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Motivation

Several dynamical approaches can simulate epidemics and vaccination strategies. Generally the models can be divided into top-down approaches like Markov models and differential equations and bottom-up approaches like cellular automata and agent based models. Top-down approaches are characterized by cumulative values that are representing groups of people. Bottom-up approaches in contrast consider individuals. Both approaches have advantages and disadvantages. Top-down approaches can be analyzed very well with mathematical methods while bottom-up approaches require comparison of the outcome of simulation runs with different parameter sets. To improve validity of model structures a method that compares different approaches for epidemic models is introduced.

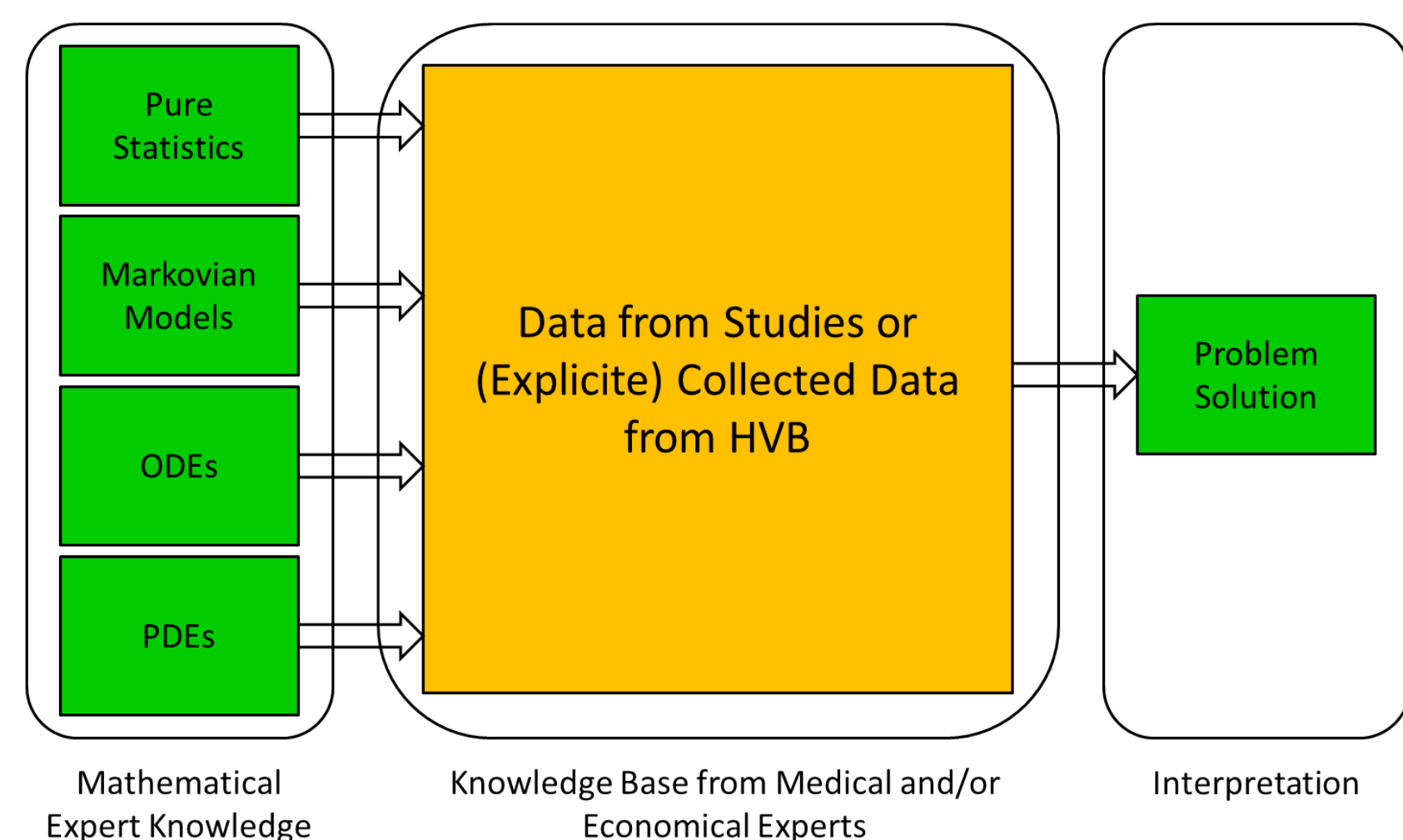


Figure 1: Actual solution approach in modeling of health technology problems. Straight forward solution using one predefined method.

