

# PREDICTIVE, PREVENTIVE AND PERSONALIZED MEDICINE & MOLECULAR DIAGNOSTICS

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## Developing useful prognostic tools for risk assessment: Predictors of mortality in catheter-related bloodstream infections

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**Introduction & Aim:** Catheter-related bloodstream infections (CRBSIs) remain a common challenge in critically ill patients. Predictors of mortality in this population across different treatments have not been well studied. This study was aimed at developing useful prognostic tools and predictive models for relative risk adjustment for mortality in patients with CRBSI.

**Methods:** We used a recent trial data of 731 patients with CRBSIs randomized to drug (x) and vancomycin (VAN). Our mortality analysis plan involved a sequence of specific step; data mining, non-parametric methods and finally parametric (logistic) modeling.

**Results:** Both CART and logistic regression identified MPMS, age, baseline corticosteroid exposure, region of world of enrolling study site and infection with a Gram negative pathogen as the most important factors associated with mortality. Together, these five predictors contained more than 95% of the prognostic information in the clinical data (baseline, developed). Logistic modeling allowed us to combine and investigate the effect of different prognostic variables on mortality. The validated model accurately estimated likelihood of mortality across different patient population with unique characteristics.

**Conclusions:** Appropriate antibiotic therapy remains a key driver of mortality in CRBSI. Efforts to improve outcomes can be facilitated with using a validated predictive models and the use of prognostic tools, like nomograms, to calculate the probability of mortality for any specific patient. The early prognosis would assist clinicians to identify high risk patients and to select the appropriate therapy.

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## Identifying effectiveness of the antitumor drugs and predicting the tumor response prior to therapy for personalizing cancer medicine

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Identifying effectiveness of antitumor drugs enables to predict and optimize chemotherapies to personalize cancer medicine. The processes of tumor formation and cancer therapy are based mainly on the concept of doubling time-energy conversion (DT-EC) in which the conversion of doubling time into growth energy takes place. Monitoring the mechanical behavior of tumor response of the treated groups by that of the control groups with respect to the growth/or shrinkage constants along the corresponding periods determines the accumulated energy yield by the drug doses. Assessment of the efficient regimen for optimizing therapy would be based on achieving an accumulated DT-EC in the tumor cells by the regimen doses. The higher the energy yields by the same drug dose the more effectiveness of the applied regimen and vice versa. Then, efficiency of those applied regimens on different types of tumor models would be determined to assess the specifications of the personalized treatment schedule. The correlation and regression between the energy yield by the applied drug doses in optimal schedules (dependent variable) and value of those doses (independent variable) would be investigated to determine values of both variables that in perfect correlation. Thus, a dose-energy model with perfect fit for the studied drug would be constructed to administer the optimal dose in an efficient schedule. Accordingly, the therapeutic response of cancer to the studied drug could be predicted prior to therapy by identifying each of patient's histologic grade in vitro or in vivo and energy yield by the proposed (personalized) dose using the constructed dose-energy model of the antitumor drug.

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