

## IBES Invited Talk 2

### The Long Path to Usable AI

Prof. Barbara Di Camillo

Department of Information Engineering, University of Padova,  
Padova, Italy



The barriers limiting the impact of practical application of artificial intelligence methods in health care have been inherent, besides to the characteristics of big data, to the unmet needs of the final users. This includes, from the very beginning of the data analysis path, the difficulty to manage in an automatic way huge amounts of input data, often of a different nature (continuous, discrete, categorical variables) and collected as a time series of sparse and not equally distributed events. Other barriers to AI use in public health management include the need to use models and biomarkers that can truly generalize on different datasets and the need to be able to visualize the clinical data as a process that highlights the relationship between clinical decisions and events.

In this contribution, I would like to suggest some paths that, in my experience, lead the data mining and machine learning approaches toward a real use in clinical research and healthcare practice. In particular, I will touch, through real examples, the management of input data and how this can be solved automatically using deep learning; the problem of model recalibration; the problem of turning long and numerous series of clinical events into a process that includes and gives insight into clinical actions and their effects.

Bio:

Barbara Di Camillo is a full professor in computer science with the Department of Information Engineering, University of Padova. Her research activity is centered on the development and application of advanced modeling, data mining, and machine learning methods for high-throughput biological data analysis in the field of Bioinformatics and Health Informatics. This includes model/methods development and application in the field of systems biology, reverse engineering, and predictive medicine. In particular, she has been working on omics data studying metagenomics and transcriptomics regulatory networks and cell-cell communication networks from scRNAseq data. She is working on the use of dynamic Bayesian networks to model disease dynamics and the effect of the interaction of different variables (societal, clinical, environmental,

and genetic) and their effect on complex clinical phenotypes.

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