

BRIGHAM HEALTH



BRIGHAM AND
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Imaging Advances in Smoking-related Injury: From COPD to Interstitial Lung Disease

Raúl San José Estépar, PhD



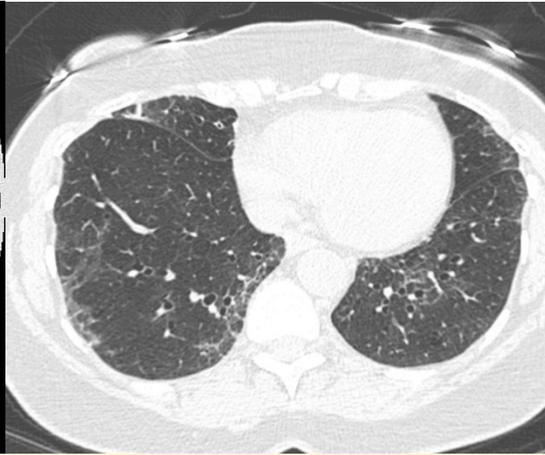
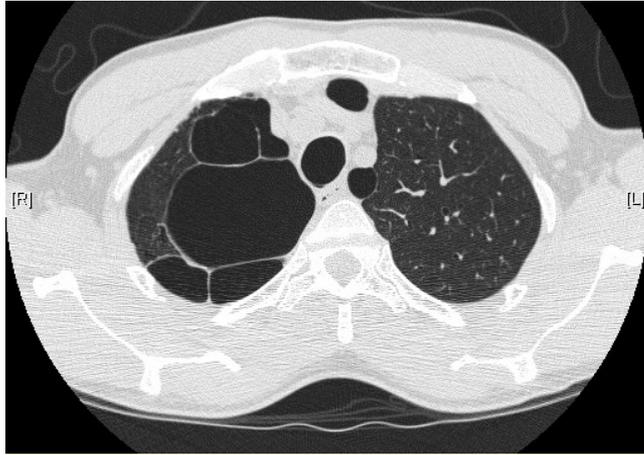
Applied Chest Imaging Laboratory
Brigham and Women's Hospital



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Smoking Related Lung Disease



Emphysema/COPD

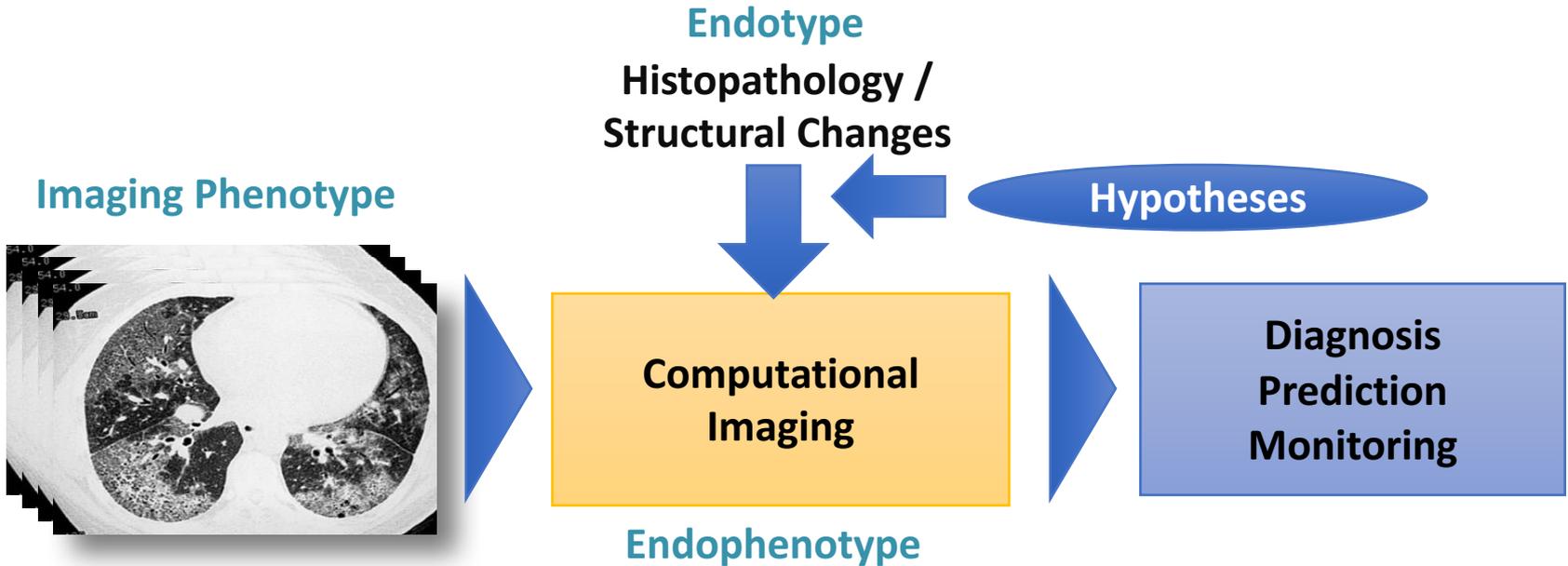


Overlap



Pulmonary Fibrosis

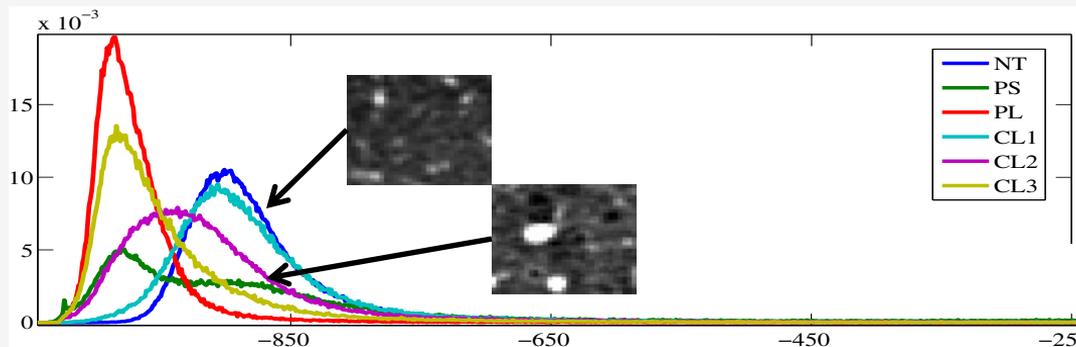
Designing Imaging Phenotypes: Computational Imaging



What are the *imaging endophenotypes* that are linked to the clinical manifestation and the prognostication of smoking related injury and *poor lung development*?

