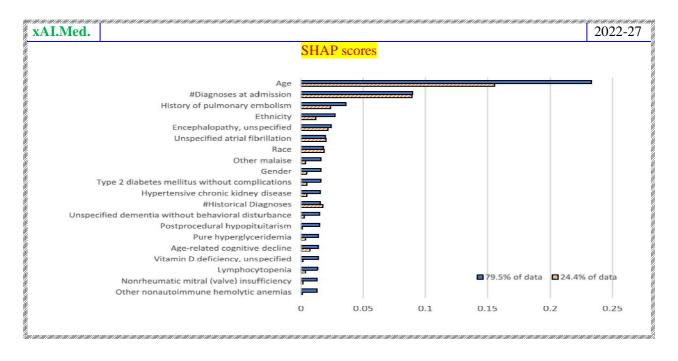
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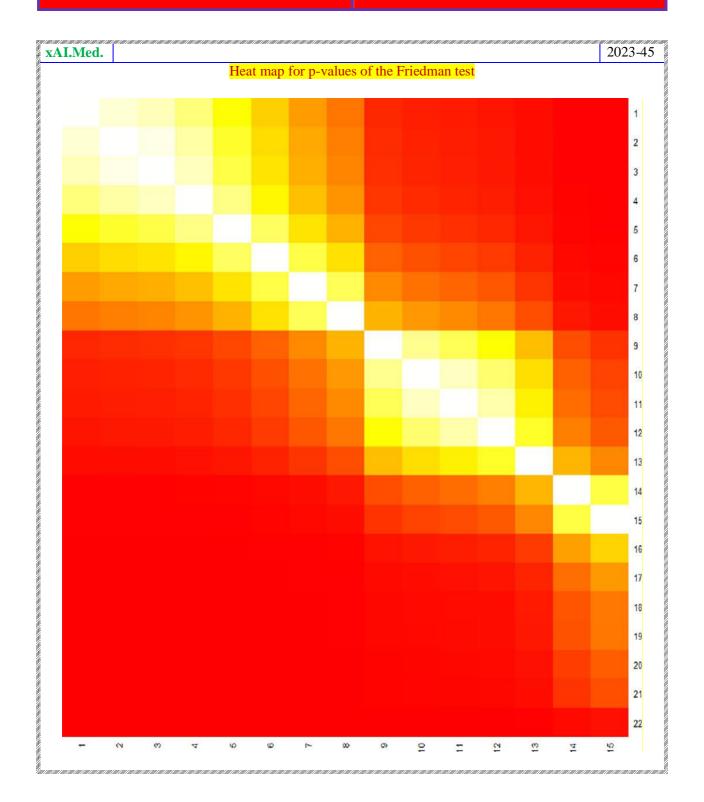
- contributions of each variable to the final prognosis.
 Green bars indicate positive contributions, meaning that the value of a certain variable implies an
- Green bars indicate positive contributions, meaning that the value of a certain variable implies an increase in prediction
- Red bars suggest a negative contribution
- ✓ Shapley values indicate positive and negative contributions to the final prediction

