Understanding Myelome Multiple patients relapse by automatic reasoning on an integrated model of transcriptomic data and large-scale signaling pathways

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Methods and tools

Problematic
Multiple Myeloma (MM) is an incurable haematological malignancy cancer; representing 1% of cancer, and 2% of the associated mortality. This disease is particularly aggressive and the current treatments can’t ensure the survival of patients.

Our aim is to better understand mechanisms of relapse by comparing cancer cells expression profiles with the regulation network of a normal cell.

In this work, we studied the consistency of a large-scale causal network of signaling and transcriptional events with respect to gene expression profiles [Guziolowski et al., 2012] from 32 patients (9 healthy, 11 measured at MM diagnosis and 12 at MM recall).

Constraint based model

Confrontation between the data and the regulatory network [Guziolowski et al., 2009]

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Reference:


Conclusions

Further work

Discussion

References