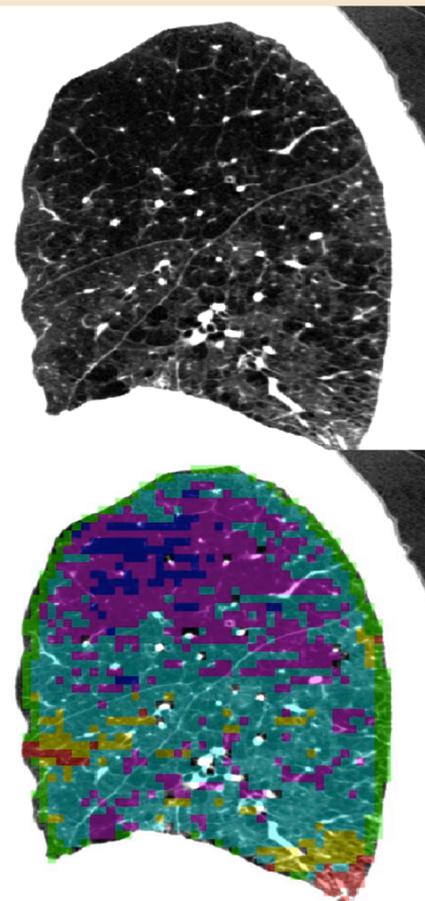
Emphysema Subtyping via Local Histogram

Mean Local Histogram for Emphysema Patterns



NT: Normal (non emphysema)
PS: Paraseptal
PL: Panlobular

CL1: Mild Centrilobular
CL2: Moderate Centrilobular
CL3: Severe Centrilobular

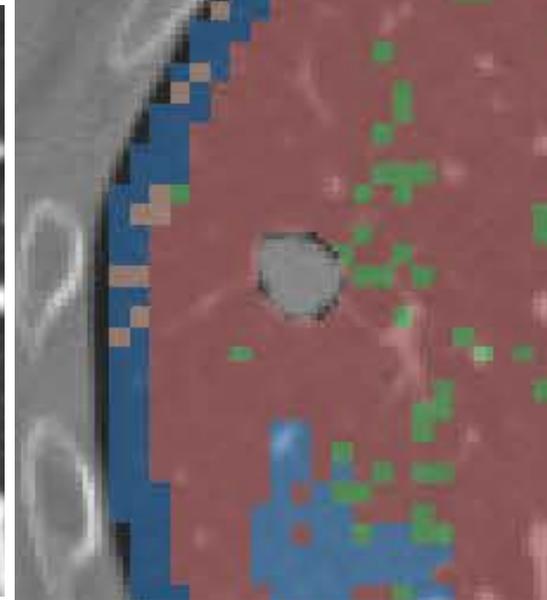
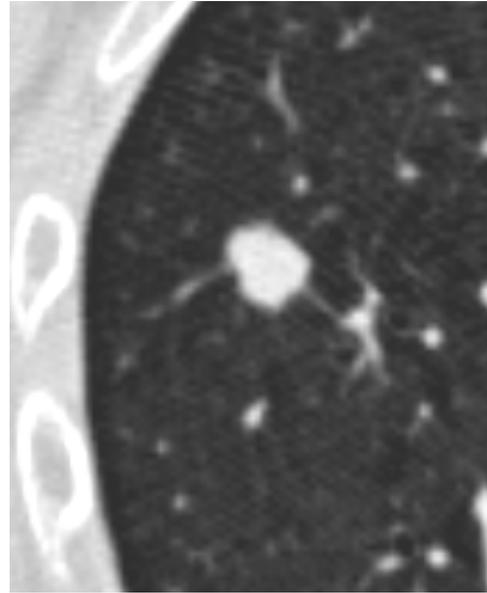
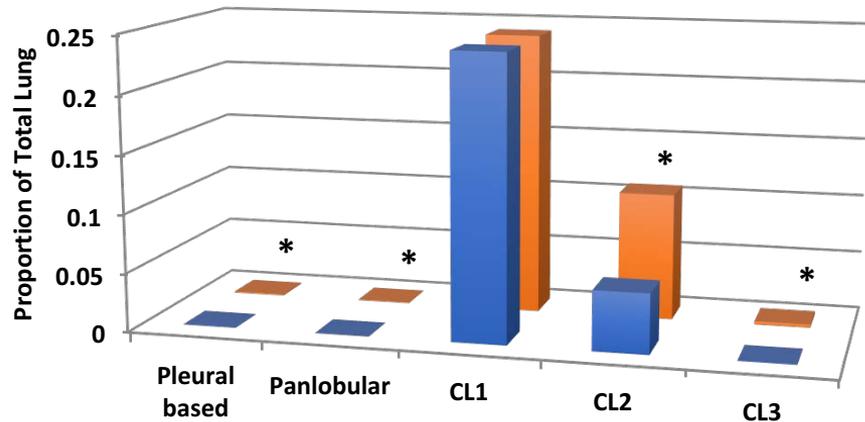


Local Histogram Subtypes have novel GWAS

LHE Pattern	Lead SNP	Nearest Gene	Locus	Position (BP)	Effect Allele	P Value Meta
Normal	rs17486278	<i>CHRNA5</i>	15q25	78867482	A	8.3×10^{-13}
	rs138641402	<i>HHIP</i>	4q31	145445779	A	1.7×10^{-9}
	rs1690789	<i>TGFB2</i>	1q41	218698027	C	2.9×10^{-8}
	rs17368659	<i>MMP12</i>	11q22	102742761	G	1.1×10^{-8}
Moderate centrilobular	rs114205691	<i>CHRNA3</i>	15q25	78901113	C	3.1×10^{-13}
	rs56113850	<i>CYP2A6</i>	19q13	41353107	T	1.3×10^{-9}
	rs17368582	<i>MMP12</i>	11q22	102738075	G	2.7×10^{-9}
	rs1690789	<i>TGFB2</i>	1q41	218698027	C	7.9×10^{-9}
Severe centrilobular	rs9788721	<i>AGPHD1</i>	15q25	78802869	T	1.8×10^{-13}
	rs379123	<i>MYO1D</i>	17q11	30891814	T	1.5×10^{-8}
Panlobular	rs11852372	<i>AGPHD1</i>	15q25	78801394	A	1.5×10^{-10}
	rs9590614	<i>VWA8</i>	13q14	42175588	G	1.1×10^{-8}

- Novel associations within genes associated with cell migration (*MYO1D*) and cell signaling (*VWA8*).
- GWAS observed at previously established COPD-associated loci
 - 14q31 (nearby gene *HHIP*), 15q25(*CHRNA3/5/IREB2*), 11q22 (*MMP12*), and 19q13 (*CYP2D6*).

Emphysema Subtypes and Lung Cancer



Lung Cancer Risk by Emphysema Subtype

Lung Parenchymal Feature	OR	CI	P value
%LAA -950 (density threshold alone)	1.01	[0.99, 1.02]	0.146
Mild centrilobular (CL1)	0.26	[0.17, 1.61]	0.263
Moderate centrilobular (CL2)	2.41	[1.09, 5.32]	0.029
Severe centrilobular (CL3)	6.12	[0.97, 38.6]	0.054
Panlobular (PL)	4.99	[0.23, 108.8]	0.306
Pleural-based (PB)	13.4	[0.00, 1137]	0.713

Each model includes one of the above lung parenchymal features and is adjusted for age, gender, pack years, and airflow obstruction

With the exception of %LAA-950, all morphologies were measured by the LH method at the level of the secondary pulmonary lobule.

