

Book review

Review of "Mining Imperfect Data" by Ronald K. Pearson Francisco Azuaje*

Address: Computer Science Research Institute, University of Ulster, Jordanstown, Co. Antrim, BT37 0QB, Northern Ireland, UK

Email: Francisco Azuaje* - fj.azuaje@ulster.ac.uk

* Corresponding author

Published: 18 July 2005

Received: 08 July 2005

BioMedical Engineering OnLine 2005, 4:43 doi:10.1186/1475-925X-4-43

Accepted: 18 July 2005

This article is available from: <http://www.biomedical-engineering-online.com/content/4/1/43>

© 2005 Azuaje; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Book details

Pearson RK: *Mining Imperfect Data: Dealing with Contamination and Incomplete Records* Philadelphia: SIAM; 2005. 305 pages, ISBN 0-89871-582-2, \$70.

Imperfect data are prevalent in health informatics and biomedical engineering. Therefore, data analysis and modelling tools in real world applications must be able to represent, recognise and process imperfect data. Several studies have aimed to classify the different types of data imperfections and their possible sources. Incompleteness, imprecision, inconsistency and uncertainty are some of the problems associated with data imperfection [1]. In data-driven application domains, such as bioinformatics and medical informatics, these types of problems may originate from unreliable data acquisition sources, faulty sensors, data collection errors and the lack of data representation standards. Although these factors and constraints are widely accepted by the health informatics and data mining communities, most applications have traditionally ignore the need for developing appropriate approaches to representing and reasoning with imperfect data.

Ronald Pearson's book discusses the detection of different types of imperfect data, their potential sources, implications and methods to treat them. It mainly focuses on three types of data imperfections: Outliers, missing data and misalignments. The introductory chapter defines these anomalies, presents a rationale for their analysis and overviews important approaches to pre-processing and detection. The second chapter is a deeper discussion of these types of imperfections, their causes and consequences for data analysis. The third chapter describes techniques for detecting univariate outliers followed by a

chapter on data pre-processing, which covers techniques for dealing with missing data, time-series and multivariate outliers. Chapter 5 concentrates on the application of functional equations and inequalities to characterise data. Chapter 6 further discusses the generalised sensitivity analysis (GSA) framework, which is one of the key data analysis tools applied in the book. Pearson summarises the basis for GSA with the following statement: "A 'good' data analysis result should be insensitive to small changes in either the methods or the datasets on which the analysis is based". Chapter 7 describes different data sampling strategies that may be applied to implement GSA. The last chapter discusses some of the challenges and open questions for mining imperfect data. This book emphasises the application of boxplots for summarising, visualising and comparing results. Examples are illustrated using real data sets relevant to medicine, bioinformatics and industrial applications.

The book provides the reader with clear descriptions and accessible discussions of problems, motivations, methods and interpretations. The author excels when describing the importance of tools and their applications. The first chapter is a prime example of how to introduce important concepts and methods to a wide readership that may be composed by students, researchers and non-specialists.

The book should not be seen as a comprehensive, detailed description of methods for dealing with different types of data imperfections. For example, with regard to missing value estimation, it might be complemented by Little and Rubin's *Statistical Analysis With Missing Data* [2] or Allison's *Missing Data* [3]. *Statistical Analysis and Data Display* by Heiberger and Holland [4] may be a relevant reference

for summarising and comparing data analysis results [5]. Although the chapter on functional equations is important, I would have expected a stronger rationale for stressing this particular approach. The final chapter offers an interesting discussion on key challenges for mining imperfect data. Nevertheless, readers could have been benefited from a concluding chapter that also summarises the author's suggestions on when and why specific approaches should be applied. Moreover, the discussion on analysing large datasets could be enriched by including other, more recent investigations from the areas of data mining and visualisation, as well as different applications domains, such as bioinformatics.

Having said that, it is necessary to highlight that this book represents a significant contribution, which should benefit anyone interested in developing or assessing data mining and machine learning applications in medicine and biology. I will certainly keep it as a key reference and recommended reading for final year undergraduate and post-graduate students.

References

1. Parsons S: **Current approaches to handling imperfect information in data and knowledge bases.** *IEEE Transactions on Knowledge and Data Engineering* 1996, **8**:353-372.
2. Little RJA, Rubin DB: *Statistical Analysis With Missing Data* Second edition. New York: Wiley; 2002.
3. Allison PD: *Missing Data* Oaks, CA: Sage Publications; 2001.
4. Heiberger RM, Holland B: **Statistical Analysis and Data Display: An Intermediate Course with Examples in S-PLUS, R, and SAS.** New York: Springer; 2004.
5. Azuaje F: **Review of "Statistical Analysis and Data Display" by Richard M. Heiberger and Burt Holland.** *BioMedical Engineering OnLine* 2005, **4**:18.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

