Deep Learning based Segmentation of Tumors from TNBC PDX MR Images and Sensitivity of Radiomics Features to Segmentation Probability Boundaries

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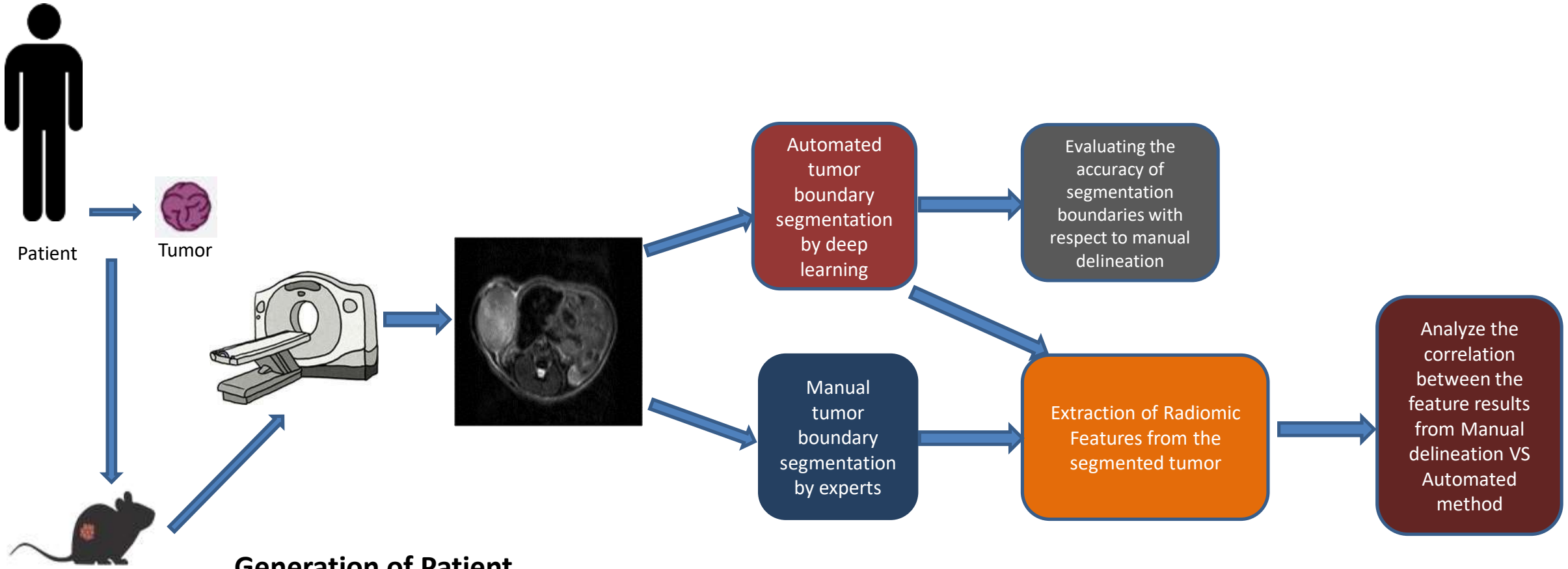
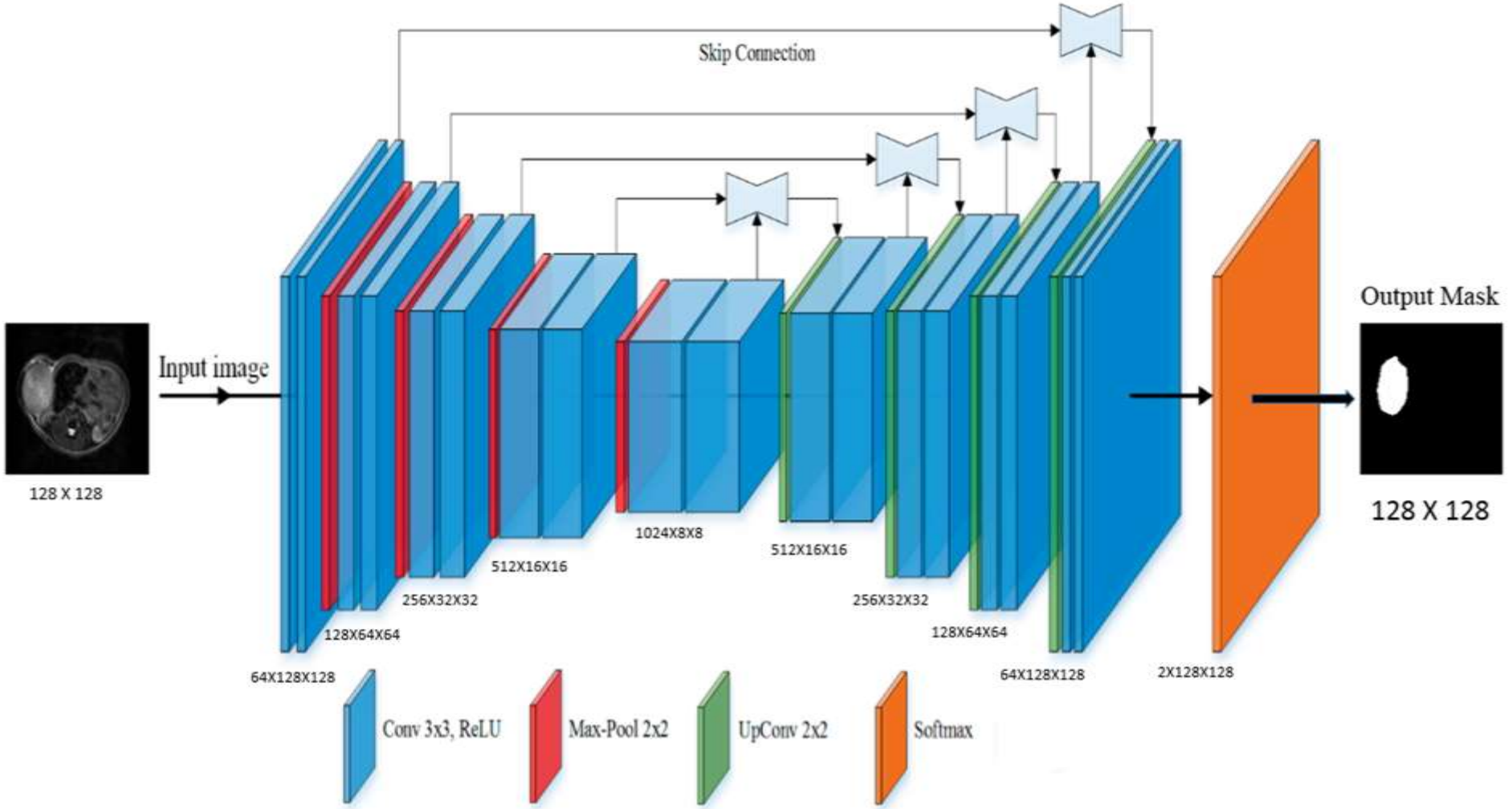
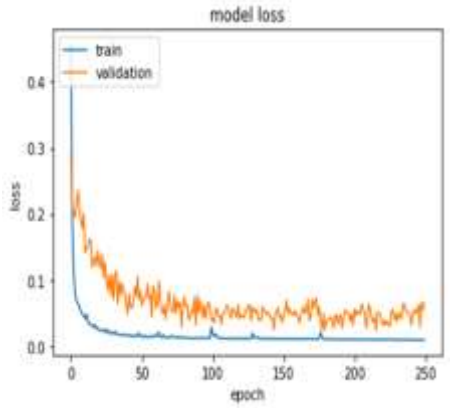
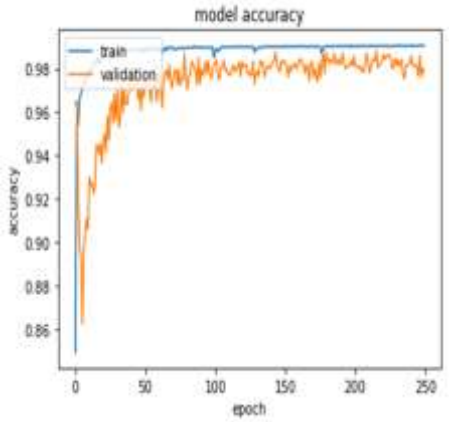
Proposed methodology to analyze the sensitivity of radiomics features on segmentation boundary