Interstitial Lung Abnormalities

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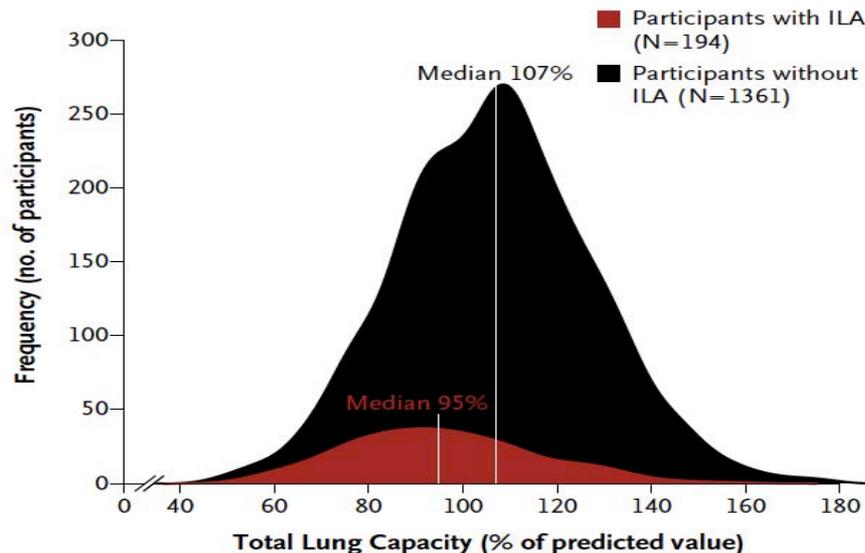
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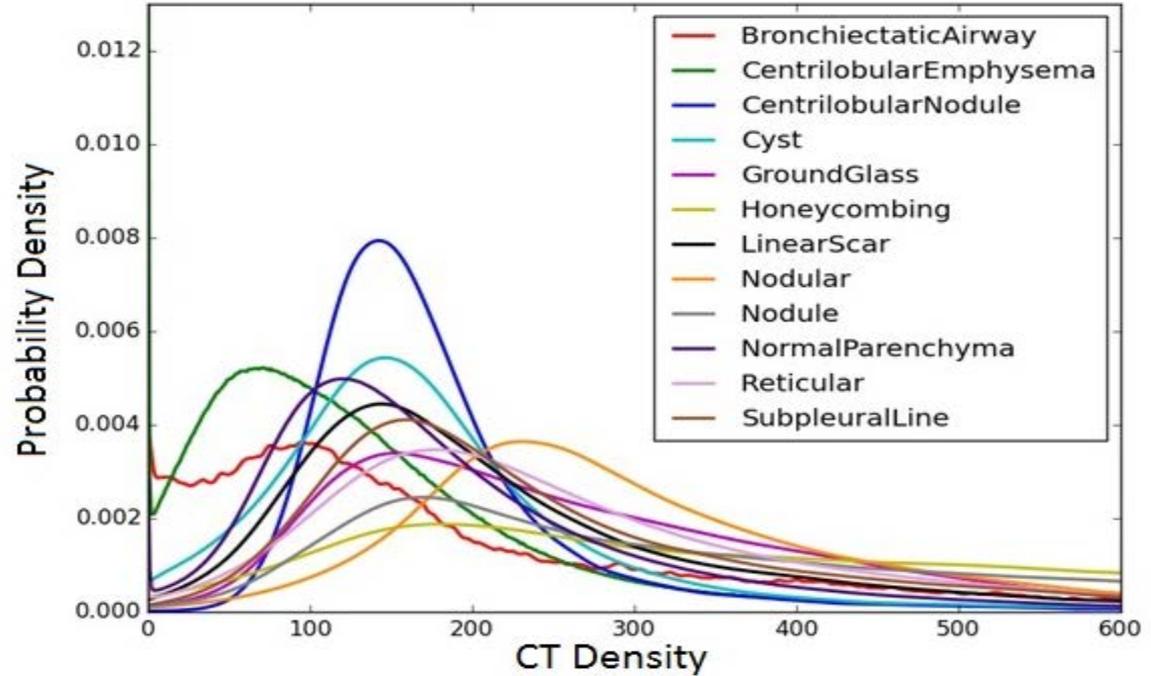
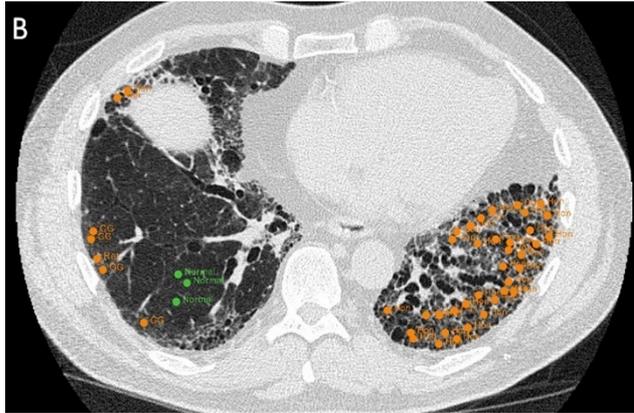
ORIGINAL ARTICLE

MUC5B Promoter Polymorphism and Interstitial Lung Abnormalities

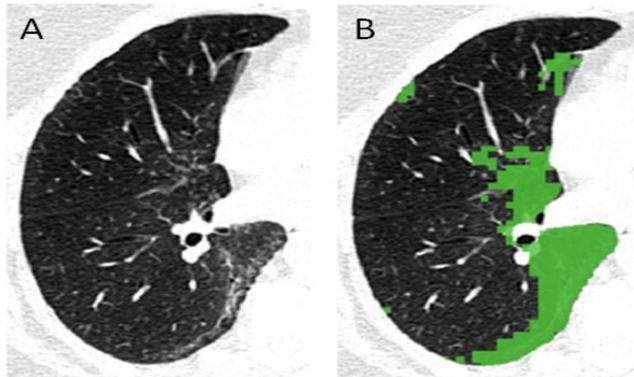
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Local Histogram with Interstitial Patterns

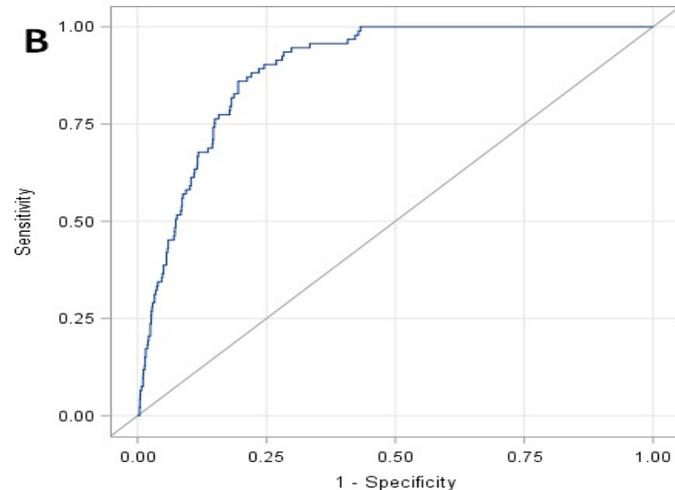
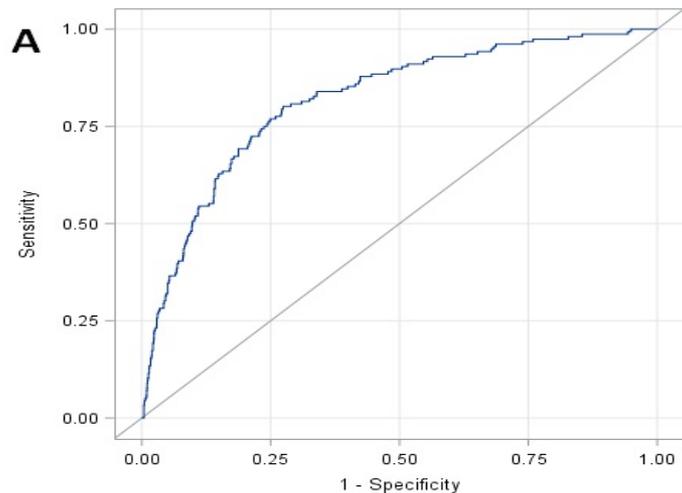


Detection of ILA matches visual diagnosis



AUC 0.82 for the detection of visually defined interstitial lung abnormalities

AUC 0.89 for the detection of visually defined fibrotic parenchymal abnormalities



