



Feature Disentanglement to Aid Imaging Biomarker Characterization for Genetic Mutations

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How? Life atures of 19/20 co-gain

Mutated ⇒ Higher median survival





Challenges

- Lack of data
- High class imbalance

- High inter-class similarity
- High intra-class diversity

Inter-class similarity







Assessment pipeline

- Do visual indicators exit?
- Classification using multiple state-ofthe-art models and validation methods

Presence

Characterization

- What are these features?
- Isolate and quantify various macrofeatures

• Are these features reproducible?

• Use GAN to try and recreate these indicators

Reproducibility





Reproducibility of Biomarkers

- If we use biomarkers to generate synthetic images, does it suggest mutation presence?
- We propose a generative model which can tackle the following problems:



FeaD-GAN: Feature Disentanglement GAN







Texture Loss

Shape Loss



Results: Quantitative

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RX: Representation of data (extent of features represented); ACC: Accuracy; SEN: Sensitivity; SPEC: Specificity and DIC: Dice Score. IL: Image Level; PL: Patient Level

Dataset	RX	ACC (PL)	ACC (IL)	SEN (IL)	SPEC (IL)	DIC (IL)
38	R1	0.92(0.08)	0.89 (0.06)	0.85(0.07)	0.95(0.05)	0.87(0.08)
	R2	0.95(0.03)	0.92(0.05)	0.88(0.06)	0.98(0.02)	0.88(0.08)
Dataset A	R3	0.85(0.08)	0.80(0.08)	$0.67\ (0.09)$	0.84 (0.06)	0.69(0.09)
	R4	0.70(0.06)	0.68(0.07)	0.65(0.09)	0.75(0.05)	0.66(0.08)
	R1	0.92(0.09)	0.88(0.07)	$0.85\ (0.08)$	0.94(0.04)	0.86(0.08)
Synthetic	R2	0.95(0.03)	0.90(0.08)	0.87(0.07)	0.98(0.02)	0.88(0.09)
$(Dataset \ A)$	R3	0.85(0.08)	0.82 (0.10)	0.70(0.08)	0.86(0.06)	0.68(0.08)
	R4	0.68(0.06)	0.66(0.07)	0.62(0.07)	0.74(0.5)	0.62 (0.08)





Results: Qualitative







Conclusions

- Visual indicators of mutations that correlate to median survival are present in MRI
- Location, texture and shape are significant indicative features
- The features are reproducible
- FeaD-GAN:
 - Can faithfully generate good quality images from limited dataset
 - Can capture data diversity

Thank You!

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