METSCAN™, a novel and proprietary algorithm to predict the metastatic potential of primary tumor patients

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The 19th Biennial Congress 2022 MRS METASTASIS RESEARCH SOCIETY

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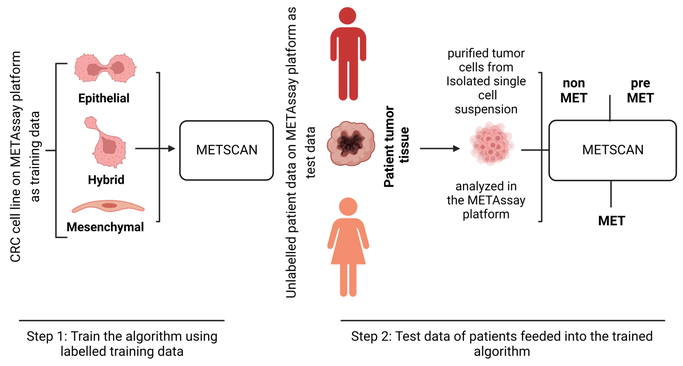
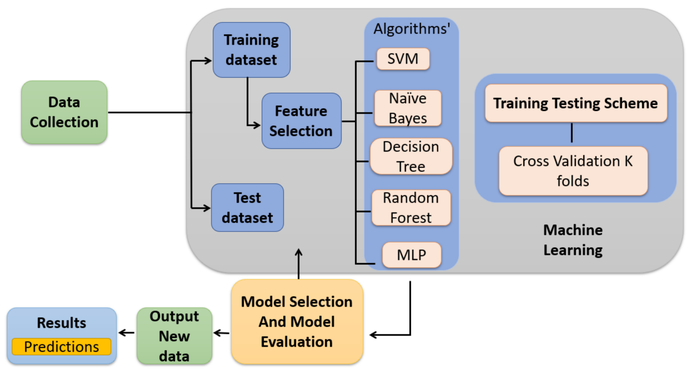
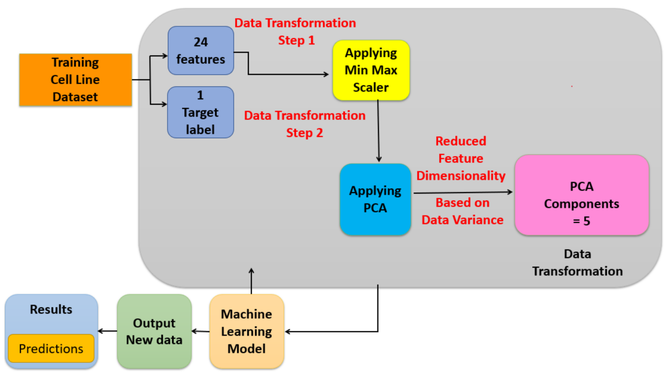
INTRODUCTION



- The probability of primary colorectal tumor patients developing metastasis is currently dependent on their node status, which is not always accurate.
- Mestastop has integrated the functional properties from primary patient tumor-derived cells into a learning algorithm to predict the metastatic potential of pathological non-metastatic grade patients, blinded of tumor staging or node status.
- We have duplicated the complete and complex metastasis biology *in vitro*, distinguishing functional differences, between moving and growing tumour cells in multiple cell lines, represented by the METAssay™ platform
- Data derived from this platform was used to train a learning algorithm METSCAN™, which distinguishes cells having different moving and growing phenotypes and summatively predicts a tumor's probability to move