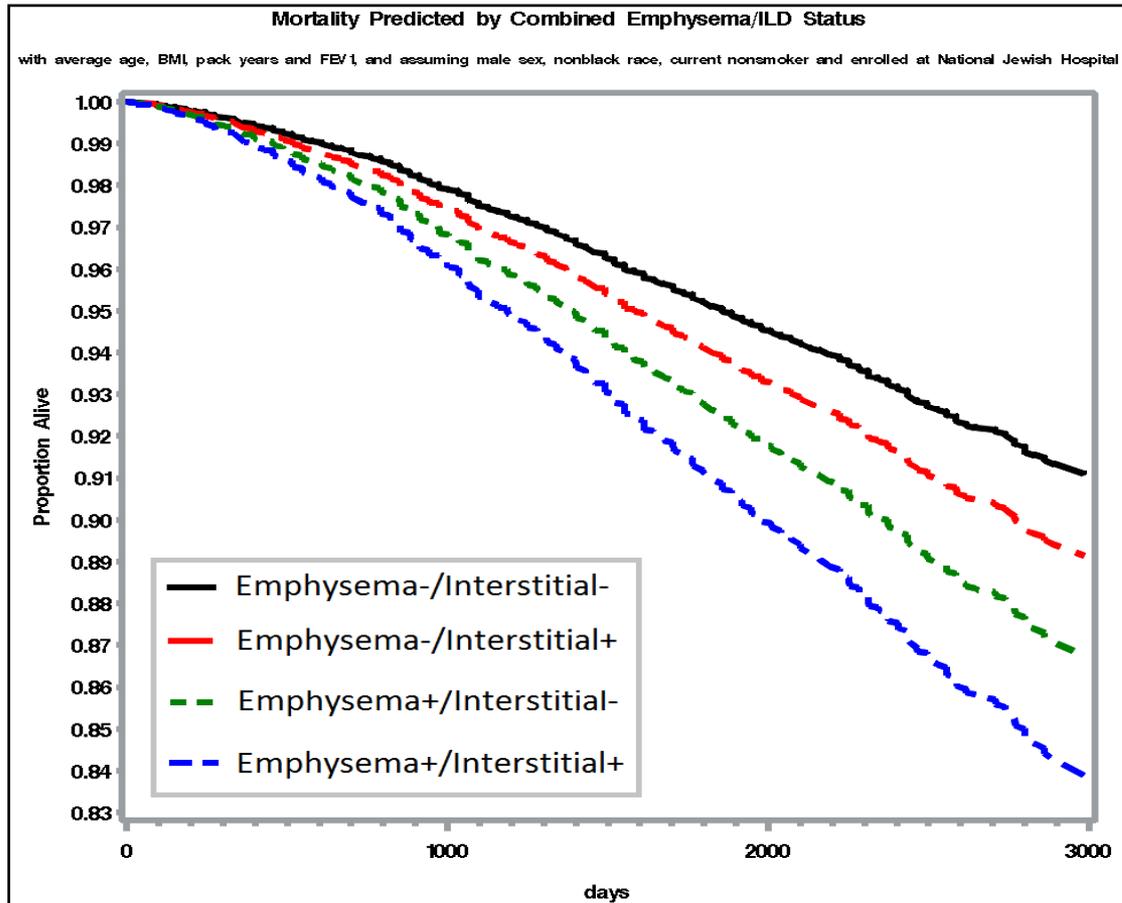
Susceptibility without visual ILA

Adjusted				All Participants
All Participants	Change per 5% Increase in Interstitial Features	CI	p	
FEV1%	-2.65	-3.15, -2.14	<0.001	
FVC%	-2.47	-2.88, -2.06	<0.001	
FEV1/FVC	-0.004	-0.007, -0.001	0.005	
SGRQ	1.36	0.92, 1.81	<0.001	
No ILA (0 only)				Without Visual ILA
FEV1%	-4.83	-5.78, -3.89	<0.001	
FVC%	-4.09	-4.85, -3.32	<0.001	
FEV1/FVC	-0.010	-0.016, -0.005	<0.001	
SGRQ	0.806	-0.027, 1.639	0.058	

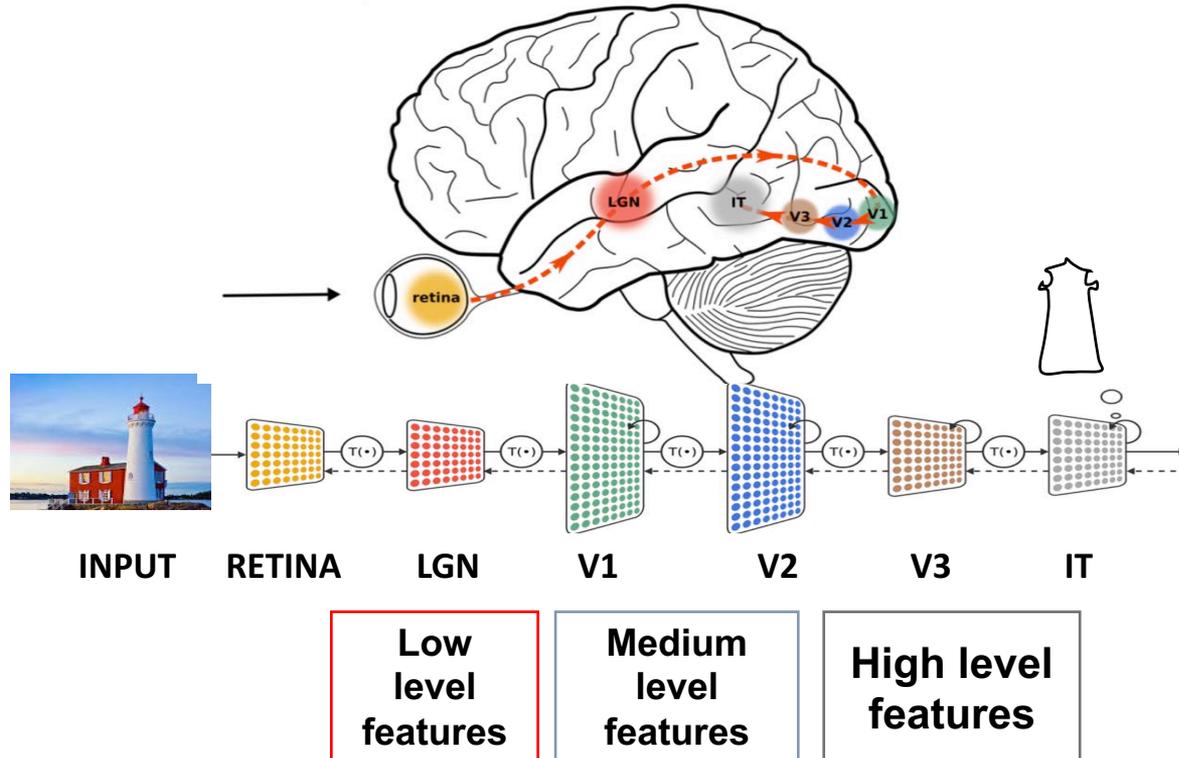
Mortality and Interstitial Features

	Hazard Ratio* (5% Absolute increase of ILA Features)	CI	p
All participants	1.29	1.21, 1.38	<0.001
Subgroup A – Those without ILA	1.27	1.16, 1.39	<0.001
Subgroup B – Those without ILA and without indeterminate findings	1.20	1.02, 1.42	0.031
Subgroup C – Those with normal spirometry	1.25	1.07, 1.46	0.004
Subgroup D – Those without chronic dyspnea or bronchitis	1.26	1.11, 1.44	0.001

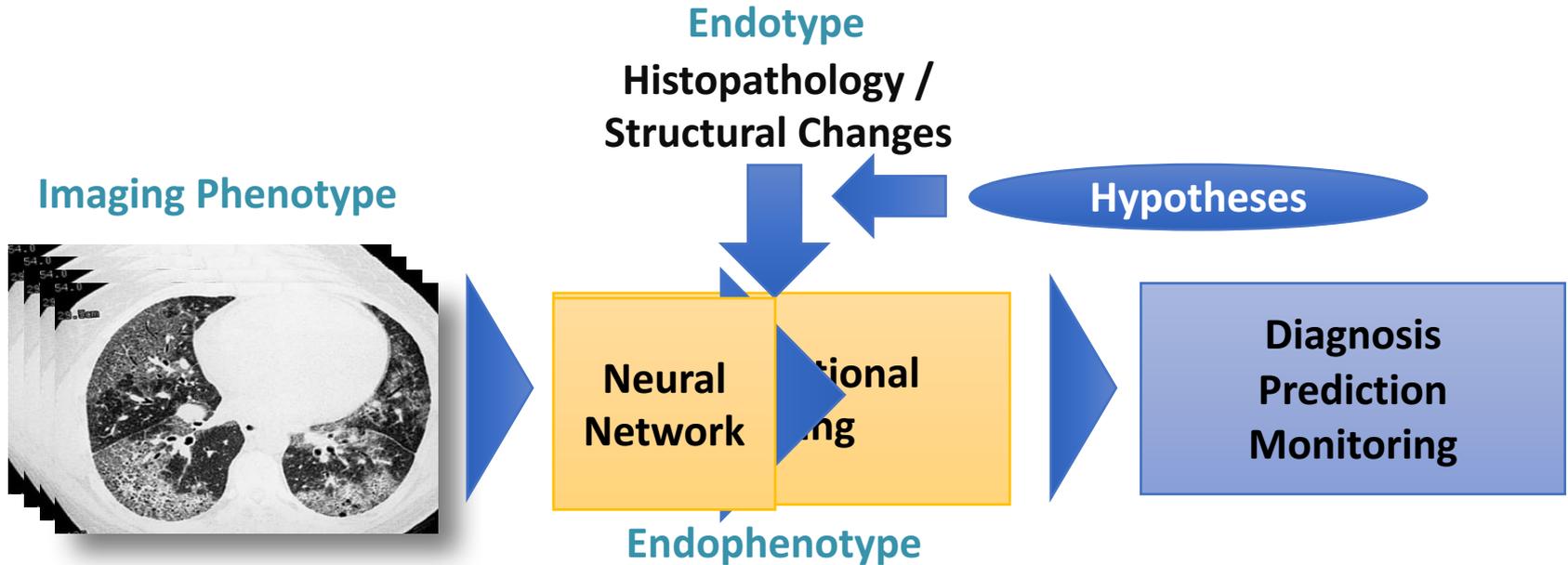
Parenchymal Subtyping Predicts Mortality



