

Outcome prediction after resection of colorectal cancer liver metastases: out with the old, in with the new?

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Colorectal cancer remains one of the commonest and most lethal malignancies worldwide (1). Up to 80% of patients with colorectal cancer develop liver metastases (CRLM), which are the main factor limiting survival (1,2). Despite advances in systemic therapy and the emergence of multimodal treatment concepts, curative surgical resection remains the best therapeutic option and provides the highest chance of long-term survival (1,2). However, liver resection is associated with perioperative morbidity and mortality, while multiple factors affect long-term prognosis (3,4). As a result, various predictive models have been developed over time, to improve preoperative patient selection and foresee unfavourable outcomes.

The first clinical risk scores (CRS) for patients undergoing resection of CRLM, were developed more than 20 years ago, with the aim to predict overall survival (OS) and recurrence-free survival (RFS) (2). Early versions by Nordlinger *et al.* (5), Fong *et al.* (6) and Nagashima *et al.* (7) comprised clinicopathological data, histological factors (such as primary tumor nodal status), size and number of liver metastases, and serum carcinoembryonic antigen (CEA) level. Later models included tumor genetic information, such as the RAS (rat sarcoma viral oncogene homolog) mutation clinical risk score (m-CS), developed by Brudvik *et al.* (8). Seeking to improve on the prognostic

power and reduce bias in these models, Sasaki *et al.* (9) proposed a "Metro ticket" model, the tumor burden score (TBS). This only included the number and size of liver metastases, so that newer scores by Margonis *et al.* (10) and Chen *et al.* (11) attempted to go further, by combining TBS with histological and genetic information, resulting in the Genetic and Morphological Evaluation (GAME) and Comprehensive Evaluation of Relapse Risk (CERR) scores, respectively. Finally, Okimoto *et al.* developed the Glasgow Prognostic Score (GPS), which predicts recurrence after liver resection for CRLM, based on systemic inflammation and nutritional status (12).

In recent years, artificial intelligence (AI) and machine learning (ML) have been increasingly integrated in various areas of industry, science, and medicine (13,14). Some studies have focused on imaging modalities, such as magnetic resonance imaging (MRI), computed tomography (CT), or endoscopy, aiming to identify pathological lesions (6-8). Others have analyzed digitized histology images to predict outcomes or response to chemotherapy (13-15). Moreover, medical record digitization and development of large registries has enabled "big data" research, where various AI applications are being put to the test (13,15).

Naturally, the potential of ML algorithms to predict outcomes after liver resection for CRLM has also been

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explored in recent years. Starting in 2013, Spelt *et al.* trained an artificial neural network (ANN) on 28 pre-, intra-, and postoperative variables from a monocentric Swedish cohort of patients operated on between 1994–2009. The ANN predicted long-term survival based on six of these variables, with a C-index of 0.72 (16). In 2020, Paredes *et al.* trained two ML-models based on logistic regression with bagging to predict recurrence in a multicentric cohort of patients operated on between 2001–2018. Ten preoperative variables were selected for model training, including Kirsten rat sarcoma viral oncogene homolog (KRAS) status for one of the models. Both were found superior to the traditional Fong CRS (6) and the m-CS by Brudvik *et al.* (8), with area under the curve (AUC) ranging from 0.67 to 0.69 for 1-, 3 and 5-year recurrence (17). A different approach was used in a further study on the same cohort: here, Moro *et al.* used classification and regression trees (CART) to predict OS using 15 prognostic factors. These were ranked according to KRAS status, resulting in different combinations and two different models, both of which outperformed the Fong score. Specifically, Akaike's information criterion was better in both the KRAS-wildtype (CART 3,334 *vs.* Fong CRS 3,341) and the KRAS-mutated (CART 1,356 *vs.* Fong CRS 1,396) groups (18). Finally, in our own study on patients operated for CRLM between 2010–2021, a novel gradient-boosted decision tree (GBDT) model was trained on 24 preoperative variables to identify patients at risk of poor OS. The GBDT model ranked 6 of these variables significantly higher than the rest, so that a version trained on only these six parameters was able to identify patients at risk of significantly reduced OS (23 *vs.* 52 months, P=0.005) with a robust predictive capability (C-index 0.70) (19).