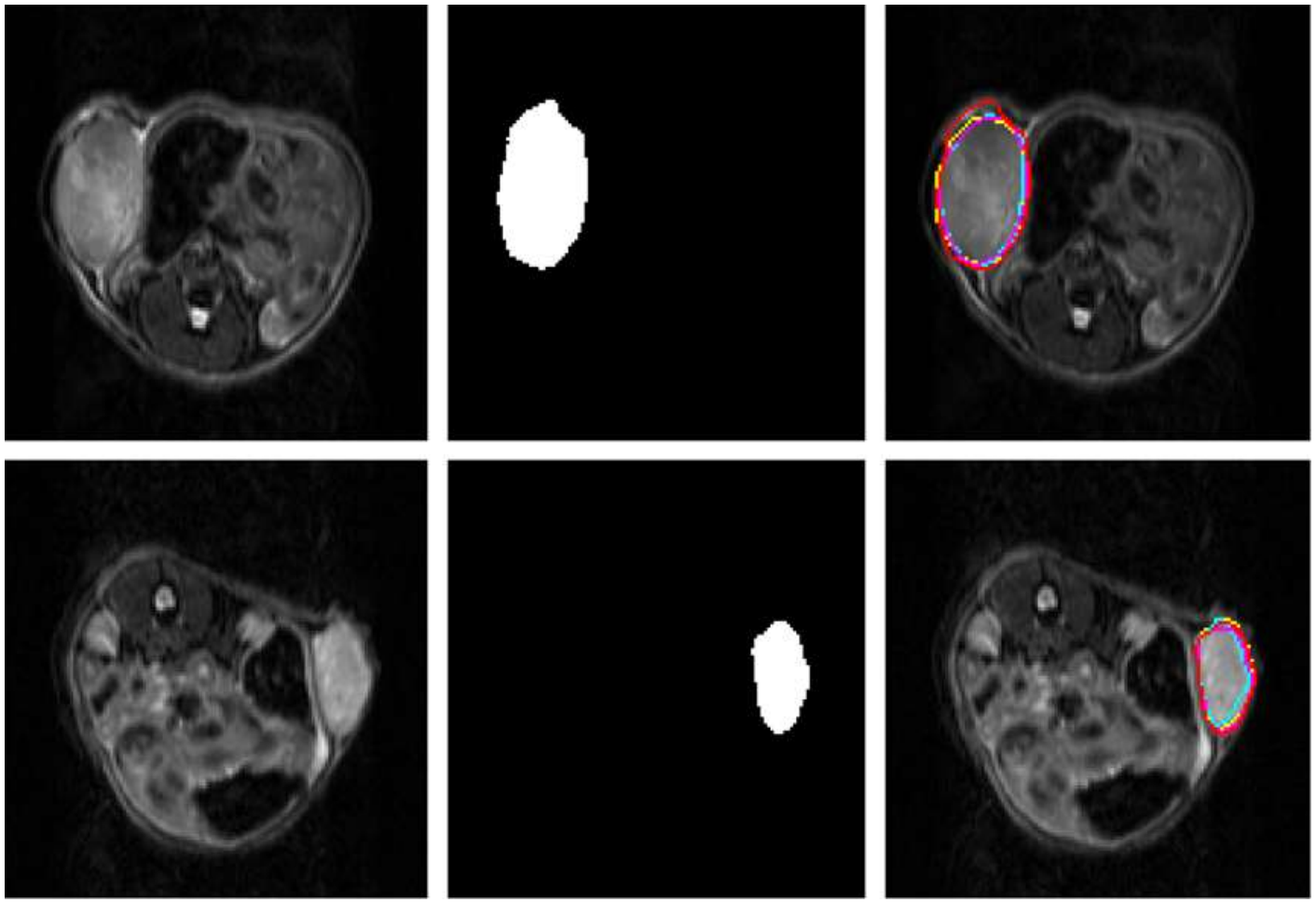
Deep Dense UNet is used to create segmentation probability masks