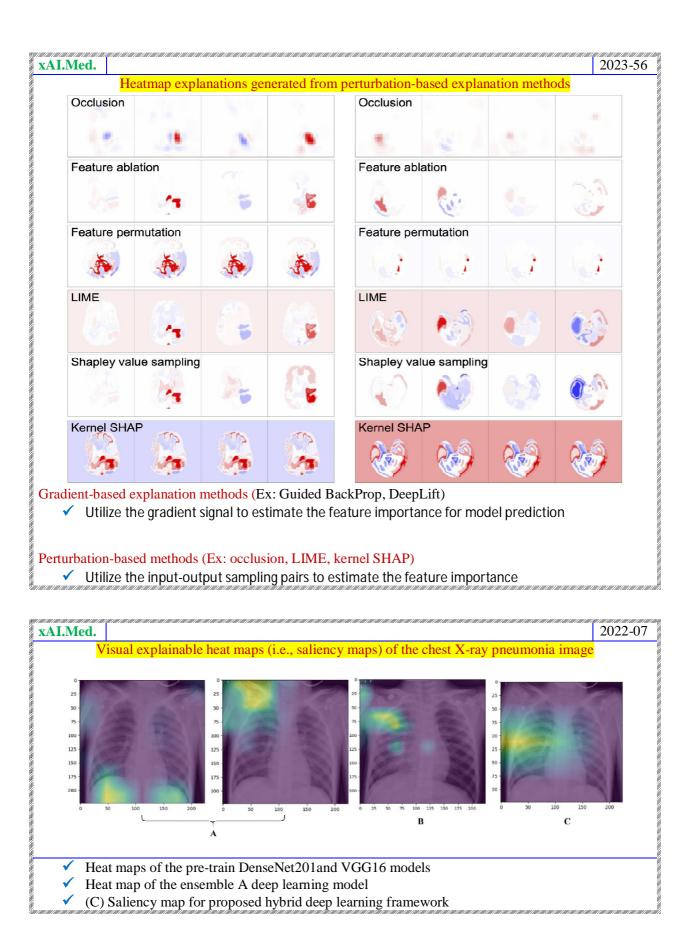


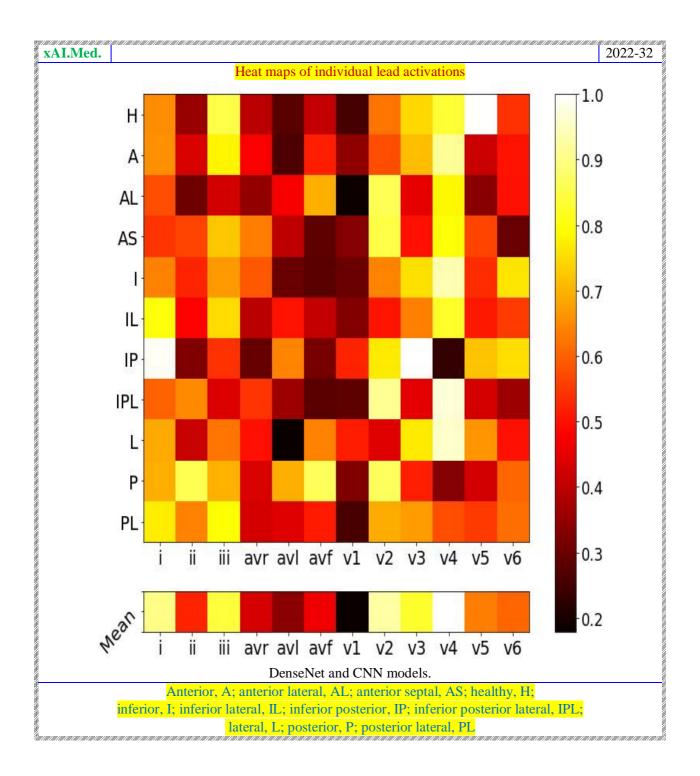




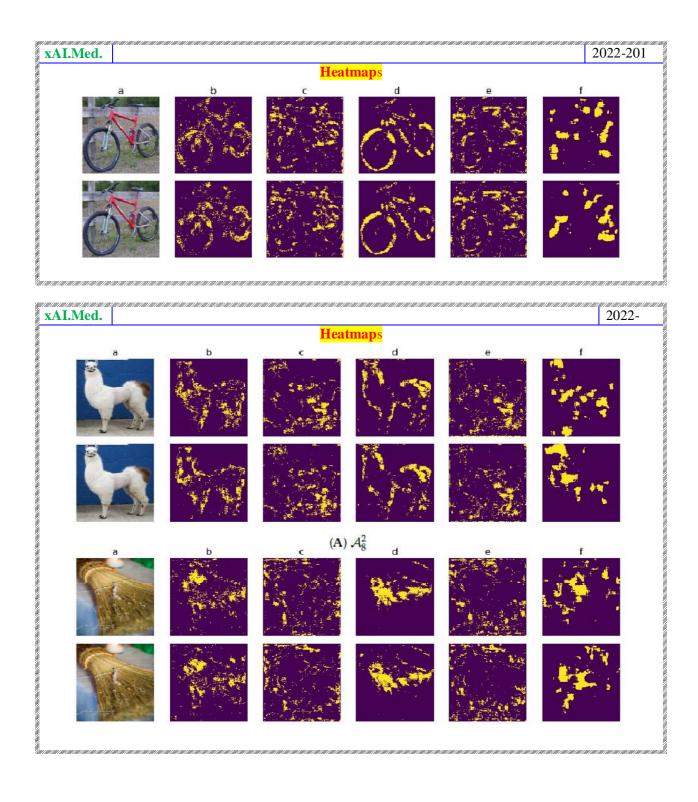
Heat maps



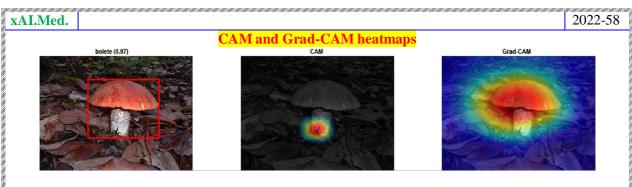




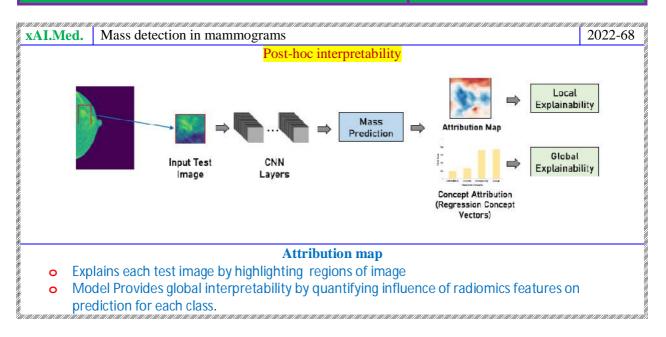




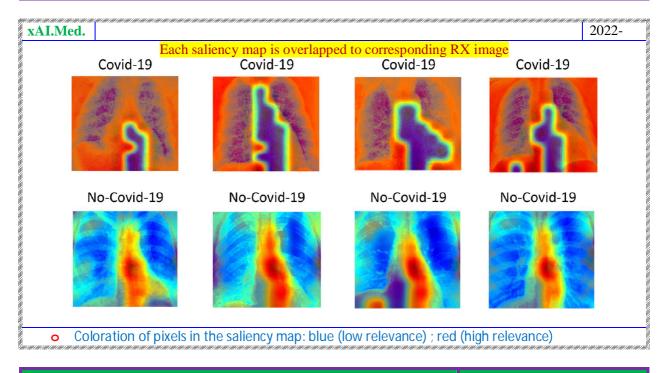
Heatmaps Grad-CAM



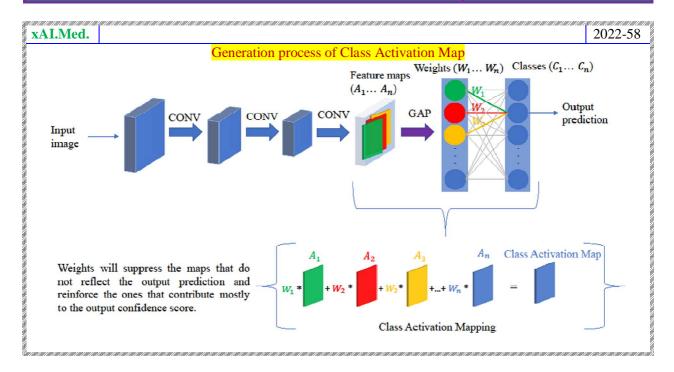
Attribution map

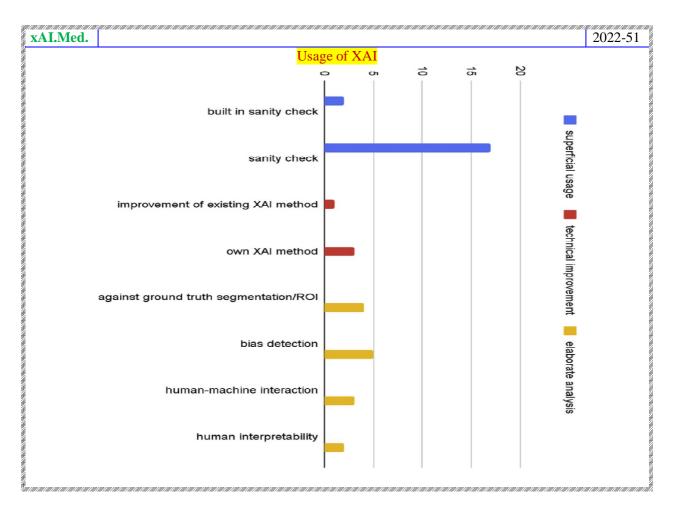


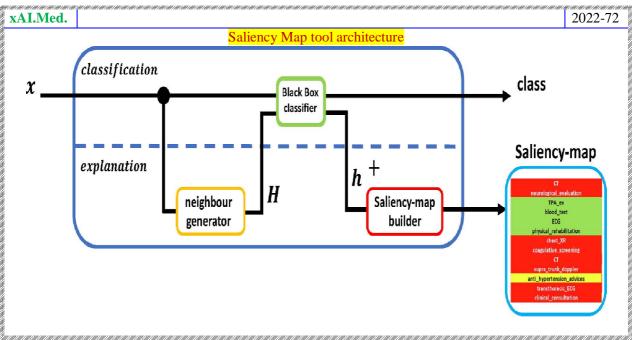
Saliency maps

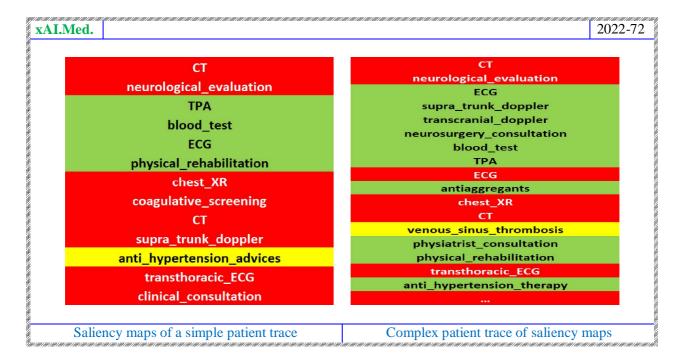


Class Activation maps

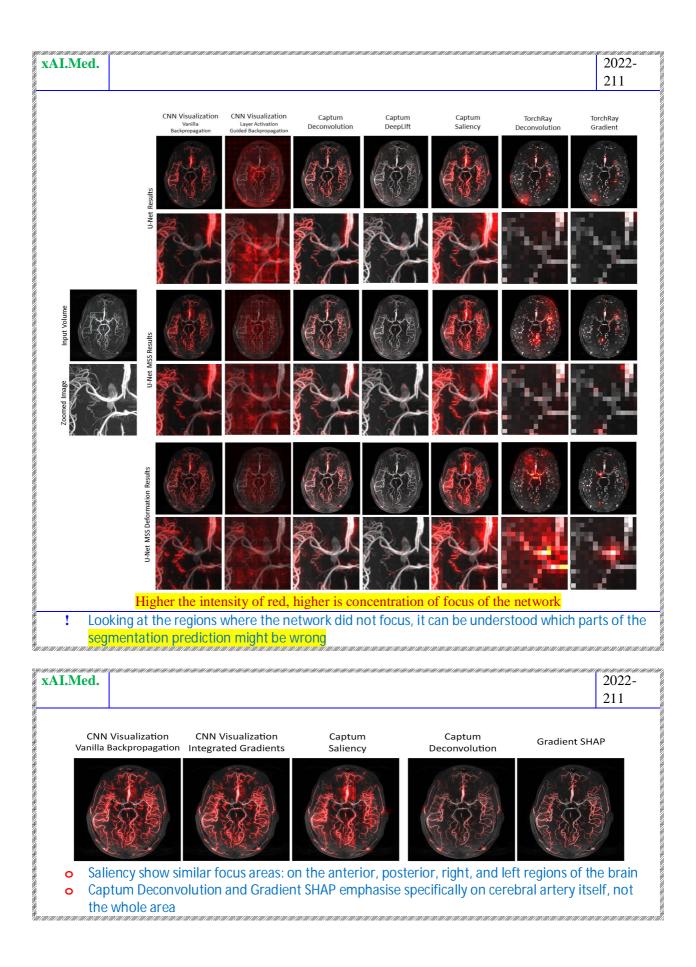




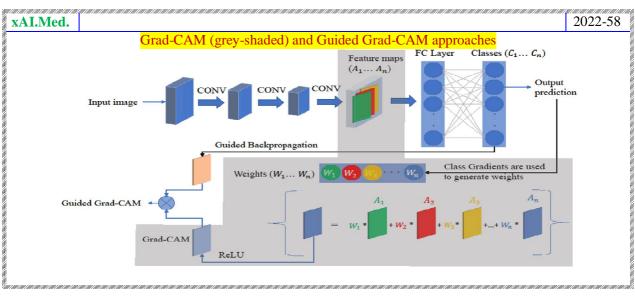


