HERD IMMUNITY AS A RESULT IN DYNAMIC AGENT-BASED EPIDEMIC MODELS
Miksch F, Popper N, Zauner G, Endel G, Schiller-Fruhwirth P, Breitenecker F
Vienna University of Technology, Vienna, Austria; DPH Simulation Services, Vienna, Austria

OBJECTIVES: Herd immunity describes a phenomenon in the area of communicable diseases. Pathogens are spread by infected persons. Protecting a part of the population—vaccination—lowers the overall appearance of pathogens as these people cannot spread pathogens any more. Not protected people profit by fewer contacts with pathogens, and further, a lower number of infections for them can be expected. Classic Markov model cannot provide herd immunity as a result. In this work, we propose calculations of herd immunity directly in real life and 2) depends on several factors.

METHODS: Classic Markov models require herd immunity as a static input parameter that cannot be provided. The developed agent-based model includes single persons with different infection states and a single pathogen. Every agent is part of a social contact model. It is possible to simulate scenarios without vaccinations and with different vaccination strategies. Herd immunity as a result of the dynamic model is calculated as the reduction of the late epidemics, and show herd immunity dynamically in different states of the model. Appearance of herd immunity is very disputed because it 1) cannot be measured directly in real life and 2) depends on several factors. METHODS: Classic Markov models require herd immunity as a static input parameter that cannot be provided. The developed agent-based model includes single persons with different infection states and a single pathogen. Every agent is part of a social contact model. It is possible to simulate scenarios without vaccinations and with different vaccination strategies. Herd immunity as a result of the dynamic model is calculated as the reduction of the late epidemics, and show herd immunity dynamically in different states of the model. Appearance of herd immunity is very disputed because it 1) cannot be measured directly in real life and 2) depends on several factors.

RESULTS: Results show herd immunity as simulation result depending not only on vaccination strategies but also on other system parameters. Further work extends the social contact structure with places like houses, schools, or workplaces that are expected to have an impact on herd immunity as well. CONCLUSIONS: Results can be implemented in systems for calculating new strategies for vaccination programs. Current work considers two or more concurrent serotypes where herd immunity and serotype replacement affects each other. In this case, different definitions of herd immunity are possible.

THE DEVELOPMENT AND VALIDATION OF A DECISION MODEL REPRESENTING THE FULL DISEASE COURSE OF ACUTE MYELOID LEUKEMIA
Leunis A, van Beers EH, Lowenberg B, Redkop WK, Uyl-De Groot CA
Institute for Medical Technology Assessment (iMTA), Rotterdam, The Netherlands; Syneo Diagnostics BV, Rotterdam, The Netherlands; Erasmus University Medical Center, Rotterdam, The Netherlands

OBJECTIVES: Acute myeloid leukemia (AML) is a heterogeneous disease, consisting of several subtypes with a variety in prognosis, a new genomics technology, the AML profiler, has been developed that identifies new genetic subtypes. Since no decision model exists that describes the full disease course of AML, the potential cost-effectiveness of this test cannot yet be determined. The aim of this study is to fill this gap and develop and validate a disease progression model for AML. METHODS: The structure of the model and the identification of relevant parameters were based on the literature and expert opinion. All input parameters were estimated from clinical trial data (HOVON data) for patients aged 16 to 80 years. The internal and external validity of the model was evaluated by comparing model-based survival results with the results from HOVON trials and the literature. RESULTS: Important prognostic factors were derived from the literature and expert opinion and a microsimulation model (i.e., individual patient sampling) was designed to incorporate all important prognostic factors in the model. The prognostic factors were included as covariates in parametric survival functions for two events: relapse and death. The model combined these survival functions with individual patient data to calculate life-years per patient. The average 5-year survival of the simulated patient cohort was 40%, which is similar to the survival found in HOVON trials and the literature. DISCUSSION: The validity of the model was achieved by involving clinical experts in the construction of the model. The survival estimated using the model corresponds with those seen elsewhere, suggesting an acceptable level of internal and external validity. Therefore, the model can be used to assess the cost-effectiveness of AML genomics technologies such as the AML profiler. Moreover, the model can be used for other cost-effectiveness analyses in the field of AML.

