Editorial

# Application of hyperbolastic growth and hypertabastic survival methods in biomedical and cancer research

## Editorial

The eminent statistician Professor George E P Box commented, "All models are wrong but some are useful." Professors Tabatabai and Singh, in collaboration with colleagues, have been developing statistical methodologies for modeling biomedical and cancer data, including longitudinal data analysis, survival analysis, and robust statistical techniques.[1-9] Longitudinal data analysis includes hyperbolastic growth models[1] and their applications in cancer growth modeling, and hyperbolastic mixed-effects models[2] for the analysis of longitudinal data, disease progression and regression, embryonic and adult stem cell proliferation,[3] and dermal and epidermal wound healing.[4] The hyperbolastic models can also be used to quantify the binding of a ligand to a macromolecule as well as modeling dose-response data to measure the effectiveness and toxicity levels of a new drug.

Hyperbolastic growth models have been used to analyze the growth of solid brain tumors by taking into account the processes of angiogenesis, tumor invasion, and metastasis.[1] The precision and flexibility of these hyperbolastic models have been tested against classical models such as Gompertz, logistic, and Weibull models, and the results of these tests have always been satisfactory. As reported in our PLOS-ONE manuscript,[2] we analyzed the cervical cancer mortality of Whites and Blacks in the US using a type II longitudinal hyperbolastic mixed- effects model. In regard to embryonic and adult stem cell proliferation, the hyperbolastic models performed better than classical models. In a recent report by the scientists at the University of Pittsburgh Live Cell Imaging Laboratory,[5] the hyperbolastic model was cited as a flexible model for analyzing stem cell proliferation.

The hypertabastic survival models[6] include the hypertabastic proportional hazards model, the hypertabastic accelerated failure model, and the hypertabastic proportional odds model. Survival analysis is a major tool in cancer research, with a wide application in modeling a variety of cancer survival time data, including analysis of breast cancer[7] and brain cancer data. We have applied the hypertabastic model to analyze breast cancer, multiple myeloma, and glioma. The model was used to analyze the survival of breast cancer patients, exploring the role of a metastasis variable in combination with clinical and gene expression variables.[8] Compared with Cox regression, the increase in accuracy was complemented by the capacity to analyze the time course of disease progression using the explicitly described hazard and survival functions. Our interest in this research was to introduce a variable representing the presence or absence of metastasis and its effect on clinical and gene expression variables. In addition to making a quantitative assessment of the impact of metastasis on the prospects for survival, we looked at its interactions with other prognostic variables. The estrogen receptor status increased in importance, but the significance of gene expression variables used in the combined model diminished. Considering only the subgroup of patients who experienced metastasis, the covariates in the model were only the clinical variables for estrogen receptor status and tumor grade. The results were published in Cancer Growth

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and Metastasis.[8] In the area of medical genomics, we published a manuscript in BMC Medical Genomics, where we analyzed breast cancer data using clinical and multiple gene expression variables using the hypertabastic proportional hazards model and compared the results with Cox regression.[7] Recently the hypertabastic accelerated failure models have been used to analyze the reliability of bridge structures in the United States.[10] This gives a new dimension in the application of hypertabastic survival models in non-biomedical settings.

## Acknowledgment

## Conflict of interest

None.

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