Methods

Markovian models are part of the top – down modeling techniques and are in general representing the behavior of one cohort over the time span of interest. Mathematically Markovian models are represented in the following form:

$$P[X_{n+1} | X_1, X_2, \dots, X_n] = P[X_{n+1} | X_n]$$

As this method is data based and is not modeling the real dynamic of the contact behavior of the population some problem occur:

- Markovian model does not allow a deeper insight into the dynamic effects of spreading of the illnesses
- With this kind of model it is not possible to represent dynamical nonlinear effects like herd immunity.
- Assumptions for heterogeneous population structures can not be modeled. Especially the influence on other age groups or serotypes is very important to be focused on.
- The lack of studies especially concerning serotype shifting is a problem and therefore it is questionable if it can be modeled in an appropriate way to estimate the effectiveness of vaccines.

Another top – down method in modeling infectious diseases are ordinary differential equations (ODEs).

ODEs use population groups in contrast to cohorts. The basic equations for an SIR epidemic are defined as follows:

$$\begin{aligned} d\dot{S} &= -\beta IS \\ d\dot{I} &= \beta IS - \mu I \quad R_0 = \frac{\beta}{\mu} \\ d\dot{R} &= \mu I \end{aligned}$$

Benefits:

- For implementation of different, for example age dependent, parameters the model structure has to be implemented parallel more often. This expands the parameter list and the complexity regarding the solution methods.
- Concurrence of different serotypes or strains can be modeled using more complex assumptions regarding parallel incidence of illnesses and carrying rates.

Disadvantages:

- Each additional feature focused on leads to a change in the equation structure and therefore to an overall model change.
- Changes or refinements are in general time consuming and often not communicable in interdisciplinary groups.
- The main problem of ODE based concepts in modeling the spread and influence of infectious diseases is the parameterization and validation of the model parameters.

Agent based models are bottom – up models of a heterogeneous population of agents and their social interactions. The summed results of the micro level interactions can be used to calculate the interesting macro level behavior. The main features of this method are:

- individual based system structure
- simple equations on the individual level raise complex system behaviour
- herd immunity is model generated, not a parameter
- serotype replacement can be modeled in a natural way

Table 1: Comparison of main features of the modeling and simulation approaches of interest

	Markov	ODE	AB
Time Axis	Discrete	Dynamic	Both
Vaccination	Steady State	Dynamic	Dynamic
Herd Immunity	Factor	Dynamic	Dynamic
Serotype Replacement	-	Dynamic	Dynamic
Population	Cohort	Age Groups	Individuals
	Static	Dynamic	Dynamic

Results

To investigate the benefits and drawbacks a problem was implemented using all three methods. A differential equation model and an agent based model could reproduce results of published Markovian models. As soon as we consider population dynamics, herd immunity and serotype replacement the Markovian model is not able to fulfil the structural requirements any more while dynamic approaches still work.

Agent based models show the best flexibility and performance regarding usage of complex data.

Outlook

Dynamic models offer more information and opportunities for epidemic simulation. Using a pool of different approaches provides at least better results, because the best suited model can be taken in each case. Therefore a new extended structure (shown in Figure 2) should be developed.

