Updating Colorectal Cancer (CRC) Survival in the CRC-SPIN Micro-simulation Model

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Simulates all modeled aspects of an individual,

program. Screening is modeled separately and

Years until non-CRC death is simulated at the

Years until CRC death is determined at time of

diagnosis which can be either at screening (pre-

Example of inverse CDF lookup algorithm:

55 year old females with Stage 3 CRC diagnosed in 1998

years since CRC diagnosis

simulated uniform(0.1)

survived years

fead within upare

clinical cancerous lesions) or by presenting

clinically (lesions in clinical disease state).

subject to individual and population-level

beginning of the natural history process.

modifies simulated natural histories.

constraints in the absence of any screening

Natural History Model

2

6.0

0.8

5

9.0

Additive Hazards Model

Annual hazard rates:

All cause mortality is modeled as the sum of the force of mortality due to CRC and the force of mortality due to all other causes:

$$\lambda_i(s) = \lambda_i^{CRC}(s) + \lambda_i^{\neg CRC}(s)$$

Interval specific survival rates:

$$p_i^D = \exp\left[-\int_{i-1}^i \lambda_i^D(s) ds\right]$$

D indicates: All causes, CRC, or non-CRC causes.

Relative Survival

GLM with complementary log-log link function:

$$\ln\left[-\ln\left(\frac{p_i}{p_i^{-CRC}}\right)\right] = \ln\left[\int_{i-1}^i \lambda^{CRC}(s) ds\right]$$

Linear on the log cumulative hazard (interval increment) scale.

Binomial error function: $N_i p_i^{CRC} \left(1 - p_i^{CRC}\right)$

Estimating: number of deaths among individuals

diagnosed with CRC relative to the number of expected deaths in a matched population in each one-year followup interval.

Executed in SAS using a call to PROC GENMOD

Hakulinen and Tenkanen, Journal of the Royal Statistical Society. Series C, Vol. 36, No. 3 (1987), pp.309-317

Implementation within CRC-SPIN



1) Results from the relative survival analysis are saved in formatted XML files. These files are read by the CRC-SPIN C# model and used to generate CRC survival curves.

2) Time from diagnosis to colorectal cancer death is calculated through an inverse CDF lookup algorithm:
•An individual's percentile within the population survival is directly simulated (sample from a uniform distribution).
•Years until death is the first year that the probability of survival

•Years until death is the first year that the pi falls below the percentile.

•The additional fraction of the year survived is another draw from a standard uniform distribution.

•CRC dod = CRC Dx date + years survived + fraction of year

3) Simulated date of death = min(CRC dod, non-CRC dod)



Secular Trends

For any number of years since diagnosis, i:

$$\ln \left(\Lambda_{i}^{CRC} - \Lambda_{i-1}^{CRC} \right) = Z_{i} \gamma + X \beta$$

Complete hazard increments are estimated:

X baseline covariates

- *i* index of years since CRC diagnosis
- Z time-varying covariates

Model stratified by:

Location (colon, rectum) and Stage of CRC

Covariates included in model: Age group at diagnosis Sex Year of CRC diagnosis Interaction between Age & Years since Dx linear spline with knots: 1981,1991,2001,2003

Data Sources

- •All (other) cause survival National Center for Health Statistics
- •Observed survival in population with CRC SEER

individuals with CRC Dx 1975-2003 with follow-up through 2009 black or white race

•Expected survival in non-CRC population SEER*Stat (NCHS)

only available for black and white races