

Modeling the cumulative incidence function of clustered competing risk data: a multinomial GLMM approach

master thesis defense



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- 1 Data
- 2 Application
- 3 Model
- 4 Contributions & challenges
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- 7 Results
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Clustered competing risk data



Key terms:

- **Clustered**: groups with a dependence structure (e.g. families);
- Causes **competing** by *something*.

Something?

- **Failure** of an industrial or electronic component;
- **Occurrence** or **cure** of a disease or some biological process;
- **Progress** of a patient clinic state.

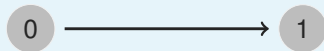
Independent of the application, always the same framework

Cluster	ID	Cause 1	Cause 2	Censorship	Time	Feature
1	1	Yes	No	No	10	A
1	2	No	No	Yes	8	A
2	1	No	No	Yes	7	B
2	2	No	Yes	No	5	A

Big picture: Failure time data

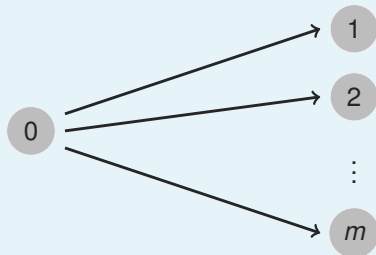


Failure time process



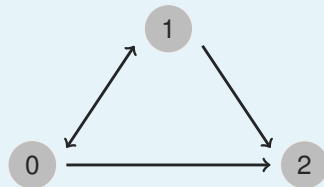
*Same methodologies,
different names.*

Competing risk process



Survival analysis Industrial life testing;
Reliability analysis Biomedical studies.

Multistate process



A comprehensive reference is

Modeling framework

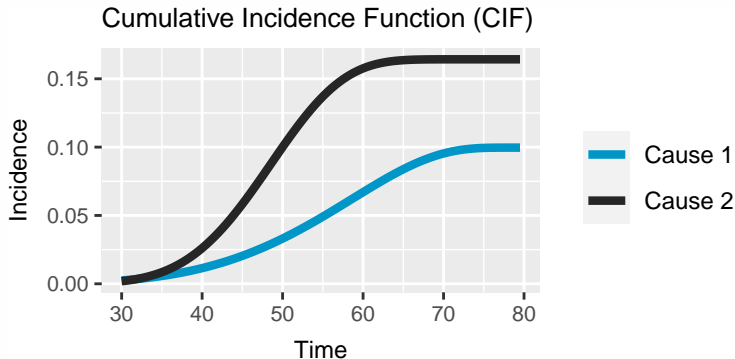
We have to choose which **scale** we model the **survival experience**.
Usually, the

hazard (failure rate) **scale** : $\lambda(t \mid \text{features}) = \lambda_0(t) \times c(\text{features})$.

In the competing risk setting ...



a more attractive possibility is to work on the **probability scale**, focusing on the cause-specific



i.e.

$$\text{CIF} = \mathbb{P}[\text{failure time} \leq t, \text{ a given cause} \mid \text{features}]$$

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Cancer incidence in twins



Clustered competing risks data

↳ Clusters? Families

↳ Family studies

↳ **Twins data**

Family studies \Rightarrow **within-family dependence**

That may reflect

- Disease **heritability**;
- The impact of shared **environmental effects**;
 - **Parental effects**: continuity of the phenotype across generations.

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Our contribution: a hierarchical approach



Thinking on two competing causes

... for the outcome y_{ijt} of a subject i , family j , in the time t , we have

$$y_{ijt} \mid \underbrace{\{u_{1j}, u_{2j}, \eta_{1j}, \eta_{2j}\}}_{\text{latent effects}} \sim \text{Multinomial}(p_{1ijt}, p_{2ijt}, p_{3ijt})$$

$$\begin{bmatrix} u_{1j} \\ u_{2j} \\ \eta_{1j} \\ \eta_{2j} \end{bmatrix} \sim \text{Multivariate Normal} \left(\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_{u_1}^2 & \sigma_{u_1, u_2} & \sigma_{u_1, \eta_1} & \sigma_{u_1, \eta_2} \\ & \sigma_{u_2}^2 & \sigma_{u_2, \eta_1} & \sigma_{u_2, \eta_2} \\ & & \sigma_{\eta_1}^2 & \sigma_{\eta_1, \eta_2} \\ & & & \sigma_{\eta_2}^2 \end{bmatrix} \right)$$

$$\begin{aligned} p_{kijt} &= \frac{\partial \text{CIF}}{\partial t} \\ &= \frac{\partial}{\partial t} \underbrace{\pi_k(X, u_1, u_2 \mid \beta)}_{\text{cluster-specific risk level}} \underbrace{\Phi[w_k g(t) - X^\top \gamma_k - \eta_k]}_{\text{cluster-specific failure time trajectory}}, \end{aligned}$$

$k = 1, 2.$

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- A clear and simpler modeling structure;
- **There is no free lunch**
Computational challenges overcome via an efficient implementation and estimation routines, the **TMB**;
- The data is very simple,
we just know the outcome (**yes** or **no**);
- We have to be able to build the **CIF** curves;
- And accommodate the **within-family dependence** properly,
that can happen in different manners;
- ...

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TMB: Template Model Builder



Quickly implement complex random effect models through simple C++ templates.
The R package combines

- CppAD: C++ automatic differentiation;
- Eigen: templated matrix-vector library;
- CHOLMOD: sparse matrix routines available from R;

to obtain an efficient implementation of the applied Laplace approximation with exact derivatives.

Also, key features are

- automatic sparseness detection;
- parallelism through BLAS;
- parallel user templates.

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Thanks for watching and have a great day



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