

Combining scenario analysis and metadata to analyse patient workflows for common diseases

Klaus Peter Schipper¹⁾, Henrik Krarup¹⁾, Søren Risom Kristensen¹⁾

1) Department of Clinical Biochemistry, Aalborg Hospital

Introduction

Clinical chemistry is a central part of every hospital. With the increasing abilities of modern medicine the hospital laboratories have lost their individual forms and turned into fully automated highly computerised work places. Even though automation makes laboratories more efficient most hospitals suffer from yearly growth in number of blood samples and results delivered. Rates of 7-10% increase per year are normal for European hospitals. Little work has been done to connect patient populations to the actual process during the hospital stay. Following diagnostic efforts still remains complicated and tedious, often just secondary result of clinical studies.

By applying metadata analysis the authors have been able to demonstrate, that isolation of patient populations across departments and local hospitals is possible and enables analysis of clinical chemistry usage.

Methods

From the LIS(laboratory information system) samples of patients are drawn with one single diagnosis. The diagnosis, extracted from the Danish patient register, is matched to the hospital information system. For the initial trials all patients with more than one diagnosis or uncertainty about the diagnosis were excluded.

One year of patient data for one diagnosis with all results was extracted, typically 1000-1400 cases. The cases were combined with all data from the other sources to construct metadata sets. During this process the datasize typically changes from 1.2MB to 36.4GB of data. On a UNIX computer running STATA and R along with specialised visualisation routines the data was mined for organisational relations to number and timing of samples.

Visualisation was then made possible by defining reference intervals for each biochemical parameter and its changes during the hospital stay. Together with a clinical reference group the visualisation of pathologic, normal and indifferent values by department was made possible. Patient groups were compared to each other with regards to other confounders.

Results

Despite the use of evidence based medicine the influence of department structure and organisation is obvious. Number of blood samples varied by 48% and number of normal results by more than 320% in the same patient group. Obviously the intention to use rational diagnostic measures is often covered by computerised systems. In all the extreme cases of unnecessary blood sample collection hospital information systems were identified as the main cause. By identifying scenarios in different departments the necessary countermeasures were quite simple changes in instructions or daily rhythm.

Conclusions

Further work is needed to allow analysis of metadata across hospitals and departments. Clinical biochemistry departments need to join the development and distribution of such tools. In simple

diagnosis such as pneumonia the difference is striking and invites to investigate the role of information technology as a negative factor in the cost development.

References

- 1) 1: Hewitt R, Gobbi A, Lee ML: A searching and reporting system for relational databases using a graph-based metadata representation. *J Chem Inf Model*. 2005 Jul-Aug;45(4):863-9.
- 2: Garcia Castro A, Thoraval S, Garcia LJ, Ragan MA: Workflows in bioinformatics: meta-analysis and prototype implementation of a workflow generator. *BMC Bioinformatics*. 2005 Apr 7;6(1):87.
- 3: Brandt CA, Gadagkar R, Rodriguez C, Nadkarni PM: Managing complex change in clinical study metadata. *J Am Med Inform Assoc*. 2004 Sep-Oct;11(5):380-91. Epub 2004 Jun 7.