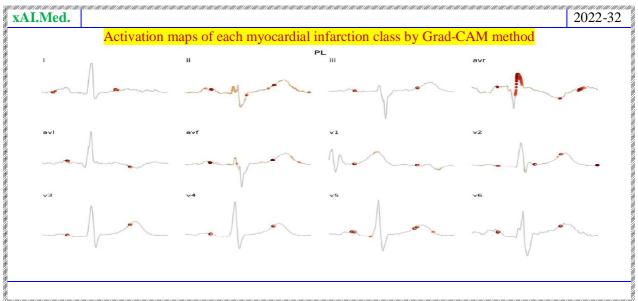


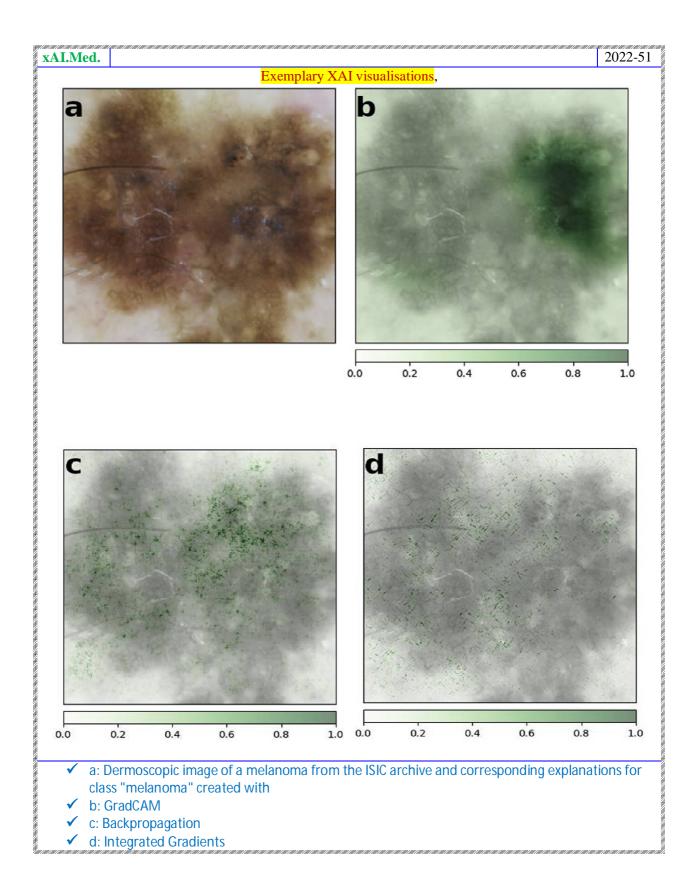
	Trace sa	liency map cor	nstruction	on procedure	202
neighborhood	ac _{i1,1}	ac _{i1,2}		ac _{i1,k}	 ac _{i1,m}
exemplars –	:	:			1
	ac _{in,1}	ac _{in,2}		ac _{in,k}	 ac _{in,m}
	μ_1	μ_2		μ_k	 μ_m
trace $x \rightarrow$	ac ₁	ac ₂		ac _k	 ac _n
	$ ac_1-\mu_1 $	$ ac_2 - \mu_2 $		$ ac_k - \mu_k $	 $ ac_n - \mu_m $

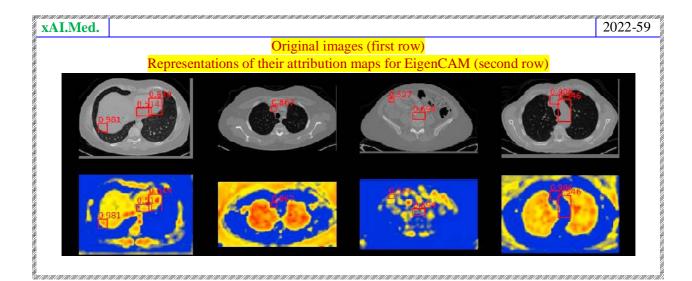


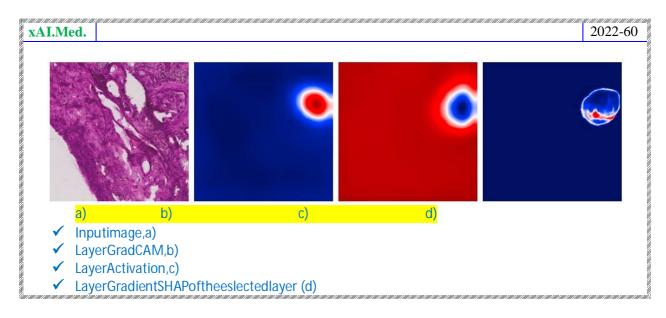
CAM					
EigenCAM	CAMs Aconv				
Grad- CAM	Guided Grad-CAM				
LayerGradCAM	1				