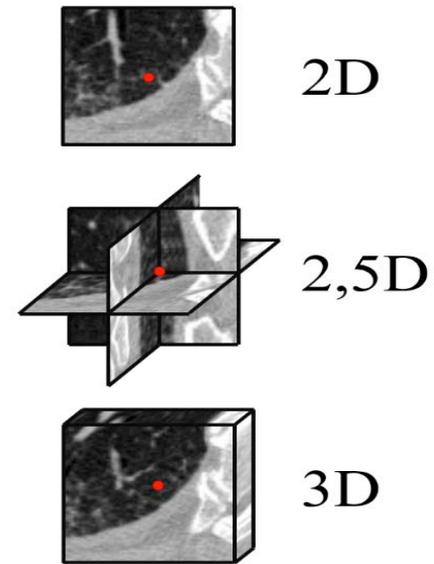
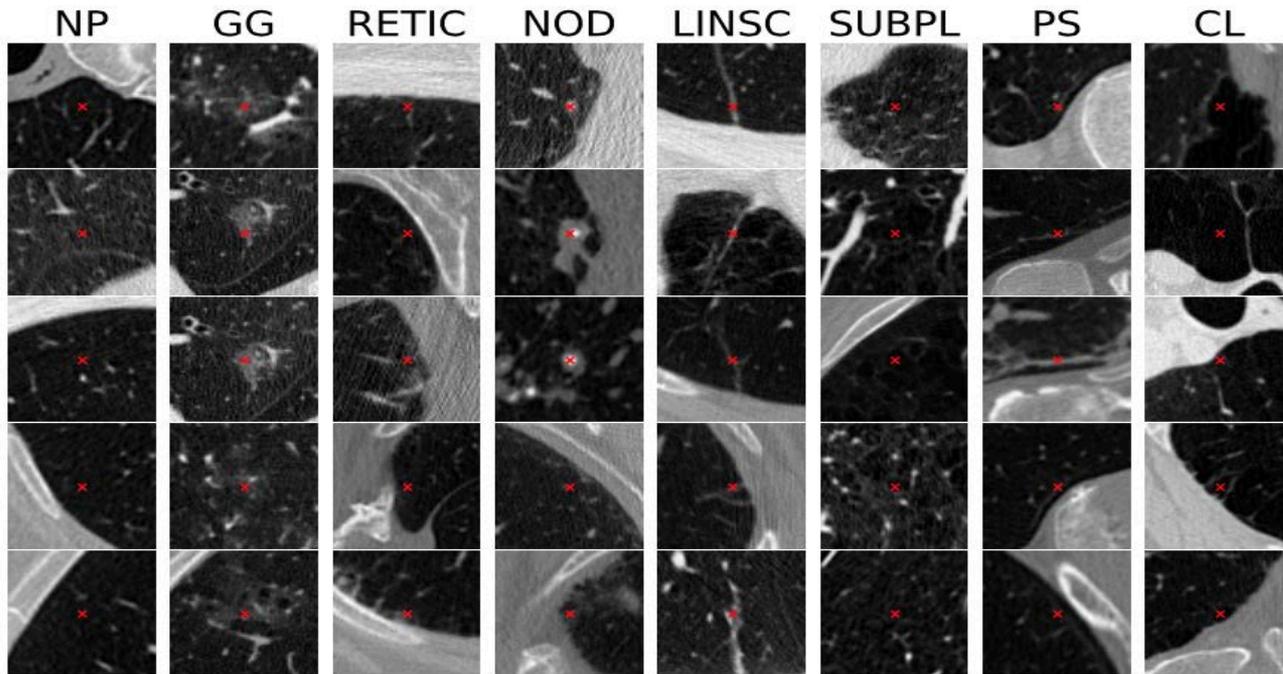
The AI Revolution: A new paradigm?



