

Data Assimilation: Mathematical Concepts and Instructive Examples

Editor(s): Rodolfo Guzzi

Affiliation(s): Department of Experimental Medicine, Systems Biology Group Lab, Sapienza University, Rome, Italy

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A typical problem in applied mathematics and science is to estimate the future state of a system, given its dynamics and its current state. First of all, one needs to understand the behavior of the system, usually defined by a set of equations of partial or ordinary differential equations. Then model parameters are compared by experimental data with specific methods optimization fitting the dynamical system by any relative time-series data that is available.

However, the mathematical modeling, although it is significant in itself, may have limited predictive value due to its idealized assumptions, the measurement error and parameters, and chaotic behavior of the system. Despite these limitations, we have complex macro-models that can make weather forecasts and predict

the climatology of planets. The question is: are we able to predict the evolution of a biological micro-systems, with the same approach adopted for meteorology and climatology?

The book by Rodolfo Guzzi entitled “Data assimilation: mathematical concepts and instructive examples” contains the answer. Data Assimilation is a mathematical technique allowing us to get all the information, including observational data, any a priori information and a deterministic model describing our system, available within a time window. Data assimilation is based on the estimation theory or theory of the inverse problem that is an organized set of mathematical techniques by which we get information about the physical world by observation. In a conventional problem, usually called a “forward problem,” one uses a set of known a priori parameters to predict the state of the physical system. Data assimilation is an “inverse problem” where one attempts to use available observation of the state of the system to estimate poorly known parameters of the system’s state itself. The reason why the Data Assimilation is so compelling is that it seeks to produce an analysis that fits a set of observation, taken over a time window (not just the remarks made at one instant in time), subjects to the strong constraint that the evolution of the analyzed quantities is governed by a deterministic model describing the given observation. Thanks to its flexibility Data Assimilation has been applied to several fields, from the numerical weather prediction, where it was born, to planetary climate analysis, up to the evolution of biological cells or in the robotic system. One begins with a forecast model, often called background, frequently updated with noisy and sparse measurements. The upgraded background, in light of the new observation, produces an analysis, which, under suitable assumptions is the maximum estimate of the model state vector. Then, the model is restarted from analysis and provides a new background forecast. Data Assimilation and model forecast are combined into observing system simulation experiment, quantifying the effect of changes in the observation accuracy, type, location and

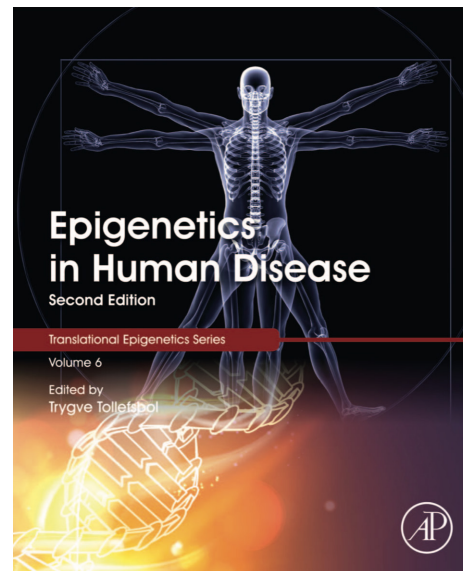
frequency on the accuracy of the numerical forecast. The method, however, suffers from severe limitations, because soon enough the forecasted parameters diverge from the actual values or become chaotic, then the optimal procedures would combine the most exhaustive theoretical and observational knowledge taking into account the errors of observation and those due to the model. To account for uncertainties, Lorenz suggested in 1965 that, instead of simulating a single initial condition by the best estimate of the state of the system under investigation, one should consider a set or ensemble of initial conditions, each from a statistically similar estimate of the true initial state. Then the ensemble gives a Monte Carlo estimate of the uncertainty in a given model. Under these assumptions, the ensemble mean constitutes an empirical maximum-likelihood estimation of the true state of the system.

The first chapter contains a right amount of historical information and background material in which are defined the historical perspective, starting from Newton to the more recent evolutions of Data Assimilation. The second chapter introduces the representation of the physical system and the different approaches developed by different authors. The third chapter presents the main effective techniques. The fourth chapter contains the advanced data assimilation methods with a particular emphasis to Bayesian inference. A final chapter is devoted to the applications. In this chapter, there are also the receipts for the data assimilation in biology and medicine.