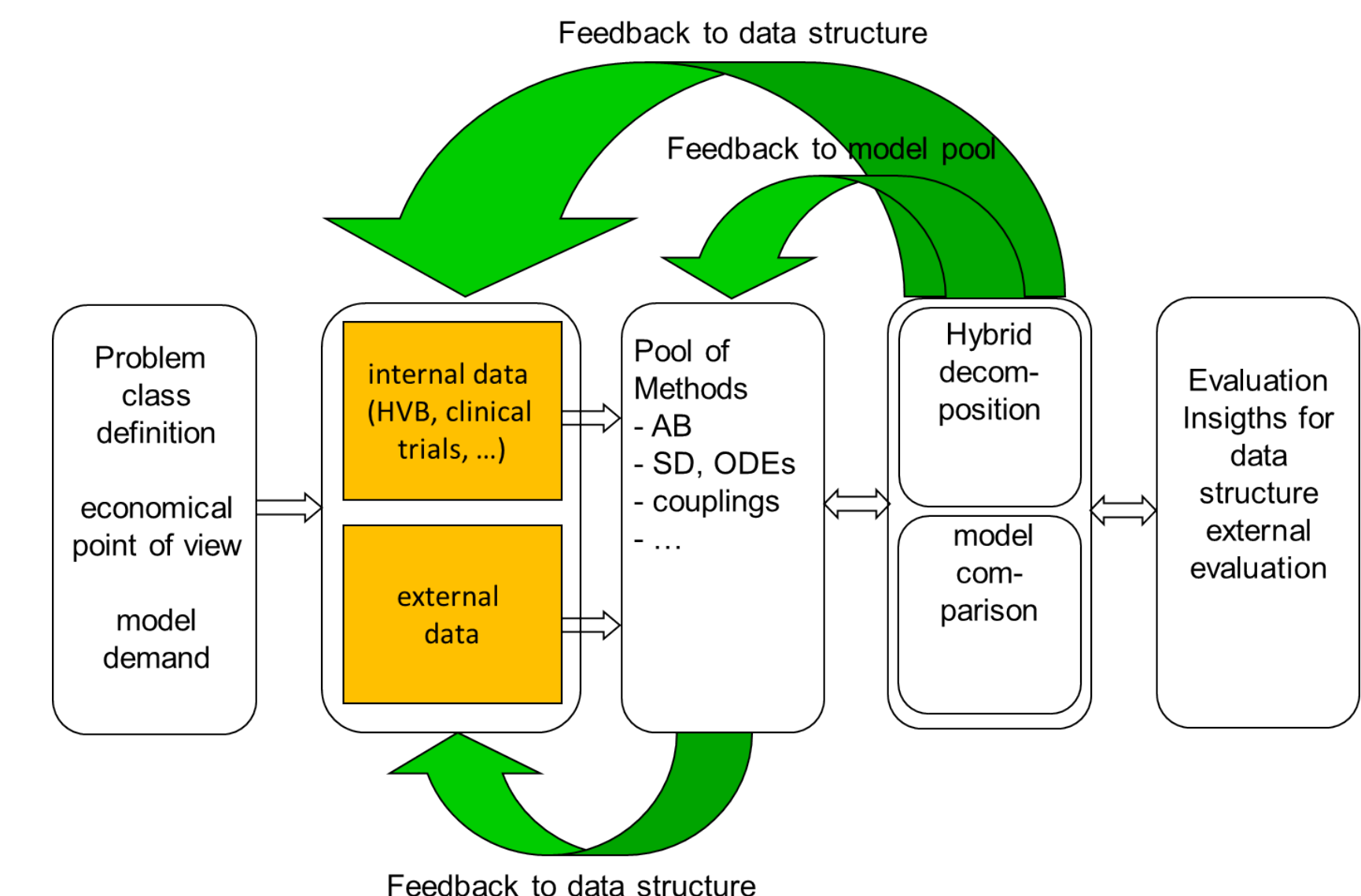


Figure 2: Flow diagram with feedback loops and model decomposition for the overall problem solving strategy for infectious disease questions

The benefits of this new structure are:

- higher flexibility in the modeling process
- better interdisciplinarity and thereby better validation opportunities
- improvement of data quality by feedback from modeling processes
- hybrid model decomposition leads to lower error ranges

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