



Why Your Protocol Mapping Is Wrong And What To Do About It

Radiology has long been plagued by the challenge of accurate protocol mapping. However, Imalogix has emerged as a pioneer in resolving this complex issue. In this article, we delve into how Imalogix has successfully addressed the critical challenges associated with protocol mapping.

Protocol mapping plays a pivotal role in the realm of radiation dose benchmarking, exemplified by the American College of Radiology Dose Index Registry (DIR). This registry relies on the comparison of similar examinations across various institutions. The reliability of DIR benchmarks hinges on the accuracy and comprehensiveness of protocol mapping nationwide. Any inaccuracies in tagging examinations by the sending facility not only skew benchmark data but also lead to inappropriate data comparisons.

Furthermore, protocol mapping is essential for identifying examinations that exceed dose thresholds. Incorrect mapping can result in the application of the wrong threshold, leading to both unnecessary alerts and the overlooking of examinations that should trigger alerts. This concern will be further compounded as healthcare institutions broaden their scope from dose monitoring to encompass comprehensive quality monitoring, in accordance with the recently introduced CMS quality measure. Consequently, the effectiveness of a radiology quality improvement initiative is intrinsically tied to the quality of its protocol mapping.

Unfortunately, conventional protocol mapping techniques have proven to be challenging. One article stated that, "The greatest challenge that remains is that exam code mapping is very difficult to do in a consistent fashion and affects the quality of the data ¹." The manual nature of the mapping task, distributed across various sites, inevitably results in inconsistencies and mismappings. A speaker with the DIR stated, "You can be certain that mismappings are going to occur²."

One major reason for these challenges is the reliance on manual configuration, often by individuals who may be doing it for the first time. Additionally, the plethora of available protocols, with subtle variations, adds complexity to the mapping process, making it difficult to determine the most appropriate protocol for a given situation. The handover of mapping tasks to different staff members over time further exacerbates the issue. In addition to their own learning curve, the new staff members must try to grasp the mapping logic used by their predecessors. Moreover, most traditional systems lack systemic error-checking mechanisms, rendering comprehensive review

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and error identification difficult. These factors combine to make manual input processes slow and error prone.

Another critical issue arises from the absence of vital data in most systems. Most mapping tools rely on either the study description or the protocol name, overlooking the wealth of additional information available at the series level. For instance, the DIR's mapping primarily relies on the study description, which disappointingly often fails to provide an accurate representation of the entire study. Our analysis indicates that study descriptions lead to incorrect exam mapping in 35% of casesⁱ. While some dose tracking software permits the use of protocol names, this approach is still far from infallible, with protocol names failing to accurately reflect the examinations performed in 32% of instances^{*}. The primary reason for the low accuracy is the prevalence of combo studies that include multiple protocols or body regions. To achieve precise protocol mapping, it is imperative to consider both study and serieslevel information.

Imalogix has successfully surmounted these challenges with groundbreaking solutions. At the heart of our innovation is a cutting-edge artificial intelligence system designed specifically for protocol mapping, offering complete automation of the mapping process. This remarkable mapping capability incorporates both series and study level data, enabling it to adeptly handle complex combo examinations. Our artificial intelligence is finely tuned through extensive training on a vast database encompassing nearly a million combinations of series descriptions, protocol names, and study descriptions. To ensure the utmost accuracy in this training set, we implement a rigorous system of checks and balances, including meticulous human curation.

The results speak for themselves, as our AI algorithm boasts a remarkable tenfold reduction in protocol mapping errors compared to traditional methods^{*}. What's more, our database continues to expand dynamically, and our artificial intelligence continues to evolve and adapt as it encounters new information, ensuring that it remains at the forefront of the ever-changing landscape of medicine. Imalogix has elevated the accuracy and efficiency of protocol mapping, ultimately enhancing the quality of radiology benchmarking and patient care.

References:

1. Robinson TJ, Robinson JD, Kanal KM. Implementation of the ACR Dose Index Registry at a Large Academic Institution: Early Experience. *J Digit Imaging*. 2013;26(2):309. doi:10.1007/S10278-012-9546-7

2. DIR All About Mapping Webinar. Accessed September 28, 2023. https://pages.acr.org/DIR_AllAboutMapping.html

ⁱ Imalogix review of protocol mapping algorithms. Data on file.