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NetSurvival.jl: A glimpse into relative survival analysis

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Data arising from large cancer studies often lack reliable information about the cause of death (supposed binary: death from the studied cancer or from other causes) for each individual. Relative survival analysis is a subfield of survival analysis specifically targeted at this particular type of datasets. The field's goal is to extract survival curves that only takes into account the deaths from cancer, the so-called net survival curves, for comparison purposes between different groups or directly for diagnostic purposes. For that, a few standard estimators were established in the last 50 years, backed by a wide literature.

Standard tools nowadays are composed of R packages, with underlying C and C++ routines, that are hard to read, maintain, and globally use. This package is an attempt to provide a fast, reliable, but most importantly easily maintainable package to implement standard estimators and routines from the field onto the StatsModels.jl API. The hope is that the junction with classical modeling API in Julia will allow later extensions of the existing modeling methods, with a simple interface for the practitioners.

In this talk, I present the current state of the implementation: the few tools and methods that were implemented, their integration into the Julian ecosystem, and showcase the functionalities and performance of the implemented methods. Note that in particular the use of native Julia allows for concision and readability of the code.

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