In their paper, Lam *et al.* present a prognostic ML model, based on Cox proportional hazards and least absolute shrinkage and selection operator (LASSO) regression (20). They included patients undergoing liver resection for CRLM between 2009–2018 at four centers, with data randomized 70:30 into training and validation sets and endpoints being OS and RFS. The model's predictive capability was assessed using Harrel's C-index and compared to that of the Fong CRS. From the significant risk factors identified in univariate analysis (27 for OS and 22 for RFS), 8 variables were selected for the final model: primary tumor nodal stage, neoadjuvant treatment for CRLM, Charlson Comorbidity Score, pre-hepatectomy bilirubin and CEA levels, diameter of the largest liver metastasis, extrahepatic metastasis detected on positron emission tomography (PET)-scan, and KRAS mutation status. The model,

named CMAP for "CRLM Machine-learning Algorithm Prognostication", was shown to be stronger than the Fong CRS at predicting 1-year (C-index 0.651 *vs.* 0.571) and 5-year OS (C-index 0.651 *vs.* 0.574).

The study of Lam *et al.* (20) is a valuable addition to the growing field of ML-prognostication for patients undergoing resection of CRLM. The advantages of ML over traditional statistics and risk scores are discussed in the aforementioned studies and boil down to this: AI and ML models are able to analyze vast amounts of data and go through countless combinations, identifying patterns which may be missed by traditional statistics. The latter, after all, rely on the human factor (for example in the selection of variables and statistical tests), suffer from limits to the number of parameters that can be analyzed, or make assumptions about risk factors and the distribution of data.

The natural conclusion would seem to be, that traditional risk scores are outdated, and ML-based algorithms are the future. However, things are not that simple, and the current state of the art is reflected in the limitations of these studies, which are not dissimilar to those of Lam *et al.*, as acknowledged by the authors themselves (20). These include retrospective study designs, limited sample sizes, and lack of external validation. The former is accompanied by well-known issues, such as bias and missing data. The latter two are especially important for MLalgorithms, to preclude overfitting, where the algorithm is particularly well adapted to a limited dataset, but cannot make predictions on new, unknown data. Some workgroups try to overcome these problems through imputation or cross-validation, with varying results (16-19). Furthermore, studies differ in the consistency of patient cohorts and treatment strategies (e.g., eras of recruitment, frequency of major or staged resections, perioperative chemotherapy), the endpoints being studied, the way variables are included (e.g., serum CEA in continuous form *vs.* cut-off *vs.* logarithmic transformation), ML-models being employed, and statistical techniques used to assess and validate their results.

The prevalent inhomogeneity in the field is exposed by the differing variables included in models predicting the same outcomes. For example, although preoperative serum CEA, the number of CRLM, and diameter of the largest lesion persist across almost all models, perioperative chemotherapy, age, primary tumor lymph node metastases and KRAS status are only a part of some. Moreover, Lam *et al.* are the only group to include the Charlson Comorbidity Score and preoperative serum bilirubin (20), Paredes *et al.*

alone included primary tumor T-stage (17), Spelt *et al.* solely took hemorrhagic complications into account (16), whereas our model was the only one comprising body mass index and primary tumor grading (19).

These disparities highlight the need for high-quality, multicentric studies, with large and complete datasets. These would allow for comparisons between different models, external validation, as well as the prediction of outcomes other than OS/RFS, such as complications or response to chemotherapy (14,21,22). Pragmatically speaking, retrospective studies combining data from multiple centers and excluding patients with missing information are the only way to generate enough data in the short term. Concurrently, well-designed prospective studies are necessary, to maximize the quality and quantity of data made available for model training, such as genetic and epigenetic information, radiological and histological images, physiological parameters, and body composition measurements. The AI models of the future could combine all these pieces of information and take part in the decisionmaking process, much like a human does. The role which generative AI models (such as ChatGPT) could play in this process, is particularly intriguing.

As of the time being, the "old" is still very much useful and the "new" is not quite ready to displace it. Nevertheless, change is inevitable.

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