Deep Survival Analysis

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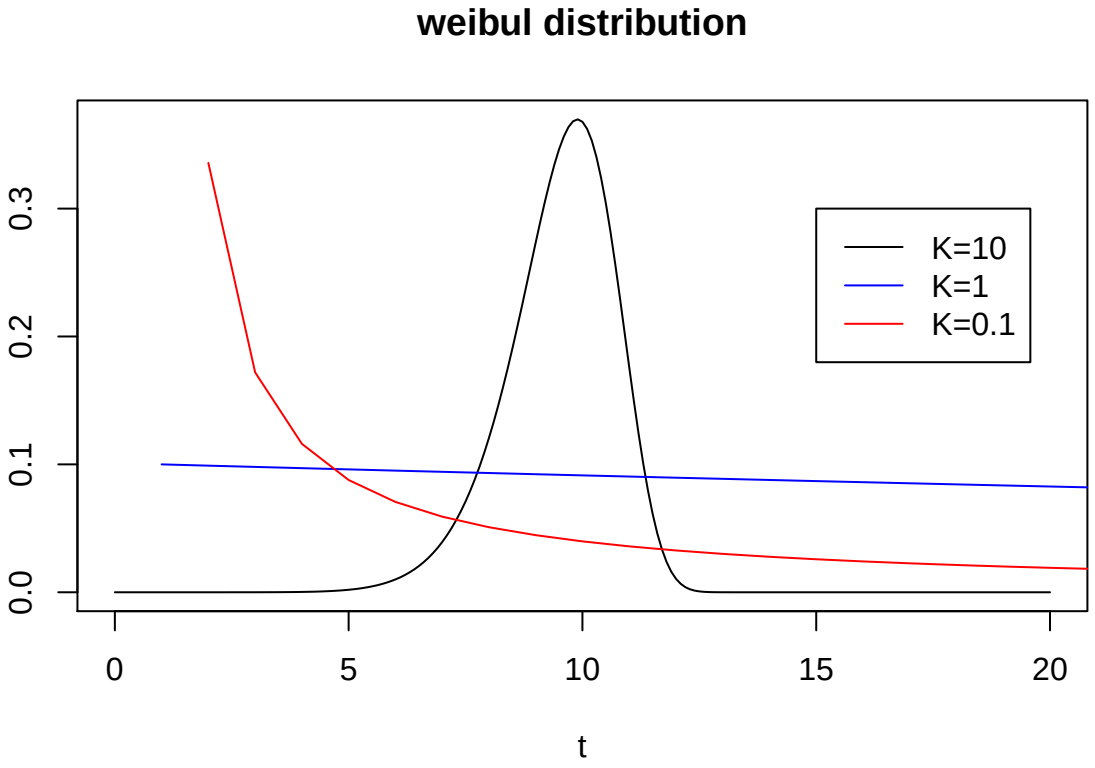
Deep Survival Analysis : EHR

- Hierachichal Generative Approach
  - survival times and covariates modeled jointly conditional on latent processes
  - records align by failure time rather than entry time
  - Each observation has L layers of latent variables
- (t,c) pairs of positive times and binary censoring status
- Limitations to traditional approches(Cox & Kaplan Meir)
  - EHR highdimensinal and sparse (missing covariates)
  - Traditional methods require aligning all patiets on a synchronizing event(i.e entry to clinical trial)
  - Regression based approaches assume linear function

```
#lamda  scale
# k shape
# mean =
# t time to failure
lambda <- 10
t <- seq(0, 20, by=0.1)

weibul <- function(k) {
  return(k/ lambda * (t/ lambda) ^ (k-1)  * exp(-(t/lambda) ^k))
}

plot(t, weibul(10), main = 'weibul distribution',  xlab='t', ylab = '', type='l')
lines(weibul(1), col='blue')
lines(weibul(0.1), col='red')
legend(15, 0.3, legend=c("K=10", "K=1", "K=0.1"), lty = c(1,1,1), col = c('black', 'blue', 'red') )
```


weibul distribution
0.0
0.1
0.2
0.3
0
5
10
15
20
t
K=10
K=1
K=0.1