METHODS





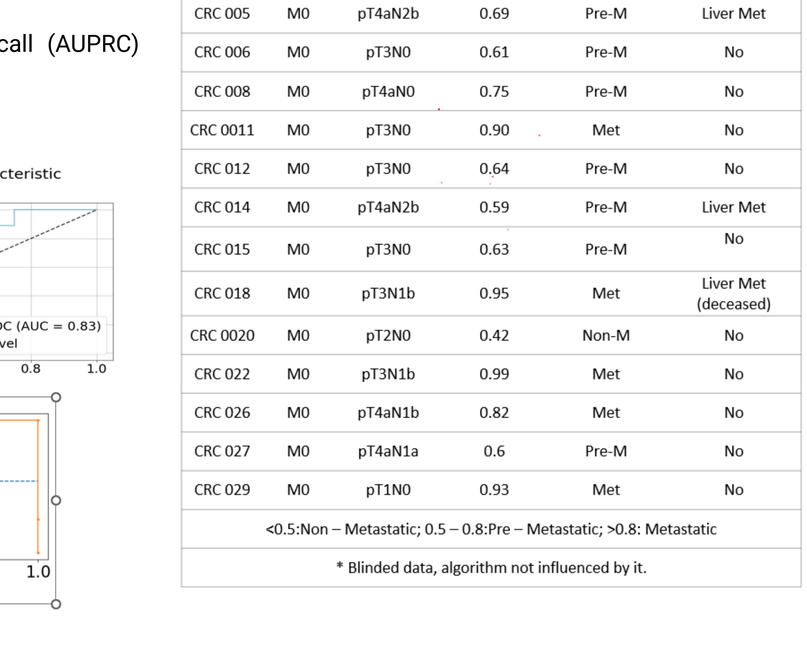
CONCLUSION

- Among the thirteen patient samples of the current blinded study, follow-up has identified three patients to be metastatic, all of which were correctly predicted by METSCAN™.
- There were no false negatives, but a few false positives, which can be indicative of higher platform sensitivity of METSCAN™
- Further studies, with head and neck tumor patients are currently ongoing
- The goal is to extrapolate this platform for multiple epithelial carcinomas

RESULTS

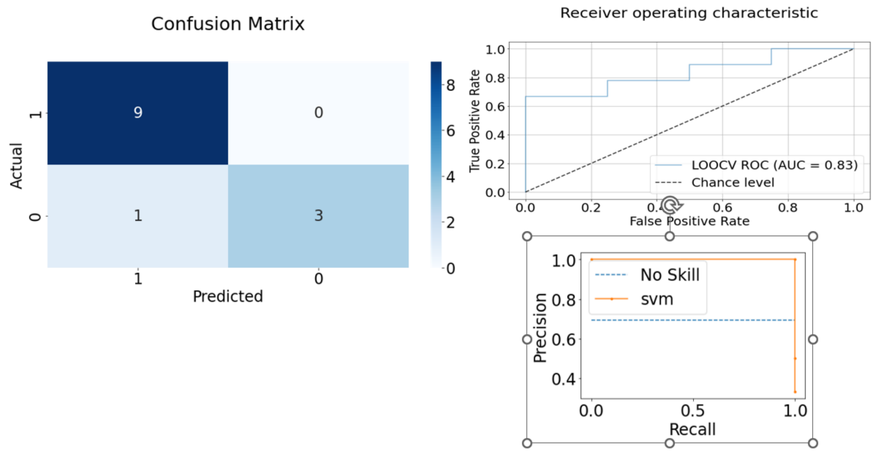
- Transformed data fed into the machine learning model gave an accuracy of 90 %
- To further improve the accuracy and predicted test results, the most important features of cell line dataset were selected using the algorithms. Feature selection using multiple methods reduced the feature size from twenty-five to eight and yielded an accuracy of ninety percent.
- To minimise false negatives and overfitting, the data set was further converted into a binary class label of metastatic and non-metastatic cells. Support-Vector-Machine showed 92.3 percent accuracy.