Direct Regression of Outcomes

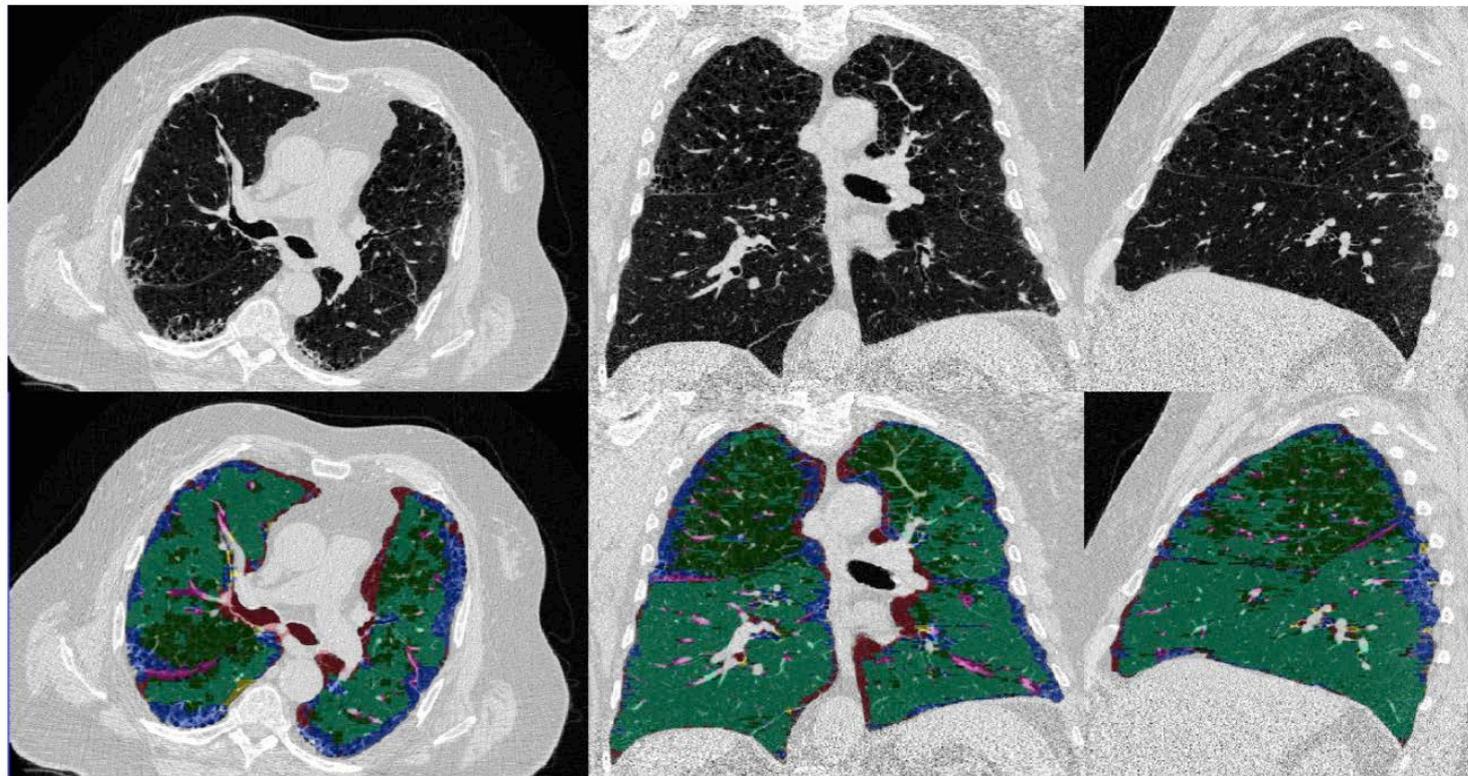


ILA subtyping with Deep Learning



Ensemble of Convolutional Neural Networks

BCNN ^{2D}	MSTAGE-CNN ^{2D}	MCONTEXT-CNN ^{2D}	BCNN ^{2.5D}	MSTAGE-CNN ^{2.5D}	BCNN ^{3D}	MSTAGE-CNN ^{3D}
<i>Input:</i> 48x48	<i>Input:</i> 48x48	<i>Input:</i> 48x48	<i>Input:</i> 3x48x48	<i>Input:</i> 3x48x48	<i>Input:</i> 48x48x7	<i>Input:</i> 48x48x7
Conv: 48@3x3	Conv:48@3x3	Conv: 48@3x3	Conv: 48@3x3	Conv:48@3x3	Conv: 48@3x3x2	Conv:48@3x3x2
Conv: 48@3x3	Conv: 48@3x3	Conv: 48@3x3	Conv: 48@3x3	Conv: 48@3x3	Conv: 48@3x3x2	Conv: 48@3x3x2
MaxPool:2x2	MaxPool:2x2	MaxPool:2x2	MaxPool:2x2	MaxPool:2x2	MaxPool:2x2x1	MaxPool:2x2x1
BatchNorm	BatchNorm	BatchNorm	BatchNorm	BatchNorm	BatchNorm	BatchNorm
Conv:48@3x3	Conv:48@3x3	Conv:48@3x3	Conv:48@3x3	Conv:48@3x3	Conv:48@3x3x2	Conv:48@3x3x2
Conv:48@3x3	Conv:48@3x3	Conv:48@3x3	Conv:48@3x3	Conv:48@3x3	Conv:48@3x3x2	Conv:48@3x3x2
MaxPool:2x2	MaxPool:2x2	MaxPool:2x2	MaxPool:2x2	MaxPool:2x2	MaxPool:2x2x1	MaxPool:2x2x1
BatchNorm	BatchNorm	BatchNorm	BatchNorm	BatchNorm	BatchNorm	BatchNorm
FC: 64	FC: 64	FC: 64	FC: 64	FC: 64	FC: 128	FC: 64
	MaxPool: 6x6	<i>Input:</i> 64x64		MaxPool: 6x6		MaxPool: 6x6x1
	BatchNorm	Conv: 48@3x3		BatchNorm		BatchNorm
	FC: 64	Conv: 48@3x3		FC: 64		FC: 64
		MaxPool:2x2				
		BatchNorm				
		Conv:48@3x3				
		Conv:48@3x3				
		MaxPool:2x2				
		BatchNorm				
		FC: 64				
	Concat: 128	Concat: 128		Concat: 128		Concat: 128
FC: 112	FC: 112	FC: 112	FC: 112	FC: 112	FC: 112	FC: 112
Softmax: 8	Softmax: 8	Softmax: 8	Softmax: 8	Softmax: 8	Softmax: 8	Softmax: 8



