Obuda University
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MINI SYMPOSIUM

2026

Andrea De Gaetano, MD, PhD (math), JD, DHC has been Researcher (1990-2001), Director of Research (full professor, 2001-2026) and Director of the Institute for Biomedical Research and Innovation in Palermo (2020-2026) within the National Research Council of Italy. A certified emergency surgeon by training (Italy) with ECFMG certification (USA), he attained both M.Sc. (USA) and Ph.D. (France) degrees in Applied Mathematics, is a Juris Doctor with Italian Bar license and is Doctor Honoris Causa (BioStatistics). He is currently Distinguished Professor (Full Professor with research endowment) with Óbuda University Dept. of Biomatics, Budapest; Adjunct Professor of Mathematical Statistics, Mahidol University Dept. of Mathematics, Bangkok; and Senior Associated Researcher with the Institute for Systems Analysis and Informatics of the National Research Council of Italy, CNR-IASI, Rome.

His research interests focus on the mathematical modelling of physiological systems with ODEs, Stochastic and Fractional differential equations, and on the attending estimation of the model parameters from experimental observations. He has published so far over 300 full-length papers on international peer-reviewed journals, largely on the mathematical modelling of energy metabolism (Google Scholar metrics: 14383 citations, h-index 52 as of June 10, 2026). He has taught Mathematical Statistics at the Universities of Urbino, Copenhagen and Mahidol Bangkok. He has obtained approx 5.1 MEuro funding for research through a series of EC-financed FP and H2020 projects, foreign financed grants and several Italian projects (Ministry of Research, Ministry of Defense). He is Past President of the European Society for Mathematical and Theoretical Biology, and has served as the Italian National Academic delegate to the NATO Scientific and Technical Organization, Human Factors and Medicine Panel and to EDA European Defense Agency, Captech Simulation.

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Obuda University-Room F09

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Continuous-time Markov chain to ordinary differential equation models via equilibrium-constrained MaxCal

We develop a methodology for modeling chronic disease progression using finite-state continuous-time Markov chains (CTMCs), establishing the connection to deterministic ordinary differential equation (ODE) models and estimating model parameters from equilibrium distributions under sparsity and holding-time constraints. The identification of the infinitesimal generator of a CTMC from a stationary distribution is a rank-deficient inverse problem. We formulate an equilibrium-constrained Maximum Caliber (MaxCal) approach for selecting generators under stationarity, sparsity, and holding-time constraints, and we connect the resulting generator to its mean-field ODE through a single fluid-limit theorem. We consider a diabetes application where the direct literature-based six-state disease model does not admit a positive exact equilibrium at the observed NHANES state proportions. We therefore augment the equilibrium-calibration step with an open-population healthy reservoir, estimate an average stationary distribution from NHANES survey cycles 2006--2020, and determine a minimal exact positive calibration compatible with the transition graph and selected literature constraints.

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