ML ALGORITHM	ACCURACY(%)
DECISION TREE	90%
SVM	80%
NAÏVE BAYES	80%
MLP	75%
LOGISTIC REGRESSION	65%



A Confusion Matrix of SVM Random Forest Regressor (cut-off 0.05) of **TRAINING DATA** shows that:

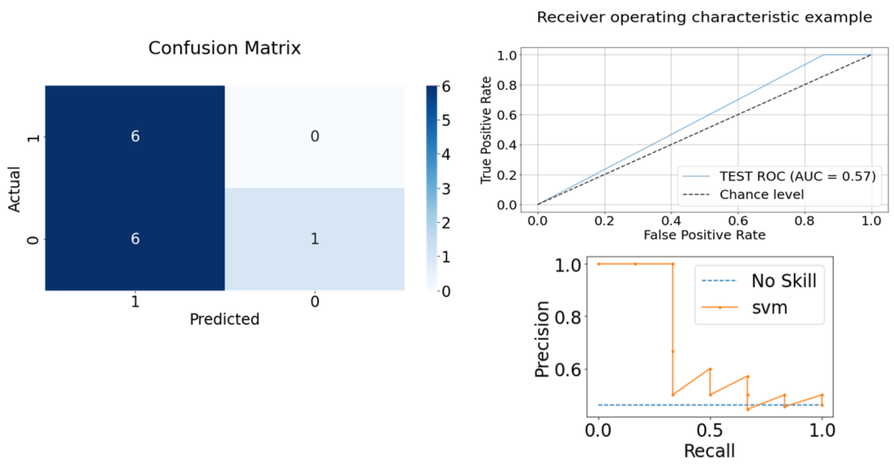
- all MET labels has been predicted correctly and
- 1 non-MET label has been predicted as MET.
- Receiver operating characteristic curve (ROC) & Precision recall (AUPRC) was used for quality check



Patient ID	Clinical Staging*	Pathological Grading*	Metastasis Probability	METSCAN Prediction	Patient follow Up, September 2022
CRC 005	M0	pT4aN2b	0.69	Pre-M	Liver Met
CRC 006	M0	pT3N0	0.61	Pre-M	No
CRC 008	M0	pT4aN0	0.75	Pre-M	No
CRC 0011	M0	pT3N0	0.90	Met	No
CRC 012	M0	pT3N0	0.64	Pre-M	No
CRC 014	M0	pT4aN2b	0.59	Pre-M	Liver Met
CRC 015	M0	pT3N0	0.63	Pre-M	No
CRC 018	M0	pT3N1b	0.95	Met	Liver Met (deceased)
CRC 0020	M0	pT2N0	0.42	Non-M	No
CRC 022	M0	pT3N1b	0.99	Met	No
CRC 026	M0	pT4aN1b	0.82	Met	No
CRC 027	M0	pT4aN1a	0.6	Pre-M	No
CRC 029	M0	pT1N0	0.93	Met	No
<0.5:Non – Metastatic; 0.5 – 0.8:Pre – Metastatic; >0.8: Metastatic					
* Blinded data, algorithm not influenced by it.					

A Confusion Matrix of SVM Random Forest Regressor (cut-off 0.05) of **TEST DATA** shows that:

- all MET labels has been predicted correctly and
- 6 non-MET label has been predicted as MET.
- Receiver operating characteristic curve (ROC) & Precision recall (AUPRC) was used for quality check



- Overall Scores were analyzed and cut-offs were assigned to distinguish between metastatic, pre-metastatic and non-metastatic tumors, in a blinded manner.
- Following which, data was matched with the clinical and pathological gradings and futher real time survival data will be used to optimize the algorithm.

- Currently study is being extrapolated into head and neck cancers, mainly tongue and buccal mucosa.
- METAssay™ platform for oral cancer is also in development to create the baseline.

Our Clinician Partners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Dr K Govind Babu
Ex-Head, Kidwai Medical College

All patient samples are consented, Ethics Commitee (EC) and Instituitional Tumor Reveiw Board (TRB) apprpoved

REFERENCES

Cancers, 2022, 14, 889 / Nature Reviews Clinical Oncology, 2019,16, 185 / Nature Genetics, 2019,51, 1113 / EACR 2021, Poster #v-0134 / PCT applications # PCTIN2021050915 & PCTIN2022050928