NP



RETIC



NOD



SUBPL



LINSC



GG



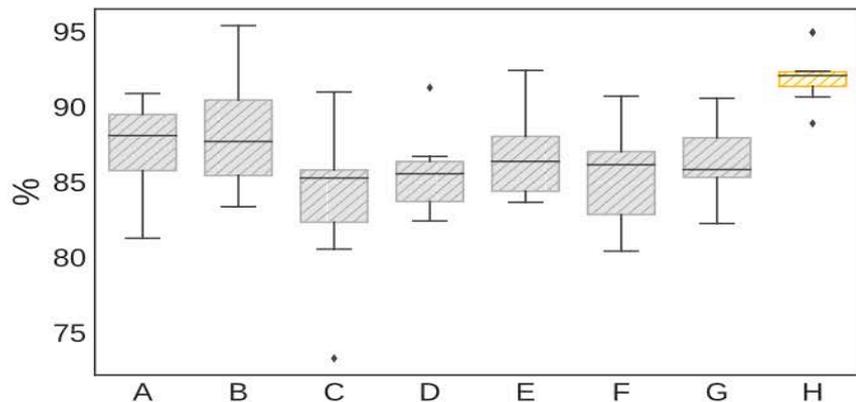
PS



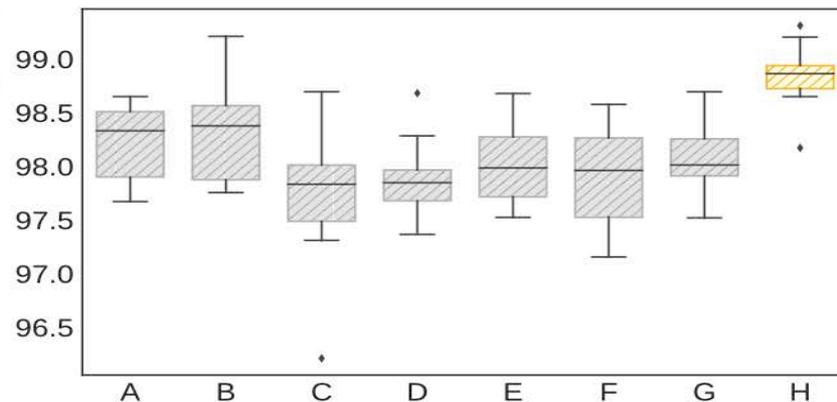
CL

Ensemble stabilize performance

- Training in 37,424 locations
- Testing in 36,336 locations



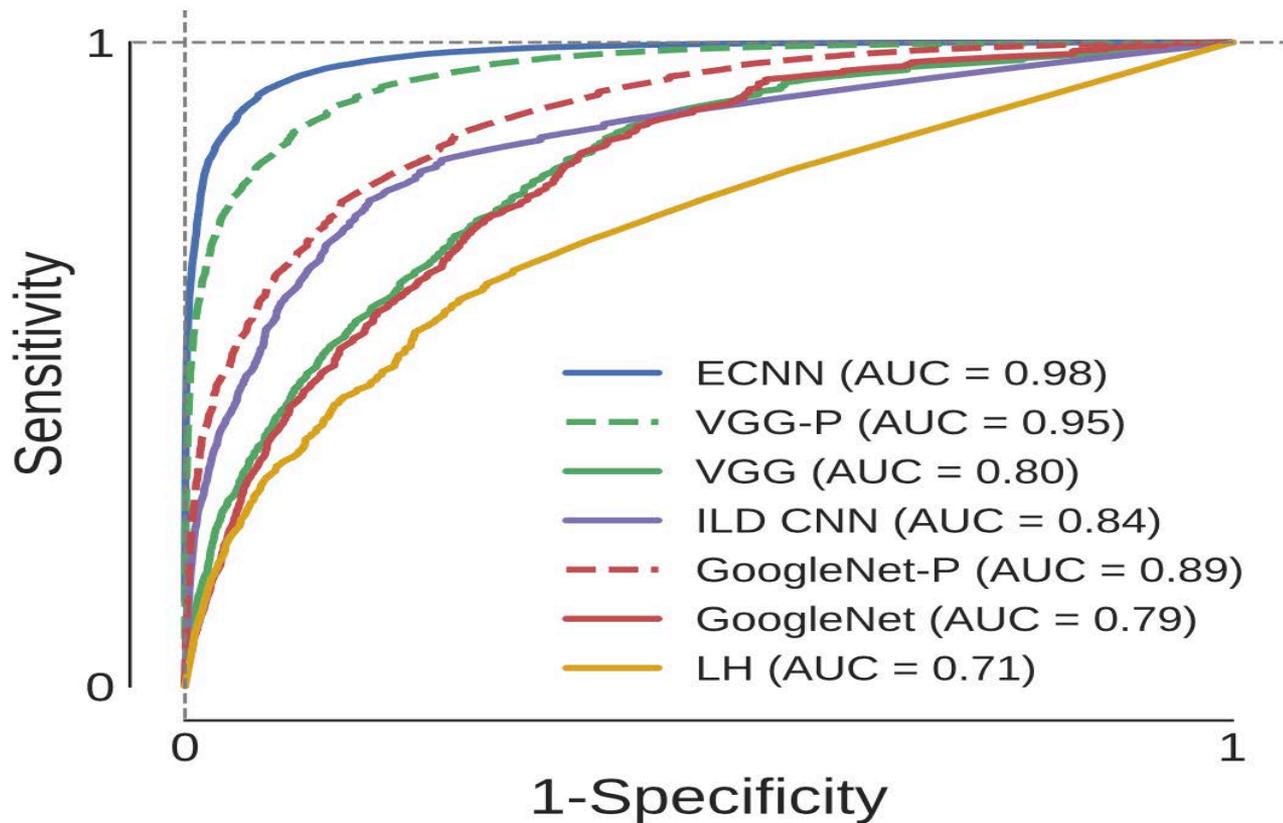
Sensitivity



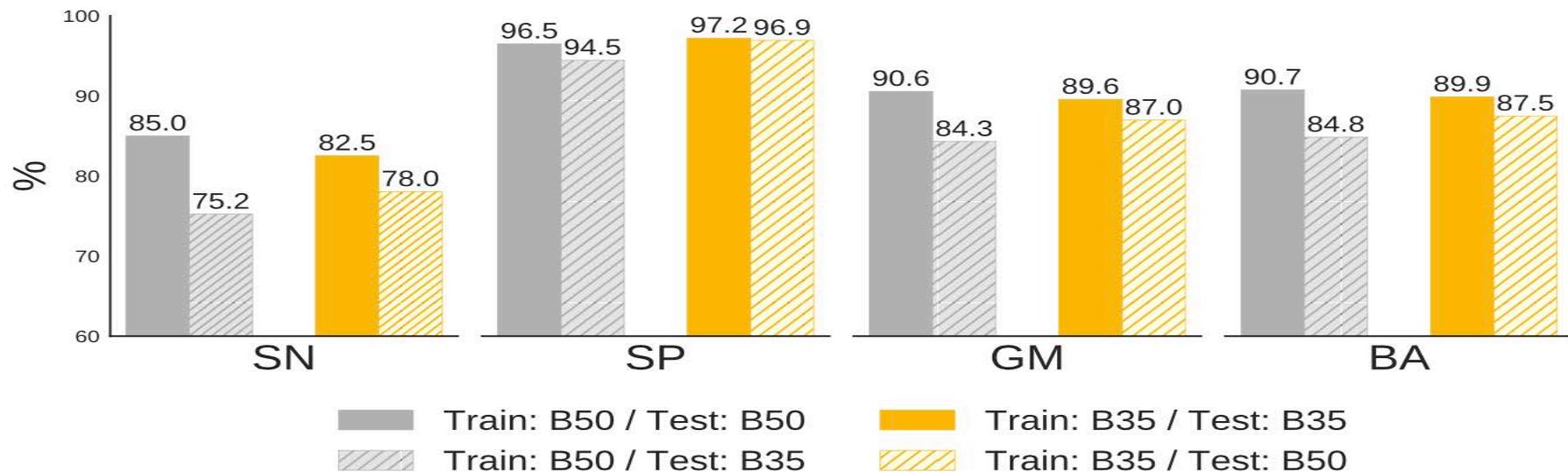
Specificity

A: BCNN^{2D} B: MSTAGE – CNN^{2D} C: MCONTEXT – CNN^{2D} D: BCNN^{3D}
E: MSTAGE – CNN^{3D} F: BCNN^{2.5D} G: MSTAGE – CNN^{2.5D} H: Ensemble

Comparison with other architectures



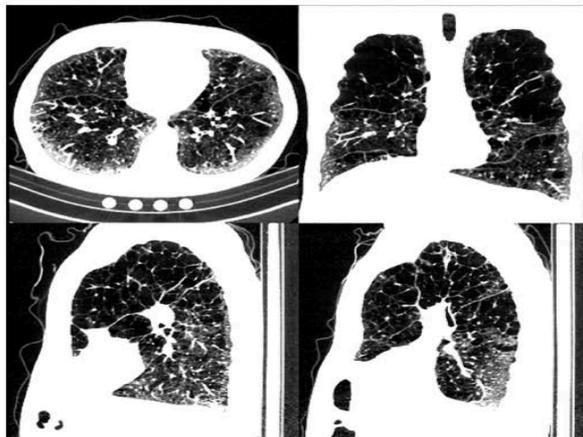
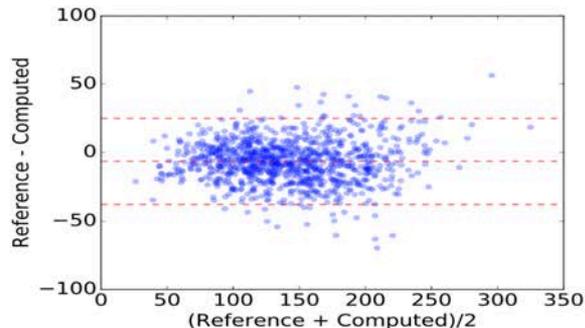
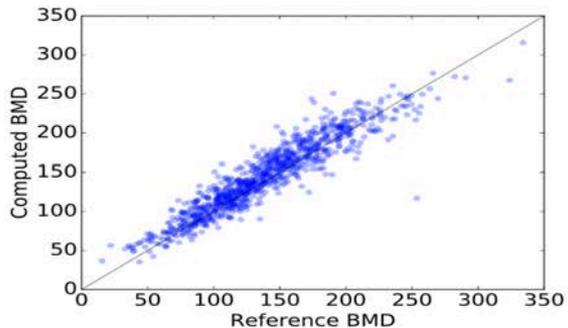
Reconstruction Stability



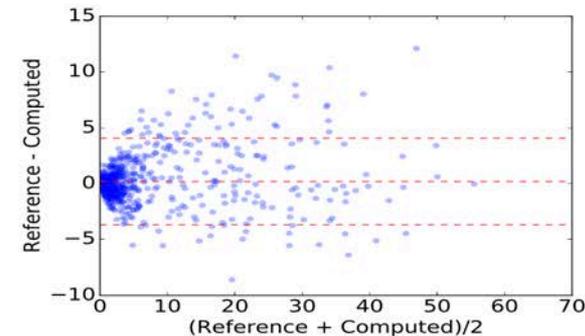
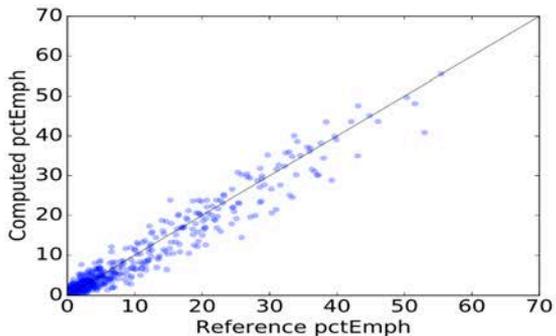
Direct Biomarker Regression



