#4028

Predicting Response to Bevacizumab in Colorectal Cancer by Integrating Radiomics to Clinical and Genomic Features

Milanese Gianluca[1], Maddalo Michele[2], Leo Ludovica[1], Lecchini Michele[1], Bottarelli Lorena[3], Gnetti Letizia[3], Campanini Nicoletta[3], Pedrazzi Giuseppe[4], Azzoni Cinzia[3], Bozzetti Cecilia[5], Zavani Andrea[5], Caruana Pietro[3], Silini Enrico Maria[3], Sverzellati Nicola[1], Negri Francesca[5]

[1]Radiological Sciences, University Hospital of Parma, Parma, Italy, [2]Medical Physics, University Hospital of Parma, Parma, Italy, [3]Pathology, University Hospital of Parma, Parma, Italy, [4] University of Parma, Parma, Italy, [5]Oncology Unit, University Hospital of Parma, Parma, Italy

Background

In our retrospective analysis, Notch signalling pathway was associated with resistance to anti-vascular endothelial growth factor (VEGF) therapy in patients with metastatic colorectal cancer (mCRC).

We tested whether radiomics might select treatment-naïve mCRC patients responding to Bevacizumab, beyond clinical and genomic (Notch Intracellular Cleaved Domain (NICD)/JAG1 expression) parameters.

Methods

76 consecutive mCRC patients treated with first-line bevacizumab were retrospectively selected.

Immunohistochemistry analysis of tissue microarrays assessed NICD, JAG1, CD44, CD3, CD4, CD8, CD20, DLL3 and DLL4 expression. Abdominal CT scans were imported into a dedicated software for tumor segmentation and extraction of 852 radiomic features (RFs), which were included into machine learning-based predictive models. Pre-processing of RFs included redundant features elimination and standardization; L2 penalized logistic regression with Monte-Carlo cross-validation were implemented for wrapper-based feature selection and model training/test. Three models were developed: clinical/genomic (C/G), radiomic (R) and the comprehensive integrated model (I), which were compared based on ROC-AUC and accuracy metrics.

Results

NICD and JAG1 expression was associated with response to Bevacizumab ($p<0.05$). Using likelihood-ratio test as inclusion criteria, the selected variables were 5 for both C/G and R models, then aggregated into the I model. C/G features included NICD expression, number of involved sites, primitive location, resection of metastases and performance status, while selected RFs belonged to both first- and higher-orders classes.

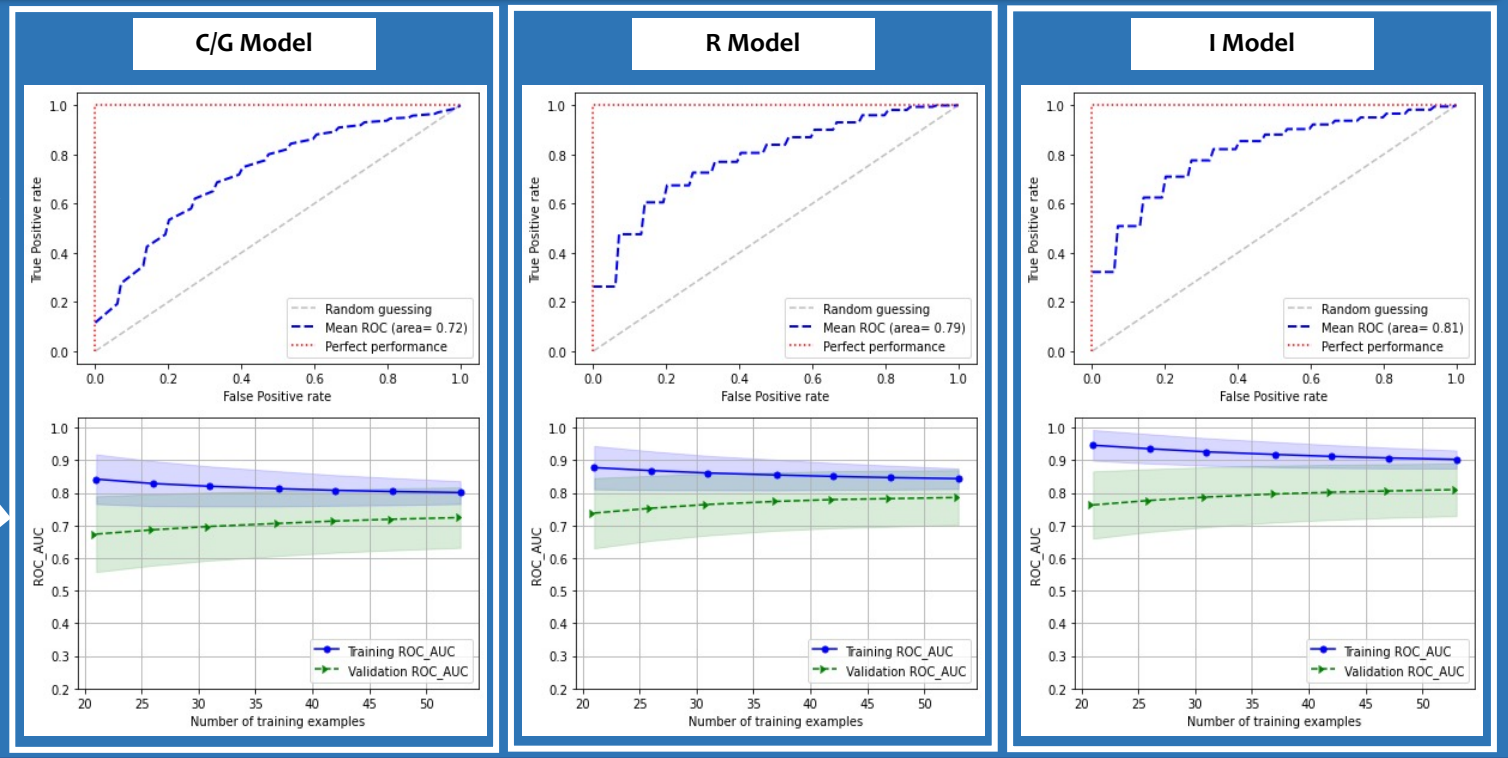
ROC-AUC and accuracy were 0.724 (95%CI:0.722-0.727) and 0.669 (95%CI:0.666-0.671), 0.786 (95%CI:0.784-0.788) and 0.710 (95%CI:0.708-0.713), 0.810 (95%CI:0.808-0.812) and 0.743 (95%CI:0.741-0.745) for C/G, R and I model, respectively.

Conclusions

The integration of clinical, genomic and radiomic features showed the highest performance in predicting response to Bevacizumab.

ROC curve

Learning curve



gianluca.milanese@unipr.it

The Authors declare no COI