Modeling the link between two genes expressions and the toxicity of some chemotherapy drugs for chronotherapy of Cancer

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Abstract

In this article, we present the mathematical model for predicting the optimal circadian timing of an anticancer drug, irinotecan using the circadian expression of two clock genes as input data. Two main classes are represented by those gene expressions signals: mutant and non-mutant mice. The data representing the input are sampled at every three hours along the twenty four hour scale , in the non-mutant case, and at every four hours in the mutant case. The data representing the output (the Body Weight Loss signal) is sampled at every four hours. Both input and output data represent the mean values of the measured data at every point. The proposed model is a linear model using a Maximum A Posteriori Bayesian inference method. The model is first implemented on mean signals, the prediction matrix being built on a certain number of available signals, the rest of signals being used for checking the accuracy of prediction. Because the number of cases in some classes is very law, another implementation (model) using the individual signals is used. When using the individual data, we study the number of training data on the accuracy of the predictions. Two measures, L_1 and L_2 relative distances are used for measuring quality of the global shape of prediction and number of times the position minimum values correspond (since the minimum value corresponds to the optimal drug administration).

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Bibliography

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