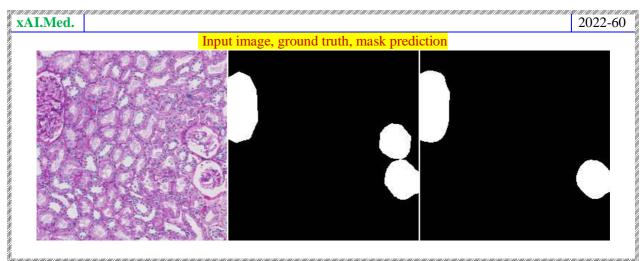


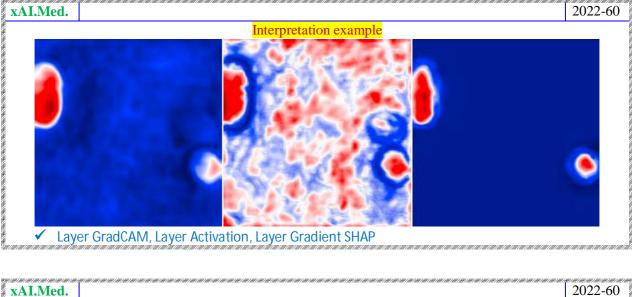


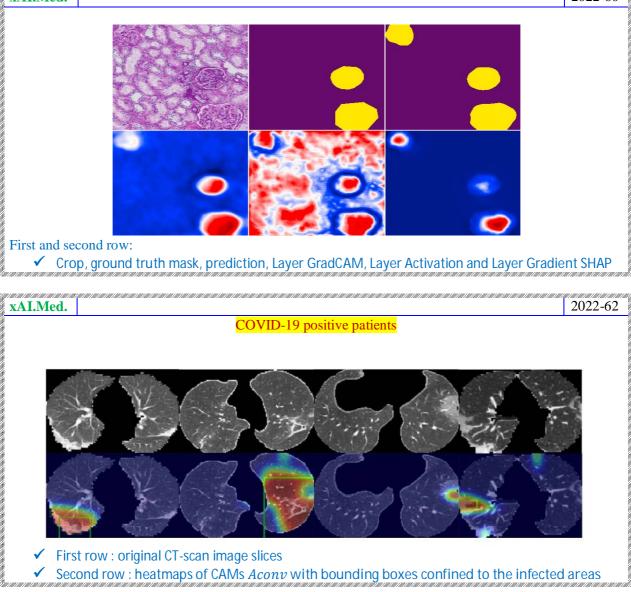


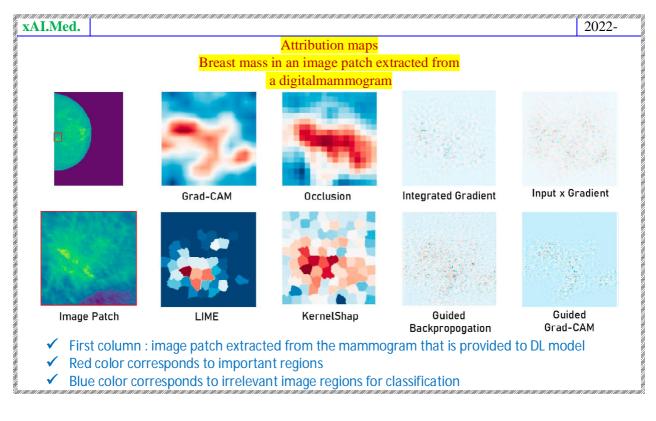


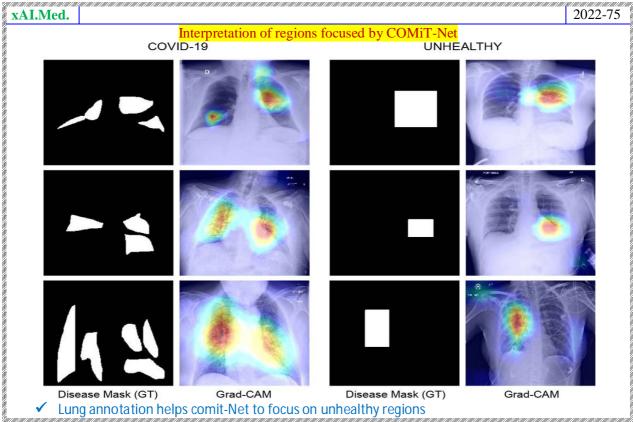




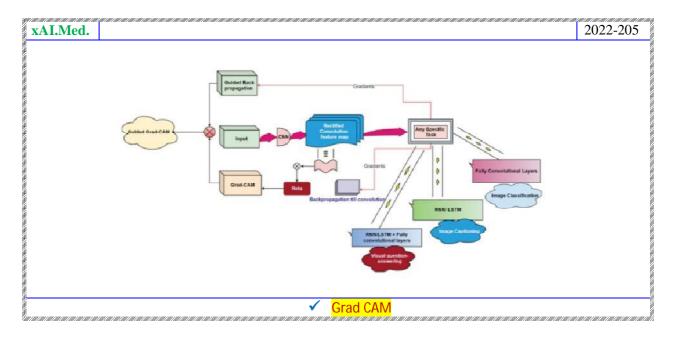


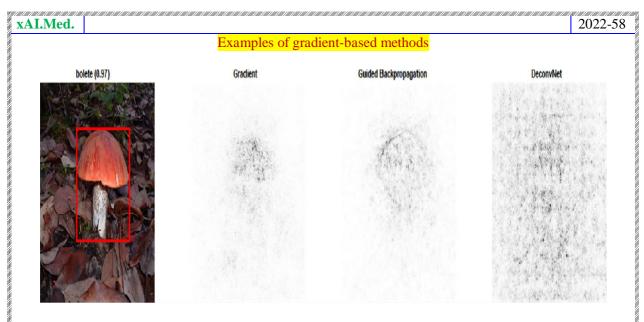






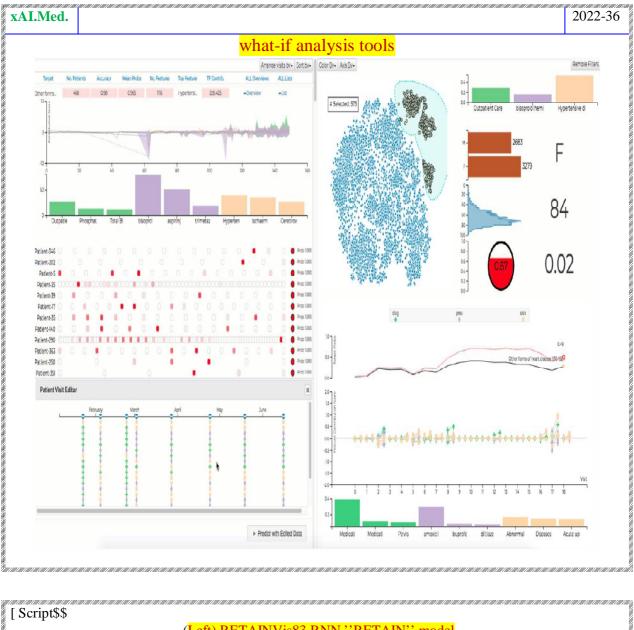
ed.		Output	e e	
E	CNN Visualization Grad Times	CNN Visualization Integrated Gradients	CNN Visualization Vanilla Backpropagation	CNN Visualization Guided GradCAM
U-Net Results Castadine Random 1 Overlav 1 Without Bandom		E B B	E SS	E B B
U-Net Results Cacading Random 1		C B B		
Cascading Random 2				
U-Net MSS Results Cascading Random 1 Overlav 1 Without Random				
U-Net MSS Results Cascading Random 1 (
Cascading Random 2				
ults Overlav 1			C 35	
: MSS Deformation Res Cascading Random 1				
U-Net Cascadine Random 2				





tSNE plot

t-distributed stochastic neighbor embedding



(Left) RETAINVis83 RNN ''RETAIN'' model

B Shows contribution to the overall outcome of patient visits through feature contribution score, representing drugs (violet), diagnosis (yellow), or physiological markers (green) for each visit

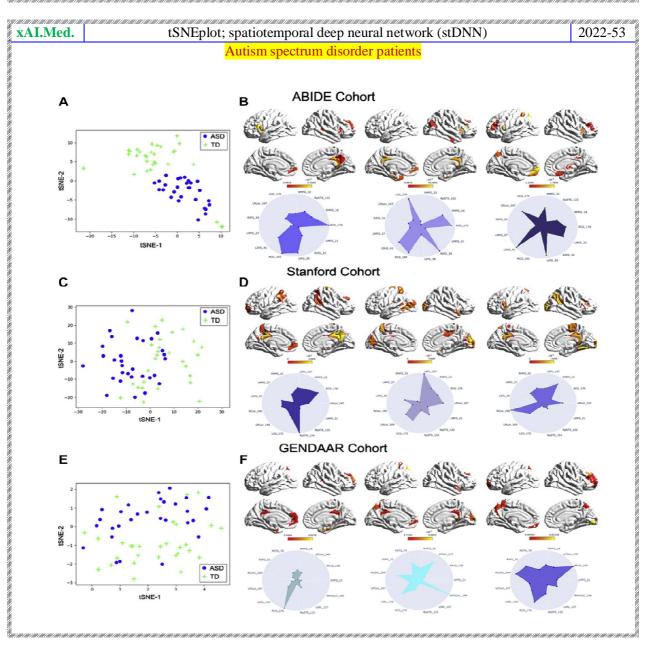
(Bottom) Patient list

- Shows individual patients in a row of rectangles. In the patient list, users can select a patient of ο interest to view details, shown below, and edit patients to conduct a what-if analysis.
- ο

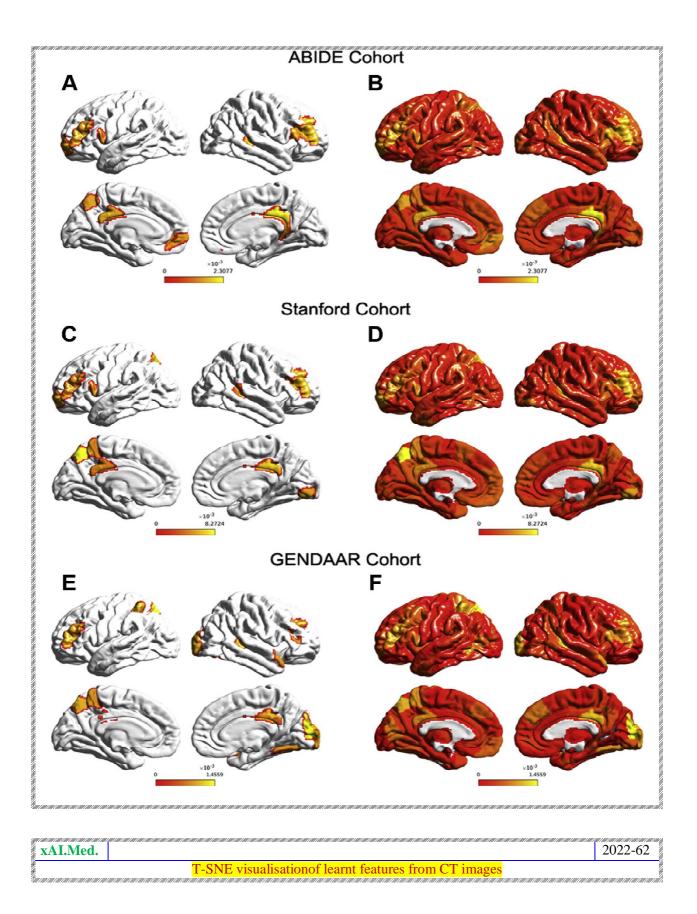
(Right top) Dimensionality reductiontechniques like t-SNE