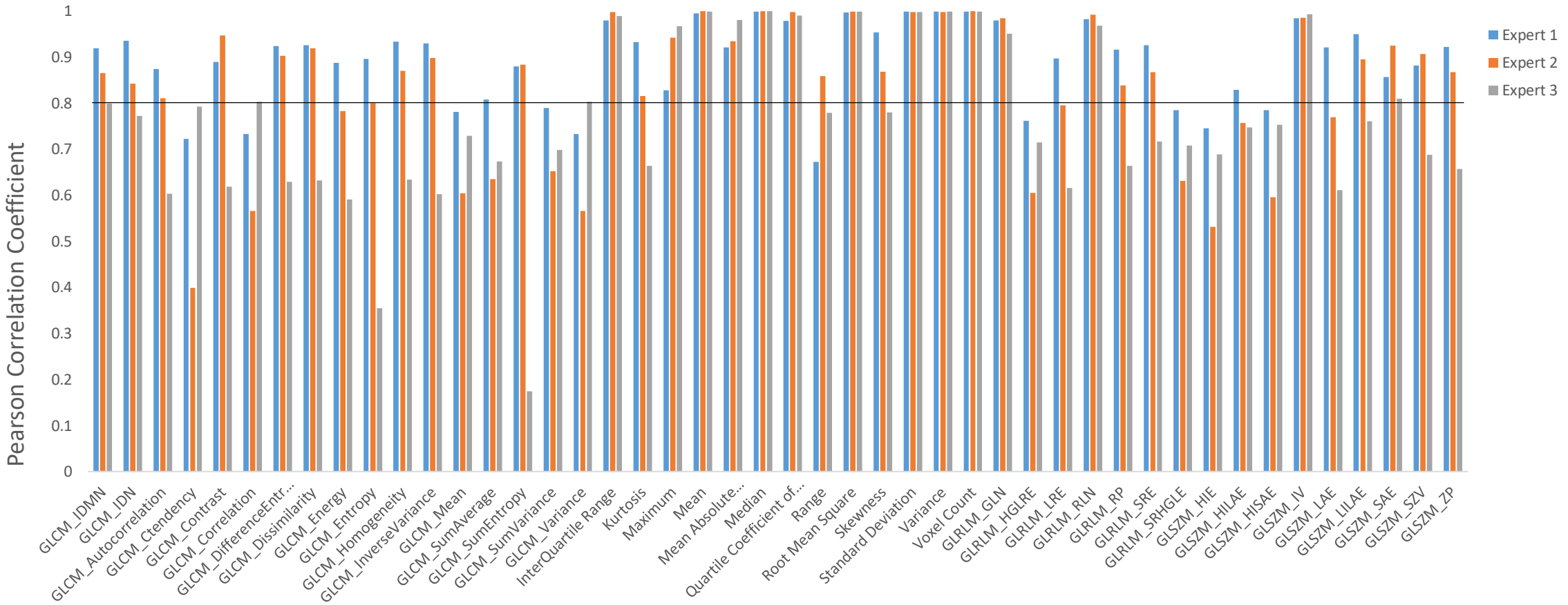
Automated Segmentation Results with respect to experts



