

## **C-mix: a high dimensional mixture model for censored durations, with applications to genetic data**

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We introduce a supervised learning mixture model for censored durations (C-mix) to simultaneously detect subgroups of patients with different prognosis and order them based on their risk. Our method is applicable in a high-dimensional setting where datasets contain a large number of biomedical covariates.

To address this difficulty, we penalize the negative log-likelihood by the Elastic-Net, which leads to a sparse parameterization of the model and automatically pinpoints the relevant covariates for the survival prediction. Inference is achieved using an efficient Quasi-Newton Expectation Maximization (QNEM) algorithm. The statistical performance of the method is illustrated on three publicly available genetic cancer datasets with high-dimensional covariates.

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