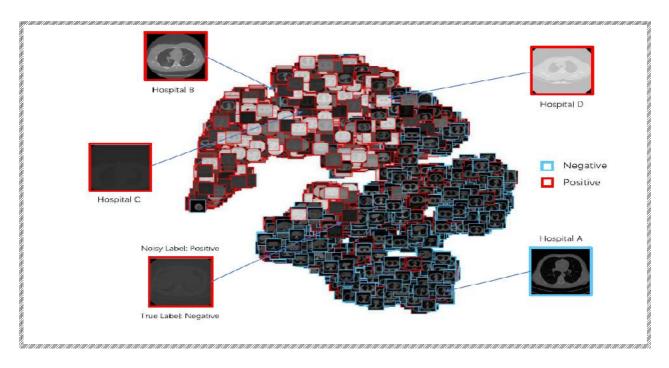
- t-distributed stochastic neighbor embedding result in the blue scatterplot to gain an overview 1 and then build patient cohorts using lasso selection tools and take a look at the distribution for demographic information like biological sex, age, and risk prediction scores (red circle). (Right bottom)
- Contribution scores for each visit and patient details are shown after the updated results of the what-if analysis

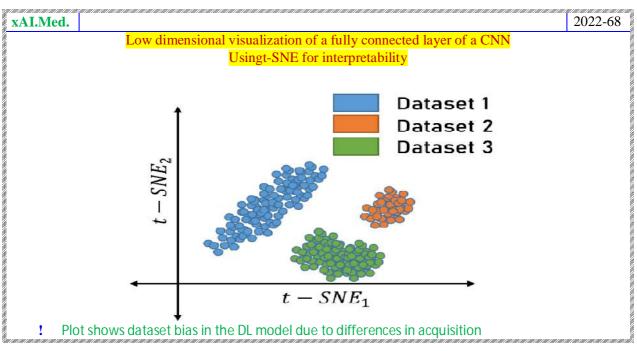
+ In the middle, an area chart shows aggregated contribution scores of nine medical codes over time. It shows mean and standard deviation as an area. Users can also see the medical codes and their mean contribution scores in bar chart " \$\$script]

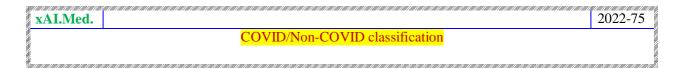


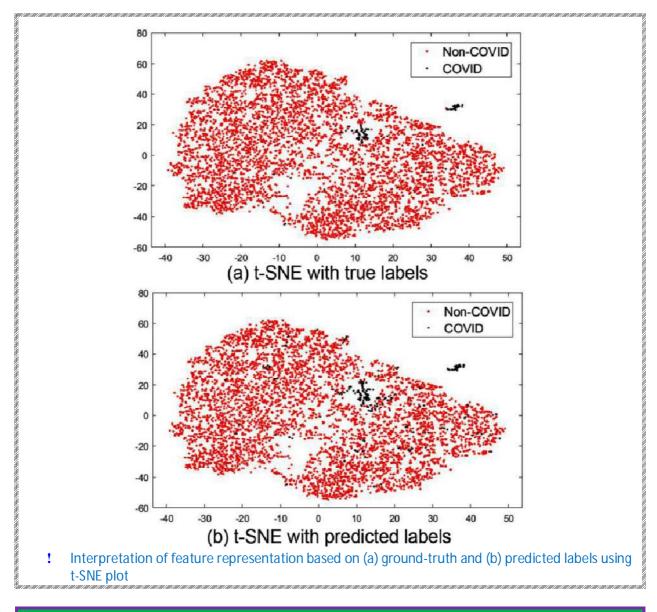
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xAI.Med.	2022-53
Autism Brain Imaging Data Exchange	





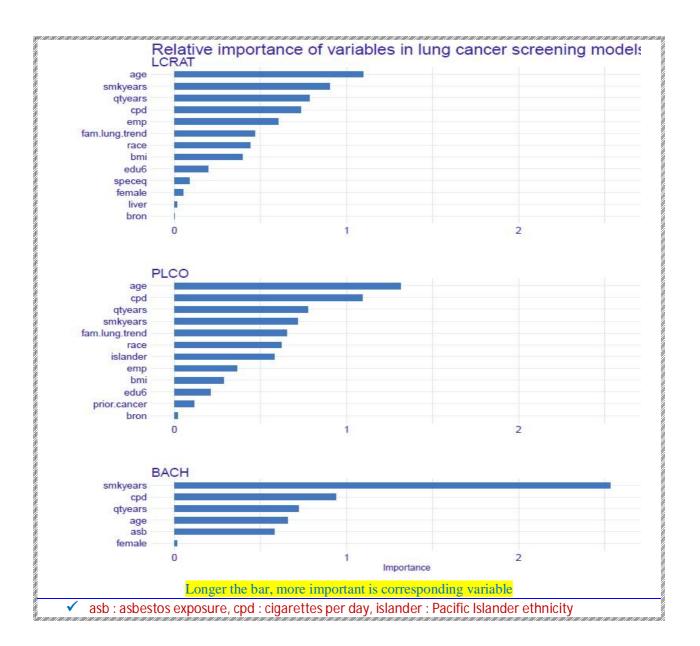


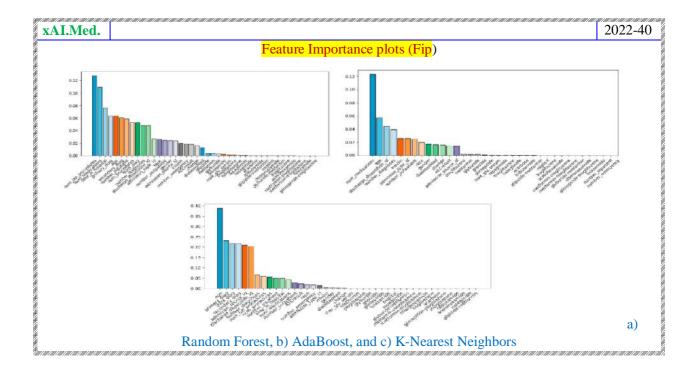




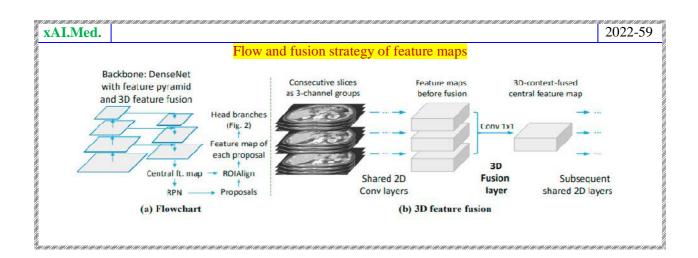
Variable ImportancePlot (VIP)

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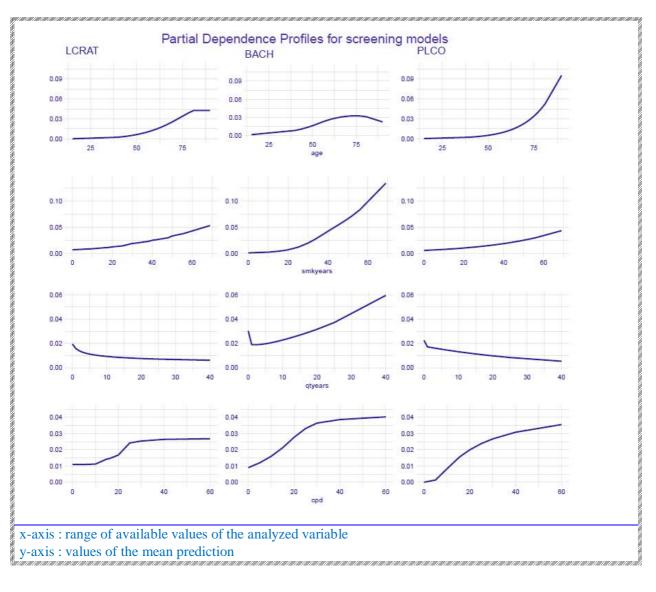
Feature Maps



