AI-based detection of molecular biomarkers directly from H&E scanned slides

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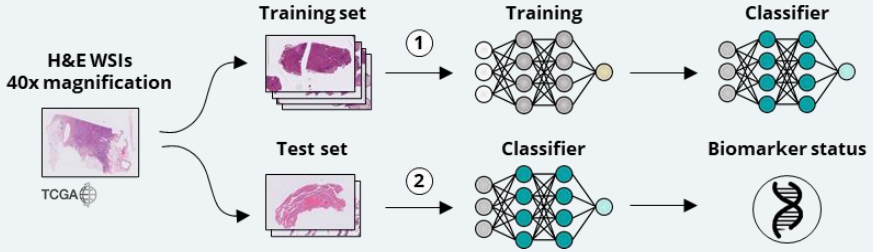
Background

Cancer diagnosis and treatment rely on the accurate identification of morphological, molecular and genetic biomarkers. As technology and science progress, the number of biomarkers and testing required increases. Professional guidelines structure the biomarkers testing methodology. Yet, testing capabilities, options, and interpretation vary significantly between countries and medical centers in practice.

Here, we present an image-based solution for molecular profiling directly from hematoxylin and eosin (H&E) stained pathology slide images. Our results show high performance of the algorithm predictions for all genes tested.

Experimental design



- H&E stained FFPE specimens whole slide images (WSIs) scanned at 40x magnification were downloaded from the TCGA database.
- The cohort was randomly split into training (75%) and test (25%) sets.
- (1) Training of neural network for biomarker status classification was performed on patches created using an on-the-fly sampling method.
- (2) Validation of classifiers was then performed using the test set WSIs, and specificity and sensitivity were calculated for each gene classifier.

Results

Biomarker	Tissue	N	Sensitivity (%)	Specificity (%)
NTRK fusion	Thyroid	3/102	100	93.9
RET fusion	Thyroid	5/102	100	95.7
FGFR3 fusion	Bladder	2/96	100	95.7
BRAF	Thyroid	48/102	91.7	90.7
KRAS	Lung	10/104	100	88.3
EGFR	Lung	6/142	83.3	97.1

Conclusions

- Molecular diagnosis in routine oncology practice using the current testing methodologies has many challenges including cost, turnaround time and interpretation.
- Image-based prediction of biomarker status provides a fast, accessible and standardized alternative.
- The AI solution presented here uses routinely prepared pathological slides that can be used for the prediction of multiple biomarker status without the requirement for additional material or substantial human labor.
- Implementation of such a system in medical centers can support real-time molecular profiling of cancer patients with different tumor origins and stages.

* Disclosure statement: Prof. Peled is a consultant for Imagene-AI

https://imagene-ai.com

* The results shown here are based upon data generated by the TCGA Research Network: https://www.cancer.gov/tcga