Supplemental Material

Supplemental A. Conversion of qualitative to quantitative measure for ROBINS-I table.

The above ROBINS-I table depicts the mean score achieved from quantifying the low, moderate, high, and unclear-bias attributes. Then these values were compared to the AP(**ai**)Bias methodology (Table 5) and PROBAST (Table 2) to find the common studies. This is shown using the Venn diagram (Figure 12).

Low Risk		Moderate Risk		High Risk		Unclear Risk		Total Score	Mean	Rank
Study	C1	C2	C3	C4	C5	C6	C7			
[62]	5	3	5	5	3	5	5	31	4.4	1
[69]	5	5	5	3	3	5	5	31	4.4	2
[56]	3	5	5	5	1	5	3	27	3.9	3
[79]	5	5	3	3	5	3	3	27	3.9	4
[72]	5	1	5	3	5	3	3	25	3.6	5
[81]	3	5	3	3	5	5	1	25	3.6	6
[47]	5	5	1	5	5	0	3	24	3.4	7
[44]	5	5	5	3	5	0	0	23	3.3	8
[42]	5	5	5	0	5	0	3	23	3.3	9
[78]	5	1	1	0	5	5	3	20	2.9	10
[64]	1	1	5	3	1	3	1	15	2.1	11
[40]	1	1	5	3	1	3	1	15	2.1	12
[76]	3	1	1	3	1	3	3	15	2.1	13
[60]	H	1	5	5	1	1	1	14	2.0	14
[43]	1	1	3	3	1	3	1	13	1.9	15
[46]	1	1	3	3	1	3	1	13	1.9	16
[55]	1	1	1	3	1	3	1	11	1.6	17
[74]	H	1	1	3	1	3	1	10	1.4	18
[45]	H	1	1	0	0	1	1	4	0.6	19
Parameters	Bias due to confounding	Bias in selection of participants into the study	Bias in classification of interventions	Bias due to deviations from intended interventions	Bias due to missing data	Bias in measurement of outcomes	Bias in selection of the reported result			
		Pre-intervention	**At-intervention**		**Post-intervention**					

Supplemental B: Acronym list

AI: Artificial intelligence; **ai**SR: AI-based systematic reviews; **AP(ai)Bias**: AtheroPoint-AI-Bias; **ARDS**: Acute respiratory distress syndrome; **BC**: Binary classification; **CAD**: Computer-aided diagnosis; **COVID-19**: Coronavirus disease 2019; **CT**: Computed tomography; **CXR**: Chest X-ray; **DL**: Deep learning; **DNA**: Deoxyribonucleic acid; **GGO**: Ground glass opacities; **IRF**: Iterative ReliefF; **LOOCV**: Leave-One-Out Cross-Validation; **LRT**: Lower respiratory tract; **MC**: Multiclass classification; **ML**: Machine learning; **NET**: Neutrophil extracellular traps; **PET**: Positron emission tomography; **PRISMA**: Preferred Reporting Items for Systematic Reviews and Meta-Analysis; **ResExLBP**: Residual Exemplar Local Binary Pattern; **ROBINS-I**: Risk of Bias In Non-randomized Studies - of Interventions; **RL**: Recurrent learning; **RT-PCR**: Reverse transcription polymerase chain reaction; **SEN**: Sensitivity; **SPE**: Specificity; **SNR**: Signal-to-noise ratio; **TL**: Transfer learning; **X-Ray**: Röntgen radiation.

Supplemental C. Conversion of qualitative to quantitative measure for PROBAST table.

The above PROBAST table depicts the mean score achieved from quantifying the low, moderate, high, and unclear-bias attributes. Then these values were compared to the AP(**ai**)Bias methodology (Table 5) and ROBINS-I (Table 3) to find the common studies. This intersection is shown using the Venn diagram (Figure 12).