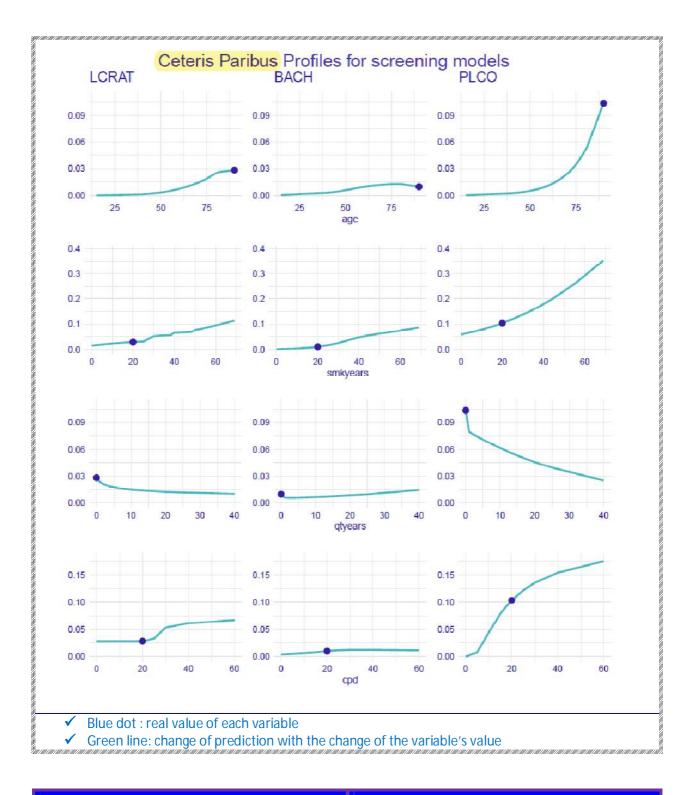
Partial depencence

Model

xAI.Med.	2022- 209
Relationship between a variable and an average model prediction	



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00. V 100. V 100.		Dependencies between continuous variables vs. Prediction for the selected patient	



Tables xAI

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xAI.Med.	2023-101
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Туре	Method	Post-hoc	Intrinsic	Local	Global	Application	Ref.
Dimension reduction	Optimum feature selection	X	1	X	1	Prediction of enhancers that are cell type specific	[109]
using XAI	Laplacian Eigenmaps	X	1	X	1	Classification of Brain tumor from MRI	[107]
	Sparse-balanced SVM	X	1	X	1	Diagnosis of type 2 diabetes at an early stage	[158]
	Cluster analysis and LASSO	X	1	X	1	Classification of lung cancer patients	[108]
	Sparse DL	X	1	X	1	Glioblastoma multiforme long-term survival prediction	[110]
	Optimal feature selection	X	1	X	1	Estimation of side effect for drug	[106]
Rule	Decision rules	X	1	X	1	Stroke Prediction	[126]
extraction and	Rule-based system	X	1	X	1	Forecasts for 30-day readmissions and pneumonia risk.	[14]
knowledge	Minic learning	1	X	1	1	Predicting outcomes in the ICU for severe lung injury	[120]

Туре	Method	Post-hoc	Intrinsic	Local	Global	Application	Ref.
distillation using XAI	Textual or visual justification	1	X	1	2	Classification of breast mass	[125]
	Visualization rules	1	X	X	5	Clinical diagnosis of diabetes and breast cancer	[121]
	Lists of Bayesian rule	X	1	X	1	Stroke prediction	[120]
	Fuzzy rules	X	1	X	1	Prediction of in-hospital mortality for all cases	[123]
Feature	DeepLIFT	1	X	X	1	Detection of splice site	[133]
importance or	Feature weighting	1	X	X	1	Prediction of ICU mortality for all-causes	[128]
selection	DeepLIFT	1	X	1	1	Ophthalmic diagnosis	[137]
using XAI	Feature marginalization	1	X	2	2	Diagnosis of inflammatory or microbiota bowel diseases from skin and gut	[131]
Attention	Attention	X	1	1	X	Prediction of future hospitalization from EHR	[143]
mechanism in		X	1	1	1	ICU clinical events predictions	[140]
XAI		X	1	1	X	HIV genome integration site prediction	[142]
		X	1	1	1	Prediction of clinical risk for cardiac cataract or failure	[145]
		X	1	1	X	Prediction of heart failure	[144]
	MILCAM	X	1	1	X	Localization of brain tumor	[145]
	Grad-CAM	X	1	1	X	Appendicitis diagnosis	[147
	Grad-CAM	X	1	1	X	Hypoglycaemia detection using ECG	[149]
Surrogate	LIME	1	X	1	X	Prediction of early puberty in the central region	[152]
representation		1	X	1	X	Construction of survival models	[153]
using XAI		1	X	1	X	Diagnosis of autism spectrum disorder	[159
	Rule-based XAI	1	X	1	X	Patient medications, diagnosis and readmission prediction	[155

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Ref	Disease Diagnosis	ML Models Used	Work Summary
[185]	Chronic Obstructive Pulmonary Disease	Gradient boosting machine (GBM)	The work ranks the attributes crucial to the GBM model according to their average absolute SHAP values that reflect the impact of each feature on a prediction.
[186]	Parkinson's disease diagnosis	deep forest (gcForest), extreme gradient boosting (XGBoost), light gradient boosting machine (LightGBM) and random forest (RF)	The classifiers determine how much the SHAP value contributes to the features. When 150 features are considered, SHAP-gcForest achieves 91.78 percent classification accuracy. With 50 features, SHAP-LightGBM combined with LightGBM yields 91.62% accuracy.
[187]	predicting acut kidney injur progression		The SHAP value increases as creatinine levels climb until it reaches about 5 mg/dL. As the Furosemide Stress Test (FST) is increased until it reaches 100 ml/min, the SHAP result decreases.

[188]	COVID-19 Prediction	XGboost model, LGBM, gradient boosting classifier (GBC), categorical boosting (CatBoost), RF	Harris hawks optimization (HHO) approach is employed to fine-tune the hyperparameters of a few cutting-edge classifiers, including the HHO-RF, HHO- XGB, HHO-LGB, and ensemble methods, in order to increase classification accuracy.
[189]	Prediction of COVID- 19 diagnosis based on symptoms	GBM	A gradient-boosting machine model created with decision-tree base-learners was used to produce predictions. SHAP values calculate the contribution of each feature to overall model predictions by average across samples
[190]	Efficient analysis of COVID 19	Support Vector Machine (SVM), Naive Bayes (NB), Multiple Linear Regression (MLP), K-Nearest Neighbors (KNN), RF, LR, and Decision Tree (DT), Keras Classifier	Simple classification techniques like random forest can outperform keras with Boruta for feature selection when the dataset size is not too large. Computing the information gain values for each attribute in Clinical Data1 shows the importance of each attribute.
[191]	COVID 19 Diagnosis	SqueezeNet, LIME	LIME and SHAP are compared for COVID diagnosis using SqueezeNet to recognize pneumonia, COVID-19, and normal lung imaging. Results show LIME and SHAP can boost the model's transparency and interpretability.
[192]	COVID-19 vaccine prioritization	Random Forest, XGBoost classifiers, XAI	CovidXAI predicts a user's risk group using Random Forest and XGBoost classifiers. CovidXAI uses 24 criteria to define an individual's risk category and vaccine urgency
[193]	COVID-19 Pneumonia Classification	XGBoost, Random Forest	The goal is to provide grounds for understanding the distinctive COVID-19 radiographic texture features using supervised ensemble ML methods based on trees through the interpretable SHAP approach. SHAP recursive feature elimination with cross-validation is used to select features. The best classification model was XGBoost, with an accuracy of 0.82 and a sensitivity of 0.82.
[194]	Lung cancer hospital length of stay prediction	Random Forest, logistic regression	This paper introduces a predictive LOS framework for lung cancer patients utilizing ML models. Using SHAP, the output of the predictive model (RF) with SMOTF class balancing approach is understood demonstrating the most relevant clinical factors that contributed to predicting lung cancer LOS using the RF model.

