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Simulation model for visualisation of small-area cancer incidence rates

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Introduction

Cancer epidemiologists are regularly asked by members of the interested public about possible associations between suspected carcinogens and apparently increased small-area cancer incidence rates. Frequently, no systematic incidence differences can be demonstrated. Under these circumstances, the large extent of random variation in small-area tumour incidence rates is difficult to convey. Nevertheless, it is necessary to address public concerns about suspected cancer clusters. To facilitate explanations about random variation of tumour incidence given to the public by cancer epidemiologists, we have implemented a software tool in R for small-area simulation of cancer incidences.

Methods

We simulate a population of size n=500 uniformly distributed over a village structure consisting of 10 streets, each with 10 houses, over a period of fifty years per simulation run. In order to obtain realistic estimates, published data on cancer occurrence are used where available to parameterize the model. Weights by 1-year age-groups corresponding to the mean Bavarian population structure of the years 2000-2002 are assigned to create the age distribution of the start population. In each year of the simulation, incident cases and deceased cancer patients are sampled based on the binomial distribution using age-specific incidence rates (1998-2000) and respective weights derived from the 1-year survival rate (period of diagnosis 1985-1989) given by the Cancer Registry of Saarland. The dying process from all causes except cancer is modelled employing an age-weighted sampling based on the Bavarian life table for the years 1996-1998. In the absence of published data, an empirical estimation of a small number of simulation parameters was necessary. These parameters were systematically changed until the simulation results were in accordance with morbidity and mortality data reported by the Federal Statistical Office and the Robert Koch-Institut. Testing of the model was based on the concept that results should correspond to published data on mean age at time of cancer incidence, mean cancer-related dying age, and mean non-cancer related dying age. Beyond graphical representation of streets, houses, and individuals with disease status, each simulation is illustrated by numerical graphs that show longitudinal changes in population size, mean age of population, birthrate, incidence, prevalence, cancer-related mortality, non-cancer mortality, mean age at cancer onset, mean age during prevalence, mean age at time of cancer-related death, mean age at time of non-cancer death, proportion of houses per street inhabited by >= 1 cancer patient, proportion of streets with each house inhabited by >= 1 cancer patient, and cancer-related 5-years Kaplan-Meier survival probability.

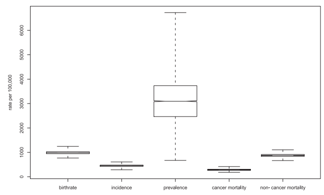
Simulation parameters
(All rates given per 100.000)

Parameter	*Value*
Number of simulations	10,000
Initial population size	500
Birthrate (Bavaria, 1998 - 2000)	1,000
Incidence (Saarland, 1998 - 2000)	470
Initial prevalence (Germany, 5-year prevalence, 1998 estimates)	1,200
Cancer-related mortality (Saarland, 1998 - 2000)	288
Non-cancer mortality (all causes except cancer; Saarland, 1998 - 2000)	878

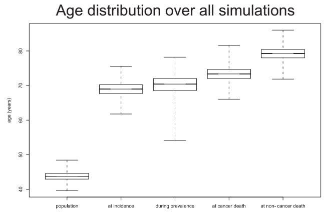
Results

The mean population size over all simulation runs was 484 (SE, 0.2). The mean proportion of houses per street with at least one person affected by cancer within the last five years was 0.2149 (SE, 0.0004). The mean proportion of streets with all houses inhabited by at least one cancer patient during the last five years was 0.000001 (SE, 0.000001). The mean cancer-related 5-years survival probability was 0.722 (SE, 0.001).

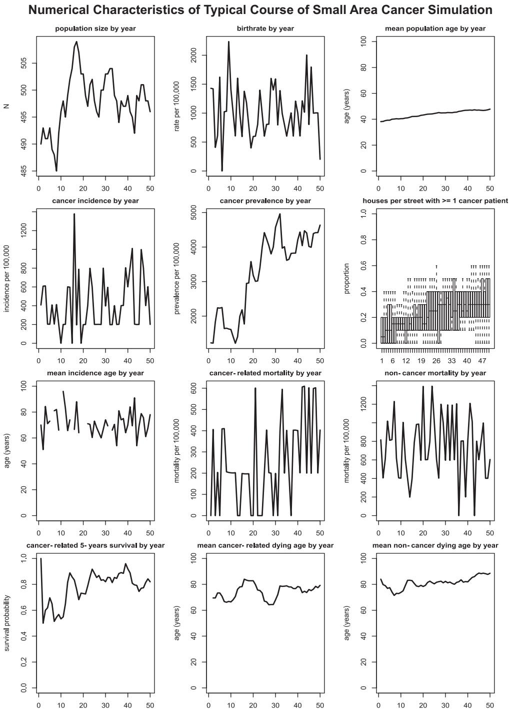
Distribution of rates over all simulations



Age distribution over all simulations



Numerical Characteristics of Typical Course of Small Area Cancer Simulation



Typical Distribution of Persons and Disease Status in Small Area Cancer Simulation

Summary

On average, two houses per street have been inhabited by at least one cancer patient during the last five years in our simulated small village. A situation where all houses in a street have been inhabited by at least one cancer patient is very rare, but possible. In the absence of cancer causes other than chance, cancer prevalence appears to be extremely variable. When applying our results, it should be kept in mind that only a limited number of parameters is used in our simulation. Real life is probably much more complex. However, we think that basic principles of cancer incidence and prevalence can be illustrated by the use of our tool. Our results may serve as a guideline for further exploration.

Conclusion

Our software tool can be used effectively for numerical and graphical visualisation of small-area tumour incidence rates. The explanation of basic epidemiological concepts to members of the public can help to increase public motivation and support for population-based cancer registration. Our simulation tool can be used to support this goal and to calm public fears of cancer clusters. It will be made available for free download in due course.

References

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