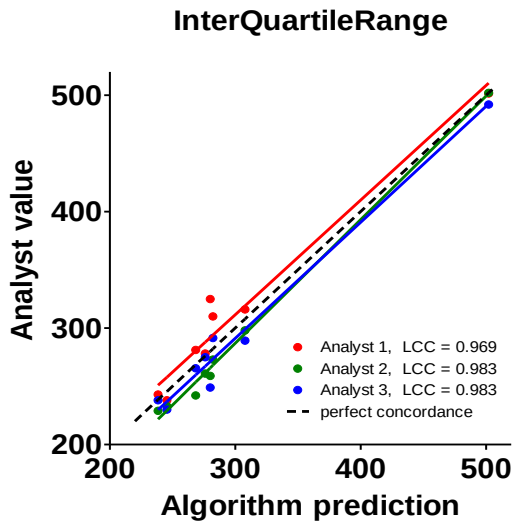
Dice Similarity Coefficient				
	Expert 1	Expert 2	Expert 3	Mean
Mouse 1	0.9327	0.9449	0.9365	0.938 ± 0.0062
Mouse 2	0.9598	0.9443	0.942	0.948 ± 0.0096
Mouse 3	0.9611	0.9527	0.9348	0.949 ± 0.0134
Mouse 4	0.92133072	0.94791756	0.9480298	0.9390 ± 0.0153
Mouse 5	0.9389288	0.93600421	0.9254403	0.9334 ± 0.0071
Mouse 6	0.9153825	0.93427186	0.9122935	0.9206 ± 0.0118
Mouse 7	0.9414543	0.92615133	0.9584756	0.9420 ± 0.0161
Mouse 8	0.9559241	0.94579806	0.9410644	0.9475 ± 0.0075