Method	Explanation	Scope	Fidelity		Interpre	tability
	type	1.660	Soundness	Completeness	Parsimony	Clarity
Post-hoc explanation	Attribution	Local	General quantitative metric	Unavailable matrices	Satisfied if an instance or feature is human-intelligible.	General quantitative metric
	Attribution	Global	General quantitative metric	Unavailable matrices	Satisfied if an instance or feature is human-intelligible.	Satisfied
	Model	Local	General quantitative metric	Satisfied	General quantitative metric	Unavailable matrices
	Model	Global	General quantitative metric	Satisfied	General quantitative metric	If the model is incapable of providing various rationales, the model is satisfied.
	Example	Local	Unavailable matrices	Unavailable matrices	Satisfied if an instance or feature is human-intelligible.	Unavailable matrices
	Example	Global	Unavailable matrices	Unavailable matrices	Satisfied if an instance or feature is human-intelligible.	Satisfied

xAI.Med.

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Learning category	Concepts	Representative methods	Applications
Supervised	learning from labeled data to predict class/clinical measures	SVM, random forest, sparse learning, ensemble learning	Disease diagnosis, prognosis, treatment outcome prediction
Unsupervised	learning from unlabeled data to uncover structure and identify subgroups	Hierarchical clustering, K-means, PCA, CCA	Disease subtyping, normative modeling, identify behavioral and neurobiological dimension
Semi-supervised	learning from both labeled and unlabeled data to perform supervised or unsupervised tasks	multi-view learning, Laplacian regularization, semi-supervised clustering	multi-modal analysis, joint disease subtyping and diagnosis, prediction with incomplete data
Deep	learning hierarchies and non-linear mappings of features for higher-level representations, can be either supervised or unsupervised	CNN, deep autoencoder, GCN, RNN, LSTM, GAN	a large class of generic learning problems
Reinforcement	solving temporal credit assignment problems, optimal control, trial-and- error learning	temporal difference learning, Q-learning, actor-critic model, dynamic programming	online control, modeling of decision-making and choiced behaviors

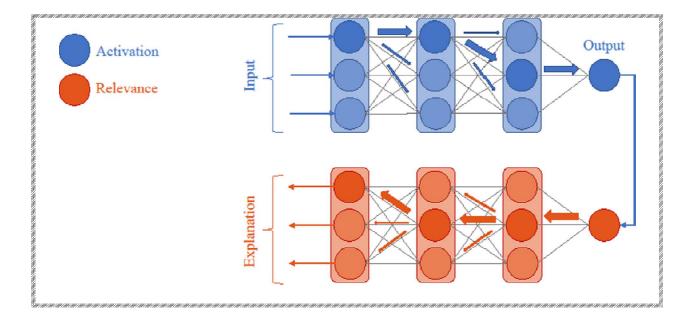
	Methods for explainability
ο	Stage (Ah: ante hoc; Ph: post hoc)
0	Scope (L: local; G: global)
ο	Forms of explanations (N: numeric; R: rules; T: textual; V: visual)
ο	Type of models

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Methods for	References	Sta	ige	See	pe		Fo	rm		Mode Is for Primary
Explainability	nerciences	Ah	Ph	L	G	N	R	Т	V	Task
Ada-WHIPS	F1101	2.11		~						FM
	[112]	1	2	5	1		-			NFM
ALMMo-0*	[116]	*		*	*	352		12	30	
Anchors	[96]		-	•	*	1	-	1	*	MA
ANFIS	[66,118,137,169]		~	*	*	1	*	*	*	FM; GA; NN;
ApparentFlow-net	[124]	4		5					1	INN
Attention Maps	[79,149,151,152]		1	5					1	INN
BB-BC IT2FLS	[178]	<		1		1	1		1	FM
BEN	[69]		5	5					5	NN
BN	[71, 165]	1		5				5	1	BM
BRL	[126]	2		•	1		1			BM
CAM	[140,141]		1		1		•		18	NN
Candlestick Plots			*,		*				*	NN
	[161]		*		*				*	
CART	[127]	4	0.041	*	2.2	102	-			TM
CASTLE	[47]		*	*	*	*			×	MA
Causal Importance	[68]		4		1	~				NN
CFCMC	61	1			1			1		FM
CGP	[122]	1			1	1				UM
CIE	[49]		1	1	1	1		1		EM; NN; SVM
CTT2FS	[134]	1	-	1	-			F	1	FM
		*	See	*	58				*	
Concept Attribution	[132]								v	INN
Counterfactual Sets	[7,55]		5	5				~		EM; NN
Cline	[108,127]	1		1			~			TM
Deconv Net	83		5	1	1				1	NN
Decision Tree	[54,75]		~	1	1		1			NN: TM
Deep-SHAP	[143]		1	5	5	1	-		1	MA
DID	[85]		-	1	•				1	NN
DIFFI			*	*	1	1			¥	EM
	[145]		~	2.2	1	v			320	
EL15	[139,142]		-	~	1	*			-	MA
Encoder-Decoder	[133]	*		*					*	NN
eUD3.5	[102]	5		5	1		5			EM
EcNN	[60]	1		1	1				1	INN
FACE	[78]		5	5					1	NN
	Fred .									EM; NN; NNM;
FDE	[170]		~	1	1	1				SVM
Feature Importance	[67, 128, 144, 172]		-	\$	5	1	1.00	4	1	MA
Feature Pattern	[163]		*		*		*			EM
FFT	[127]	~		5			5			TM
FINGRAM	88	5		5					1	TM
FormuCase Viz.	971		1	1					1	CBR
FURIA	[52]	5	-	5			1			EM
Fuzzy LeNet	[82]	1		1					1	FM
Fuzzy Relations	[64, 104]			-				0.000	×	FM
8bt-HIPS	[50]	~		~	1		~			EM
Generation	[159]		5	5				1		NN
GLAS	[77]		5	5					1	MA
GRACE	[58]		1	1				1		NN
Methods for Explainability	References	3	lage		cope			Form		Models for Primar
		Ah	Ph	L	G	N	B	2 7	1. I.	V Task
Template-Based Natural	19.2.43	1000							2	134
Language Generation	[164]	*		4				2	1	UM
Time Varying Neighbour-										
	[101]		1	1		×	6			V NN
hood			1	3	5 12	2 0	ŝ			
TreeExplainer	[84]		1	~	4	*				✓ MA
TREPAN	[89]		1	1				0		NN
Tripartite Graph	[162]	1		1		v	5			✓ UM
WM Algorithm	[157]	*			1			e		FM
XDNN	[116]	1				8		e .	1	NN
0.100.013								- 3		
XRAI	[147]		100	1						V NN

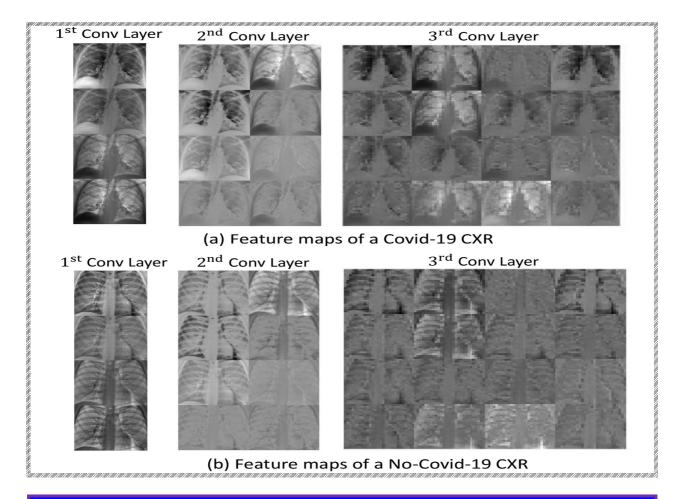
Output of Each of feature layers (CNN)

xAI.Med.		2022-58
	Layer-wise Relevance Propagation (LRP)	