USING AHP WEIGHTS TO FILL MISSING GAPS IN MARKOV DECISION MODELS
Ando G, Kowal S, Reinaud F
IHS, London, UK

OBJECTIVES: The increasing use of risk-sharing in reimbursement decisions across major markets necessitates that key stakeholders understand the role of this concept in shaping drug development and regulatory decision-making. The objective of this research was to examine global patterns in risk-sharing agreements and to provide a comprehensive understanding of the current and future impact of this fast-evolving concept. METHODS: Primary research was conducted through 50 in-depth 45-minute telephone interviews in native languages. Subjects were carefully selected and represented payers, government agencies, and HTA organizations in nine markets (Europe 5, Australia, New Zealand, United States, and Canada) to understand their assessment of the role which risk-sharing agreements have—or have not—played in their respective markets, and whether they will do so in the future. This was complemented with secondary research of reimbursement decisions around the world based on a newly created database of risk-sharing agreements around the world. RESULTS: In some countries such as the United Kingdom and Italy, for certain therapeutic areas such as oncology, these agreements almost act as a substitute for the normal reimbursement process, but primary research indicates that this practice faces significant resistance at many layers. Still, many other countries are seeking to understand the potential applicability of risk-shares to their own market. Also, risk-share agreements are being examined for their potential in several other therapeutic areas. While population- and patient-level agreements remain the most popular, we conclude that the objective of this research was to examine global patterns in risk-sharing agreements and to provide a comprehensive understanding of the current and future impact of this fast-evolving concept. METHODS: Primary research was conducted through 50 in-depth 45-minute telephone interviews in native languages. Subjects were carefully selected and represented payers, government agencies, and HTA organizations in nine markets (Europe 5, Australia, New Zealand, United States, and Canada) to understand their assessment of the role which risk-sharing agreements have—or have not—played in their respective markets, and whether they will do so in the future. This was complemented with secondary research of reimbursement decisions around the world based on a newly created database of risk-sharing agreements around the world. RESULTS: In some countries such as the United Kingdom and Italy, for certain therapeutic areas such as oncology, these agreements almost act as a substitute for the normal reimbursement process, but primary research indicates that this practice faces significant resistance at many layers. Still, many other countries are seeking to understand the potential applicability of risk-shares to their own market. Also, risk-share agreements are being examined for their potential in several other therapeutic areas. While population- and patient-level agreements remain the most popular, we conclude that the objective of this research was to examine global patterns in risk-sharing agreements and to provide a comprehensive understanding of the current and future impact of this fast-evolving concept. RESULTS: In some countries such as the United Kingdom and Italy, for certain therapeutic areas such as oncology, these agreements almost act as a substitute for the normal reimbursement process, but primary research indicates that this practice faces significant resistance at many layers. Still, many other countries are seeking to understand the potential applicability of risk-shares to their own market. Also, risk-share agreements are being examined for their potential in several other therapeutic areas. While population- and patient-level agreements remain the most popular, we conclude that the objective of this research was to examine global patterns in risk-sharing agreements and to provide a comprehensive understanding of the current and future impact of this fast-evolving concept. RESULTS: In some countries such as the United Kingdom and Italy, for certain therapeutic areas such as oncology, these agreements almost act as a substitute for the normal reimbursement process, but primary research indicates that this practice faces significant resistance at many layers. Still, many other countries are seeking to understand the potential applicability of risk-shares to their own market. Also, risk-share agreements are being examined for their potential in several other therapeutic areas. While population- and patient-level agreements remain the most popular, we conclude that the objective of this research was to examine global patterns in risk-sharing agreements and to provide a comprehensive understanding of the current and future impact of this fast-evolving concept.