Data Assimilation: Mathematical Concept and Instructive Examples" is a nice book for non-experts who would like to go in into the data assimilation area. The step-by-step introduction of the concepts with applications renders it suitable as a textbook for graduate courses and provides a right direction to young researchers.

References

Lorenz, EN. 1965 A study of the predictability of a 28-variable atmospheric model. *Tellus*, vol 17, pp. 321–333



Epigenetics in Human Disease, II edition

Editor(s): Trygve O. Tollefsbol

Affiliation(s): University of Alabama at Birmingham, AL, United States

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Epigenetics was defined for the first time in 1942 by Conrad Hal Waddington as “the branch of biology which studies the causal interactions between genes and their products, which bring the phenotype into being”. At that time, the biochemical nature of genes was unknown as well as their role as repositories and transmitters of the genetic information (Waddington 1942). At that time, and for many years after, epigenetic mechanisms were referred solely to the cellular differentiation processes and to the embryonic development. Around 1990, however, it became clear that alteration of the epigenetic homeostasis was associated to (if not directly causative for) some pathogenic process. Still in 2000 only four diseases had a recognized epigenetic basis: Fragile X syndrome, ICF syndrome, Rett syndrome and tumors (Fuso, 2013).

But, in the last two decades, increasing evidences indicate that a great number of human diseases with multifactorial origin have (or may have) epigenetic basis. This is also due to the great technical advances in the field of epigenetic research. Among the human diseases showing epigenetic components, aging-related and neurodegenerative diseases are object of the most intense research.

This could sound strange, when considering that epigenetic changes were for a long time associated to developing organisms and differentiating or, at least, replicating cells. Waddington described the epigenetic processes through a conceptual model, sustaining that the interactions between the genes and their surroundings (i.e. their “environment”) could result in different phenotypes, starting from the same genetic material. He used the famous metaphor of the “epigenetic landscape” to explain the biological development, stating that cell fates were established during the development, by analogy with a marble rolling down from high places to the point of lowest local elevation. The increasing irreversibility associated with cell type differentiation was imagined as due to ridges, rising along the slope where the stone is rolling down, directing the marble into different valleys. Today we know that the cellular environment, as well as the organism environment, can induce local and sequence specific epigenetic changes even in terminally differentiated cells, eventually causing a drift from the healthy aging process towards a diseased condition. As a consequence, we now retain the concept that epigenetic mechanisms can function as mediators of environmental and micro-environmental stimuli, possibly causing diseases throughout the whole life.

The book authored by Trygve O. Tollefsbol entitled “Epigenetics in Human Disease”, arrived to its second edition, presents the contributions from more than one hundred researchers, collected in 33 chapters, and results in a comprehensive and complete guide to understand what diseases have epigenetic basis and which epigenetic mechanisms are involved. All the modification today recognized as “epigenetic” are taken into consideration across the different chapters: DNAmethylation and hydroxymethylation, histones modifications, chromatin remodeling, non-coding RNAs. The book is organized in thematic sections. After the introduction, a section dedicated to the methodological aspect allows epigenesists and also non-experts to learn about the state-of-the-art of the epigenetic assays. The following sections present the most updated knowledge and perspectives on the role of epigenetic in cancer, neurological diseases, autoimmune diseases, metabolic disorders, allergic diseases, cardiovascular diseases, infections and gynecological disorders. Then a last section is aimed at clarifying the complex epigenetic pathways related to the transgenerational inheritance of the diseases,

the human developmental and imprinting disorders, the stem cells epigenetics and the aging associated diseases. Then, a last section highlights the future perspectives with particular emphasis to epidemiology and public health problems. One interesting aspect of the epigenetic traits is that, on the one hand, these can be induced by environmental factors but, on the other, they are potentially reversible. The potential for exploring the efficacy of epigenetic drugs and non-medical epigenetic interventions, aimed at treating or even at preventing the onset of pathologies, is incredibly large: the already existing therapies and the possible intervention are taken into consideration as well throughout the chapters of the book.

“Epigenetics in Human Disease” is therefore a complete book that can constitute a basis for a wide range of researchers, from epigenesists, to epigenetic newcomer, to undergraduate students.

References

- Fuso A 2013, The ‘golden age’ of DNA methylation in neurodegenerative diseases. *Clinical Chemistry and Laboratory Medicine*. vol. 51, pp. 523-534.
- Waddington CH 1942, The epigenotype. *Endeavour*. vol. 1, pp. 18-20.

