Hospital Simulation

Peter Krall, 2024-04-07

‚Hospital Simulation' is a program simulating spread of two competing virus strains in am open reservoir, such as a hospital patient population.

Each run start with a low frequency of the first strain. At some time, the second strain appears in initially low frequency. Both strains then compete for the resource of susceptible individuals, which is renewable since a fraction of new arrivals is susceptible.

The model is:

The open reservoir model is a SEIR model for spread in reservoirs with exchange of members between the reservoir and the environment. Computational models based on the same idea have already shown that rapid wild-type replacement is possible in reservoirs exchanging members with the environment [**Fehler! Verweisquelle konnte nicht gefunden werden.**]. The formalization given here adds the formal characterization of steady states and constraints for persistent activity, as well as a formal representation of incubation period and background immunity.

The state of the system changes in a three-step cycle:

If there is only one strain, then at any time t, $p_{new}(t) = p_{sus}(t) \cdot (1 - (1 - p_{act}(t) \cdot p_{trans})^{nc})$ get exposed in the exposition step. The interpretation is: p_{act}(t), p_{sus}(t) are the fractions of active cases, respectively susceptible individuals at time *t*. The hospital-specific parameter *nc*, p_{trans} represent contact event per person and transmission probability per contact event. To keep things simple, all individuals have the same number of contacts. and the probability not to become exposed is $(1 - p_{trans})^{nc}$ .for each contact event between an active case

If there are two competing strains with active numbers and transmission $p_{act.1}$(t), $p_{act.2}$(t) probabilities $p_{trans.1}$, $p_{trans.2}$, then the probability not to get exposed at all is the product of probabilities not to get exposed by either strain. and the conditional probabilities for getting exposed by either strain are proportional to the probabilities if the other strain were absent:

$$p_{new\text{-}1}(\mathrm{t}) + p_{new\text{-}2}(\mathrm{t}) = p_{sus}(\mathrm{t}) \cdot \left(1 - (1 - p_{act.1}(\mathrm{t}) \cdot p_{trans.1}(\mathrm{t}))^{nc} (1 - p_{act.2}(\mathrm{t}) \cdot p_{trans.2}(\mathrm{t}))^{nc}\right)$$

$$p_{new\text{-}1}(\mathrm{t}) = (p_{new\text{-}1}(\mathrm{t}) + p_{new\text{-}2}(\mathrm{t})) \frac{\left(1 - (1 - p_{act.1}(\mathrm{t}) \cdot (\mathrm{t}))^{nc}\right)}{\left(1 - (1 - p_{act.1}(\mathrm{t}) \cdot p_{trans.1}(\mathrm{t}))^{nc}\right) + \left(1 - (1 - p_{act.2}(\mathrm{t}) \cdot p_{trans.2}(\mathrm{t}))^{nc}\right)}$$

$$p_{new\text{-}2}(\mathrm{t}) = (p_{new\text{-}1}(\mathrm{t}) + p_{new\text{-}2}(\mathrm{t})) \frac{\left(1 - (1 - p_{act.2}(\mathrm{t}) \cdot p_{trans.2}(\mathrm{t}))^{nc}\right)}{\left(1 - (1 - p_{act.1}(\mathrm{t}) \cdot p_{trans.1}(\mathrm{t}))^{nc}\right) + \left(1 - (1 - p_{act.2}(\mathrm{t}) \cdot p_{trans.2}(\mathrm{t}))^{nc}\right)}$$

After exposition, a fraction p_{xch} of the individuals leave the reservoir and are replaced by new admissions, out of which p_{imm} arrive immune. The parameters p_{imm}, p_{xch} are reservoir-specific. Admission of active cases is ignored except for the possible seeding of a new mutant strain.

In the final step, individuals change from exposed to active state after the number of days given by the parameter t_{exp}, and they change from active to immune after the number of days given by the parameter t_{act}

If there is an attractive steady state, then for $t \to \infty$, $p_{new}(t) \to p^*_{new}$ for some limit value p^*_{new}. The fraction of unsusceptible individuals after exchange is the sum of those who arrived immune plus the sum of those who still are in the reservoir and have been exposed before

$\overline{p^*_{sus}} = p_{xch} \cdot p_{imm} + p^*_{new}(1-p_{xch}) + p^*_{new}(1-p_{xch})^2 + p^*_{new}(1-p_{xch})^3 \ldots$

The susceptible fraction is

$p_{sus}(t) \rightarrow p^*_{sus} = 1 - \left(p_{xch} \cdot p_{imm} + (1-p_{xch}) \cdot p^*_{new} \cdot \frac{1-p_{xch}}{p_{xch}}\right)$

$p_{act}(t) \rightarrow p^*_{act} = p^*_{new} \cdot \sum_{i=t_{exp}+1}^{i=t_{act}} (1-p_{xch})^i$

The steady states are thus characterized by the equation:

$p^*_{new} = (1 - (p_{xch} \cdot p_{imm} + (1-p_{xch}) \cdot p^*_{new} \cdot \frac{1-p_{xch}}{p_{xch}})) \cdot (1-(1-p_{imm} \cdot p^*_{act})^{nc})$

The values of the model parameter are set in a configuration. Currently, this is a header where different options can be selected by using the #define mechanism (yes, this requires re-compilation after every change – so what, the compiler is faster than my brain anyhow). A more fancy version with a GUI and R integration will follow.

Each model run produces two output file. One is a csv meant to be imported into R, matlab, Mathematica, Excel or whatever other program. The second one describes the configuration.

There is currently no graphic output. For generating graphics, the csv has to be imported into a standard program, such as matlab.