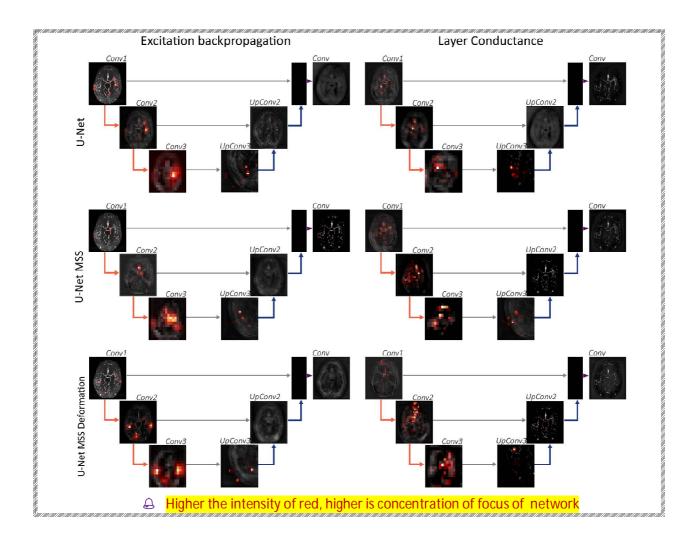
AI.Med Main different	nces	hetw	een	hacknrona	oatic	n D	econ	vNet and Guided backpropagation
Wall differen		occw	cen	ouexpropu	Sauce	л, D	ceon	file and Sudde Suckpropagation
	-1	2	-3		0	3	0	
Forward pass	-5	-4	6	ReLU	0	0	6	
	9	8	-7		9	8	0	
Paalmuand nase	0	3	0		-5	3	8	Passes only positive gradients
Backward pass 'Backpropagation'	0	0	-4	ReLU	7	-6	-4	corresponding to the preceding lower
1 1 0	-2	1	0		-2	1	9	layer
Backward pass	0	3	8	ReLU	-5	3	8	Allows only positive gradients to
'DeconvNet'	7	0	0	<	7	-6	-4	backpropagate
	0	1	2		-2	1	9	
								Allows only positive gradients
Backward pass 'Guided	0	3	0	ReLU	-5	3	8	corresponding to the preceding lower
backpropagation'	0	0	0	KeLU	7	-6	-4	layer and positive gradients from backpropagation
	0	1	0		-2	1	9	oackpropagation
								~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
<b>AI.Med.</b>	91181181181	1011101110111	911091109110	110011001100110011001100110011001100	11811811811	0110110110	, 1 <i>10</i> , 1 <i>0</i> , 1 <i>10</i> , 1 <i>1</i> 0	2022-4

### Feature maps learned by the three convolutional layers of CovNNet on (a) Covid-19 and (b)No-Covid-19 CXR image



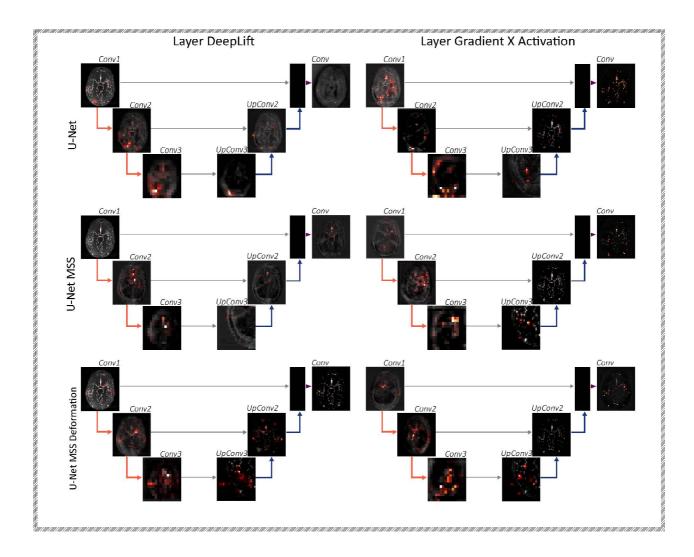
### Layer Conductance

	2022- 211
Layer-based interpretability methods	
Focus of network changes in each layer for three different models	



### Layer Gradient activation

# xAI.Med.



# Linguistic Summaries

#### xAI.Med.

2022-66

Relative linguistic summaries based on short protoforms for mania and hypomania episodes (LS with T = 1.0) and extended protoforms for mania and hypomania episodes (LS with T > 0.5).

Relative LS based on short protoform	Т
Most calls in the state of mania have low spectrum compared to the state of euthymia.	1.0
Most calls in the state of mania have low quality compared to the state of euthymia.	1.0
Most calls in the state of hypomania have low spectrum compared to the state of euthymia.	1.0
Most calls in the state of hypomania have low loudness compared to the state of euthymia.	1.0
Most calls in the state of hypomania have low qualty compared to the state of euthymia.	1.0
Relative LS based on extended protoform - HYPOMANIA	Т
Most calls with low loudness in hypomania have low spectrum compared to the state of euthymia.	1.0
Most calls with low loudness in hypomania have low quality compared to the state of euthymia.	1.0
Most calls with high loudness in hypomania have high spectrum compared to the state of euthymia.	1.0
Most calls with high loudness in hypomania have high quality compared to the state of euthymia.	1.0
Most calls with low pitch in hypomania have low spectrum compared to the state of euthymia.	1.0
Most calls with low pitch in hypomania have low loudness compared to the state of euthymia.	1.0
Most calls with low pitch in hypomania have low quality compared to the state of euthymia.	1.0
Most calls with low spectrum in hypomania have low loudness compared to the state of euthymia.	1.0
Most calls with low spectrum in hypomania have low quality compared to the state of euthymia.	1.0
Most calls with high spectrum in hypomania have high loudness compared to the state of euthymia.	1.0
Most calls with high spectrum in hypomania have high quality compared to the state of euthymia.	1.0
Most calls with low quality in hypomania have low loudness compared to the state of euthymia.	1.0
Most calls with low quality in hypomania have low spectrum compared to the state of euthymia.	1.0
Most calls with high quality in hypomania have high loudness compared to the state of euthymia.	1.0
Most calls with high quality in hypomania have high spectrum compared to the state of euthymia.	1.0
Relative LS based on extended protoform - MANIA	T
Most calls with low loudness in mania have low spectrum compared to the state of euthymia.	1.0
Most calls with low loudness in mania have low pitch compared to the state of euthymia.	0.6
Most calls with low loudness in mania have low quality compared to the state of euthymia.	1.0
Most calls with high loudness in mania have low spectrum compared to the state of euthymia.	1.0
Most calls with low pitch in mania have low spectrum compared to the state of euthymia.	1.0
Most calls with low pitch in mania have low loudness compared to the state of euthymia.	1.0
Most calls with low pitch in mania have low quality compared to the state of euthymia.	1.0
Most calls with low spectrum in mania have low pitch compared to the state of euthymia.	0.7
Most calls with low spectrum in mania have low loudness compared to the state of euthymia.	1.0
Most calls with low spectrum in mania have low quality compared to the state of euthymia.	1.0
Most calls with medium spectrum in mania have high loudness compared to the state of euthymia.	0.8
Most calls with medium spectrum in mania have low quality compared to the state of euthymia.	0.6
Most calls with high spectrum in mania have high loudness compared to the state of euthymia.	1.0
Most calls with low quality in mania have low loudness compared to the state of euthymia.	1.0
Most calls with low quality in mania have low spectrum compared to the state of euthymia.	1.0
Most calls with high quality in mania have high loudness compared to the state of euthymia.	1.0
Most calls with high quality in mania have high spectrum compared to the state of euthymia.	1.0

xAI.Med.	2022- 213
Natural Language explanations generated using GPT-3 text-davinci-003 model	
for scents observed in the Leffingwell Odor Dataset	

Scent	Why the scent?
alcoholic	The molecular property "alcoholic scent" can be explained by the presence of an ethyl/ether O group and the absence of acetal like/methyl groups, two CH2 group separated by any three bonds, an alkyne group, and an S. These are all very important for the property.
aldehydic	The molecular property "aldehydic scent" can be explained by the presence of an oxygen atom, a lack of an oxygen atom bonded to a secondary carbon atom, the absence of an aromatic/ether oxygen group, the absence of more than two oxygen atoms, and the lack of a sulfur atom.
alliaceous	The molecular property "alliaceous scent" can be explained by the presence of more than one CH2 group that is bonded to two neighbors, one of which is a heteroatom an atom bonded to three other atoms, one of which is an S, and the presence of an S The lack of an O and an oxymethylene group (-CH2O-) is also very important for the property.
almond	The molecular property "almond scent" can be explained by the presence of an oxygen atom, an aldehyde/aromatic group, and the absence of an atom bonded to two methy groups, a CH2 group bonded to two neighbors by non-ring bonds, and an S atom These are particularly important structure-property relationships for the almond scent

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