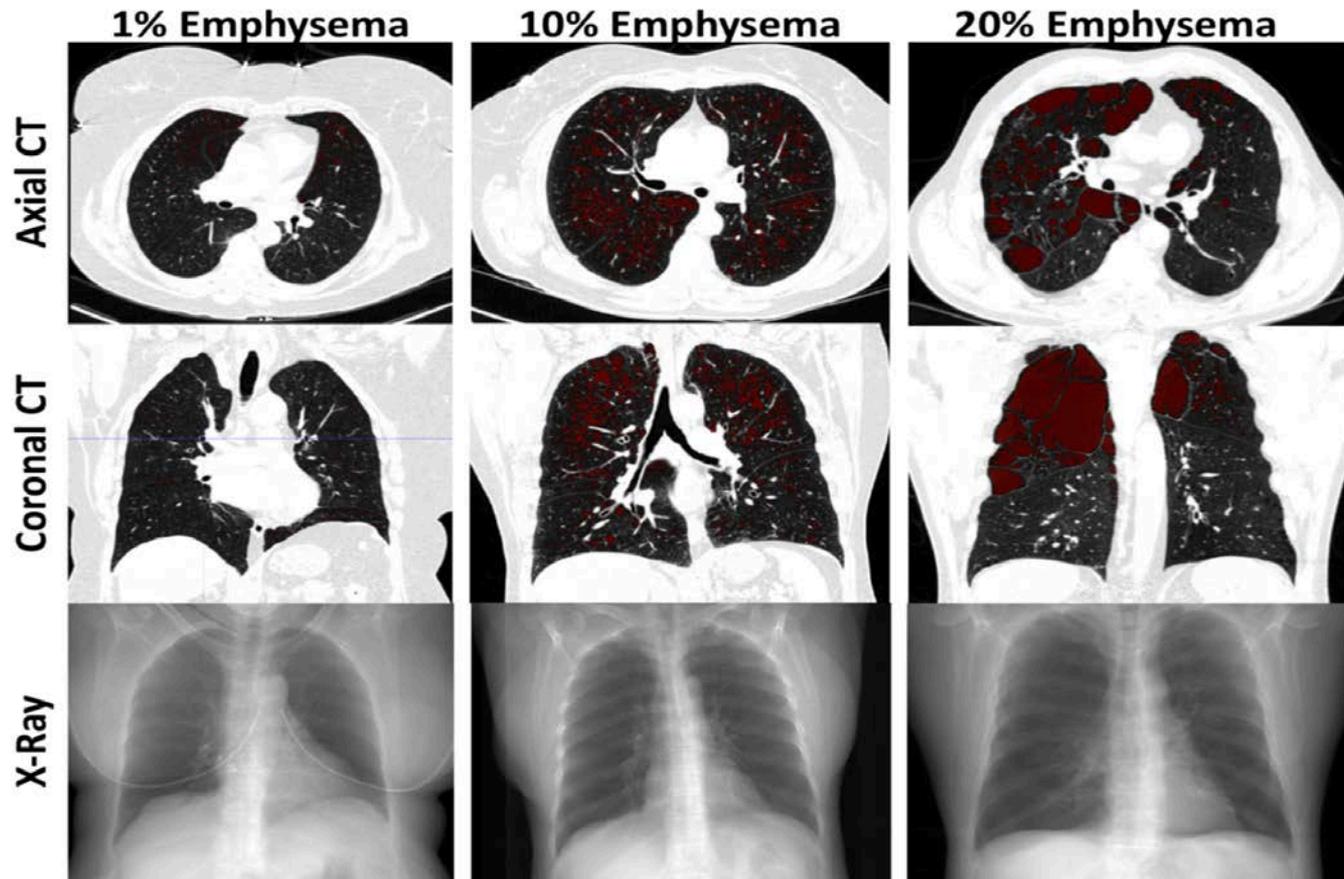
Bone Mineral Density



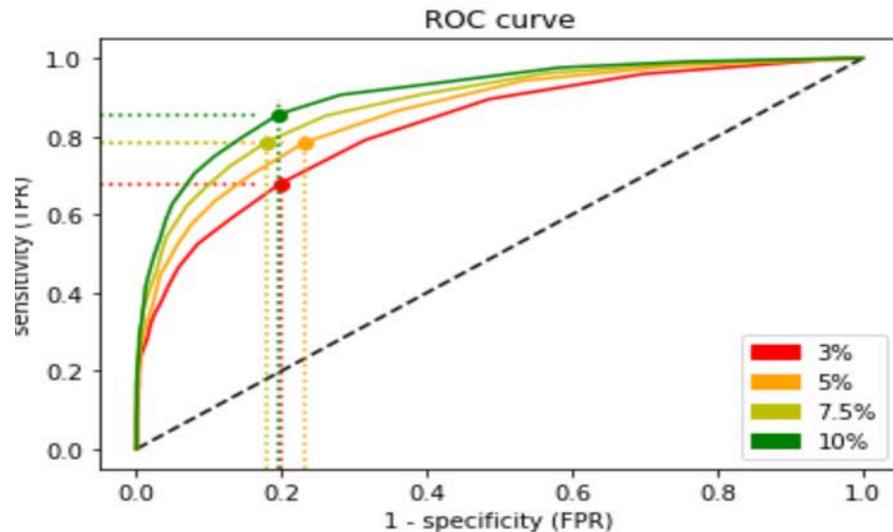
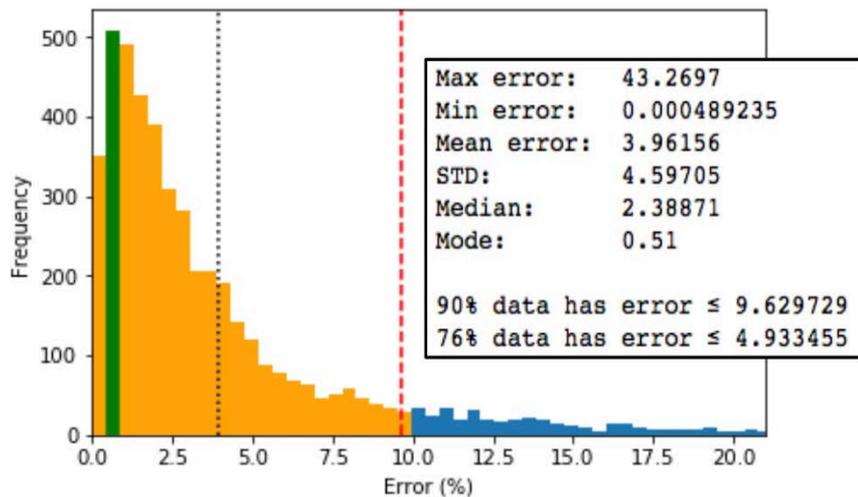
Emphysema Score



Emphysema Scoring From X-Ray



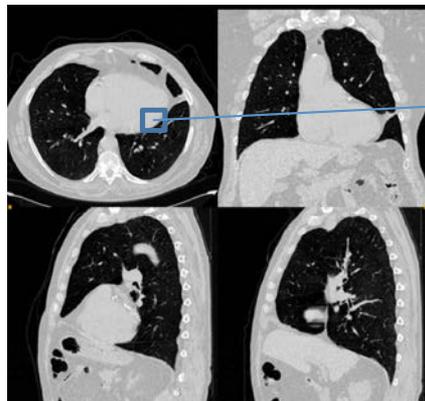
Emphysema Scoring From X-Ray



Artificial Intelligence and Integral Diagnosis

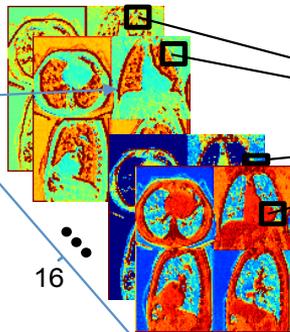
X_i

Input: 512x512x1



Conv + MaxPooling

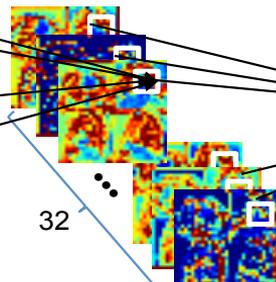
C1: 128x128x16



$\{w_n\}_{L1}$

Conv + MaxPooling

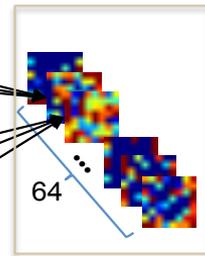
C2: 32x32x32



$\{w_n\}_{L2}$

Conv + MaxPooling

C3: 8x8x64



$\{w_n\}_{L3}$

FC1: 1024



$\{w_n\}_{L4}$

Outcome \ Clinical Phenotype

Y_i

Deep Learning Performance for COPD Assessment

	COPDGene		Replication
	Reconstruction Kernel		ECLIPSE
	STD (n=1,000)	SHARP (n=1,000)	(n=1,547)
FEV1 (r coef.)	0.735 [0.705 - 0.762]	0.735 [0.705 - 0.762]	0.64 [0.542 - 0.756]
GOLD Stage (Accuracy)	51.2% / 74.7%	52.0% / 73.8%	29.4% / 74.6%
ARD AUC	0.633 [0.602 - 0.663]	0.627 [0.597 - 0.658]	0.55 [0.51 - 0.62]
Mortality AUC	0.72 [0.6 - 0.78]	0.709 [0.58 - 0.737]	0.6 [0.52 - 0.71]

Conclusions

- Parenchymal Injury is a crucial marker of the host inflammatory response to tobacco injury.
- Quantitative assessment of parenchymal injury (emphysema and ILD) is clinically relevant even in asymptomatic.
- Artificial Intelligence may offer a new paradigm for image-based biomarker computation
 - Quality and thorough testing are a key factor for translation

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- George Washko

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 - COPDGene Study
- COPDGene Investigators



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