INPUTS

Genomic-clinical data

	Disease transition times			Clinical variables			Genomic variables		
Patient	state 1	state 2	...	male	age	...	gene 1	gene 2	...
PT1021	0	135	...	1	44	...	0	1	...
PT3421	0	NA	...	0	47	...	1	NA	...
⋮	⋮	⋮	⋱	⋮	⋮	⋱	⋮	⋮	⋱

Hazard rate model

state 1 $\xrightarrow{\lambda_1(t)}$ state 2

state 2 $\xrightarrow{\lambda_2(t)}$ state 3

state 2 $\xrightarrow{\lambda_3(t)}$ state 4

$$\lambda_i(t \mid z, \beta_i) = \lambda_i^{(0)}(t) \exp\left[\beta_i^\mathsf{T} z\right]$$

$z :=$ covariate vector

$\beta_i :=$ unknown coefficients

Prior:

$\beta_i := (\beta_{i1}, \beta_{i2}, \dots)$

$\beta_{ij} := (\beta_{ij1}, \beta_{ij2}, \dots)$

$\beta_{ijk} \sim N\left[\mu_{ij}, \sigma_{ij}^2\right]$

OUTPUTS

State transition x

age
male
...
gene 1
gene 2
...

relative hazard (log scale)

0.1   1   10

Probability

state 4

state 3

state 1

state 2

years since diagnosis