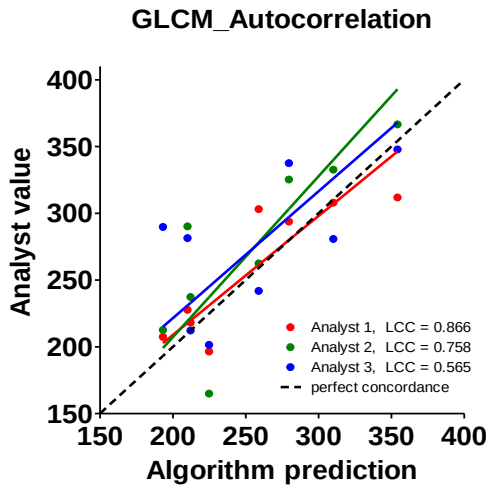
Jaccard Index				
	Expert 1	Expert 2	Expert 3	Mean
Mouse 1	0.8754	0.8961	0.8809	0.8841 ± 0.0107
Mouse 2	0.9234	0.8948	0.891	0.9030 ± 0.0177
Mouse 3	0.9232	0.91	0.8783	0.9038 ± 00231
Mouse 4	0.85419366	0.90105166	0.9012233	0.8854 ± 0.0271
Mouse 5	0.88506939	0.88011896	0.8713384	0.8788 ± 0.0069
Mouse 6	0.85574947	0.87672449	0.8492987	0.8605 ± 0.0143
Mouse 7	0.88962699	0.8626382	0.9202713	0.8908 ± 0.0288
Mouse 8	0.91590742	0.89743256	0.8906753	0.9013 ± 0.0130

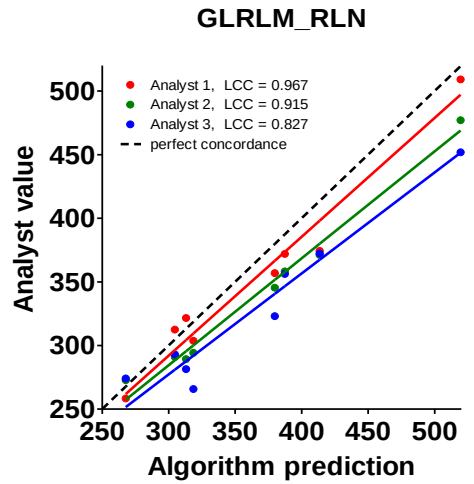
Pearson Correlation Coefficient shows the correlation between the feature values extracted from manual delineation VS automated method

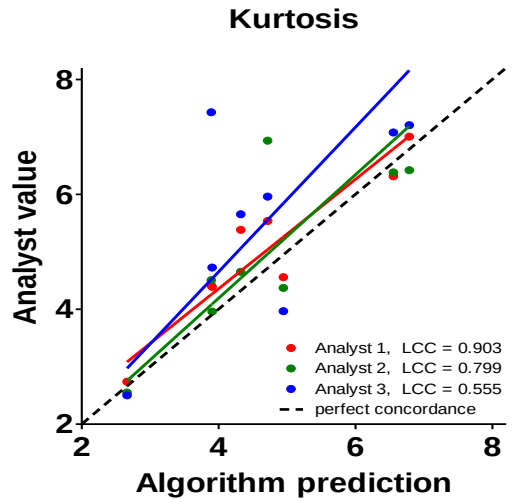


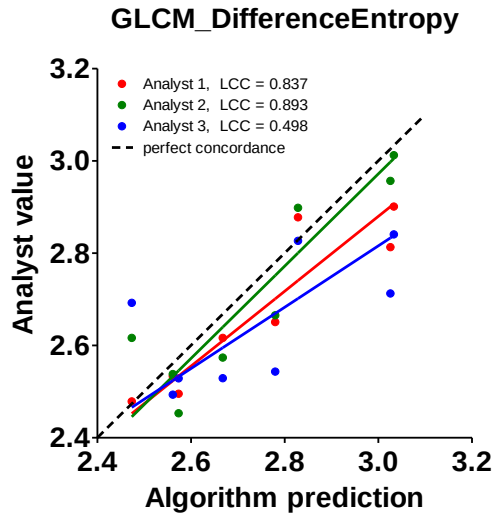
Lin's Concordance Correlation is used to show the concordance between the manual delineation and the algorithm prediction

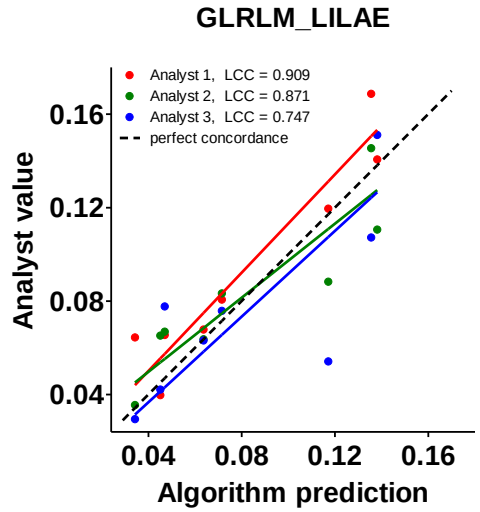












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