ID	Participants	Predictors	Outcomes	Analysis	Total Score	Mean	Rank
[62]	5	5	5	5	20	5.0	1
[69]	5	3	3	5	16	4.0	2
[79]	5	3	5	3	16	4.0	3
[81]	3	5	5	3	16	4.0	4
[72]	3	5	3	3	14	3.5	5
[78]	3	3	5	3	14	3.5	6
[44]	5	5	3	0	13	3.3	7
[47]	5	3	5	0	13	3.3	8
[42]	5	3	5	0	13	3.3	9
[56]	3	5	3	0	11	2.8	10
[43]	1	3	3	3	10	2.5	11
[60]	1	5	3	1	10	2.5	12
[40]	1	3	3	1	8	2.0	13
[64]	1	3	3	0	7	1.8	14
[76]	3	1	3	0	7	1.8	15
[55]	1	1	3	1	6	1.5	16
[45]	1	1	3	1	6	1.5	17
[46]	1	0	3	1	5	1.3	18
[74]	1	1	3	0	5	1.3	19

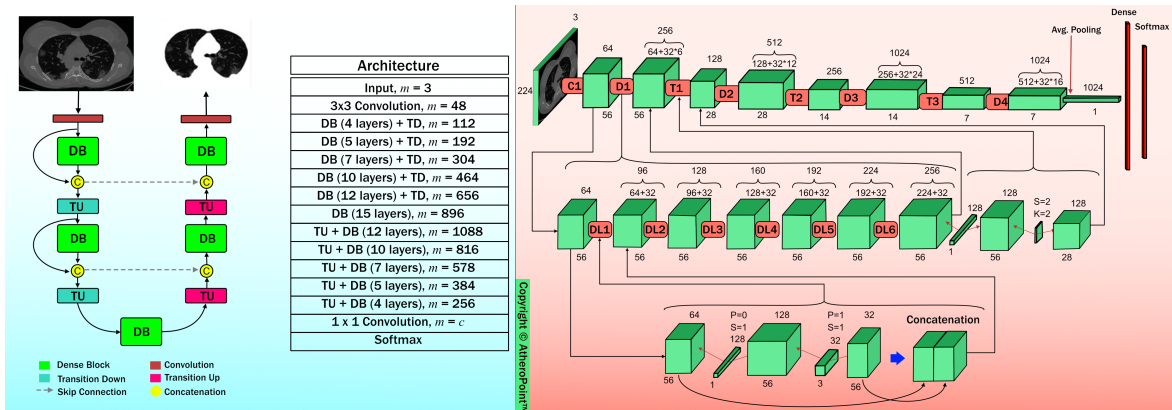## Supplemental D. DL Architectures

Figure A. **Left**: Arch. of FC-DenseNet103 and parameters of FC-DenseNet103 architecture; **Right:** DenseNet121-FPN arch. (Courtesy of AtheroPoint™, CA, USA).
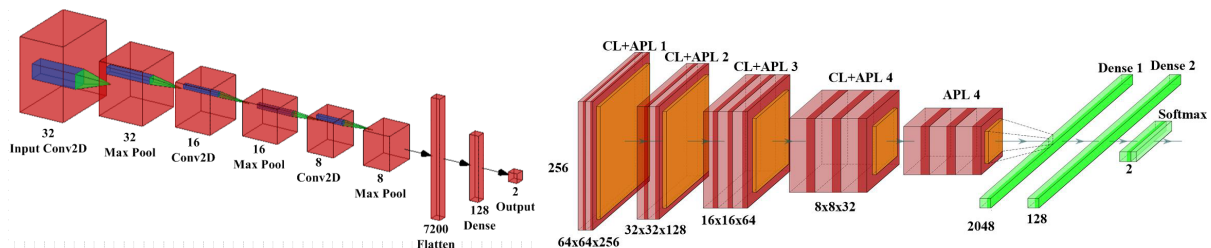

Figure B. **Left**: DL architecture CNN; **Right**: TL architecture VGG-Net (Courtesy of AtheroPoint™, CA, USA).