

Workflow Optimized Reporting of Multi-Region MR Exams with a Novel Image Reading Software – Experiences with a Prototype

Christian Müller-Horvath¹; Christian Plathow¹; Burkhard Ludescher¹; Matthias Philipp Lichy^{1,2}; Valer Canda²; Christoph Zindel²; Claus D. Claussen¹, Heinz-Peter Schlemmer^{1,3}

¹University of Tübingen, Department of Diagnostic and Interventional Radiology, Tübingen, Germany

²Siemens Healthcare, Erlangen, Germany

³German Cancer Research Center, Heidelberg, Germany

Introduction and background

Accurate evaluation of systemic malignancies for optimized and individualized therapy regime involves a reliable TNM classification of all relevant body regions. Within the last decade, whole-body / multi-region cross-sectional imaging became an invaluable clinical tool and the available technologies for this purpose are not limited to CT and PET/CT alone; with the introduction of the Tim technology, there is no doubt that MRI – with its superior soft tissue contrast – also plays an important role in multi-region imaging. While not only true for oncologic whole-body imaging, it is especially clear for these types of MR exams that MRI faces the problem that in clinical routine the almost unlimited numbers of images generated (at our institution the radiologist has to read 1,000 to 1,500 images per patient for a standard whole-body MRI) with their different contrasts and information content are one of the major threats for the reporting radiologist and referring physician. This problem is aggravated when it comes to exact documentation of tumor load, presence of further suspicious lesions and other relevant findings and their presentation at, for example, inter-

disciplinary conferences. But even relatively simple tasks during the reading process, like the generation of cross-references between the different image contrasts / image series and the anatomic sorting of the images, are a daily challenge for radiologists and have a clear impact on the required time for reading and on the accuracy of the final report.

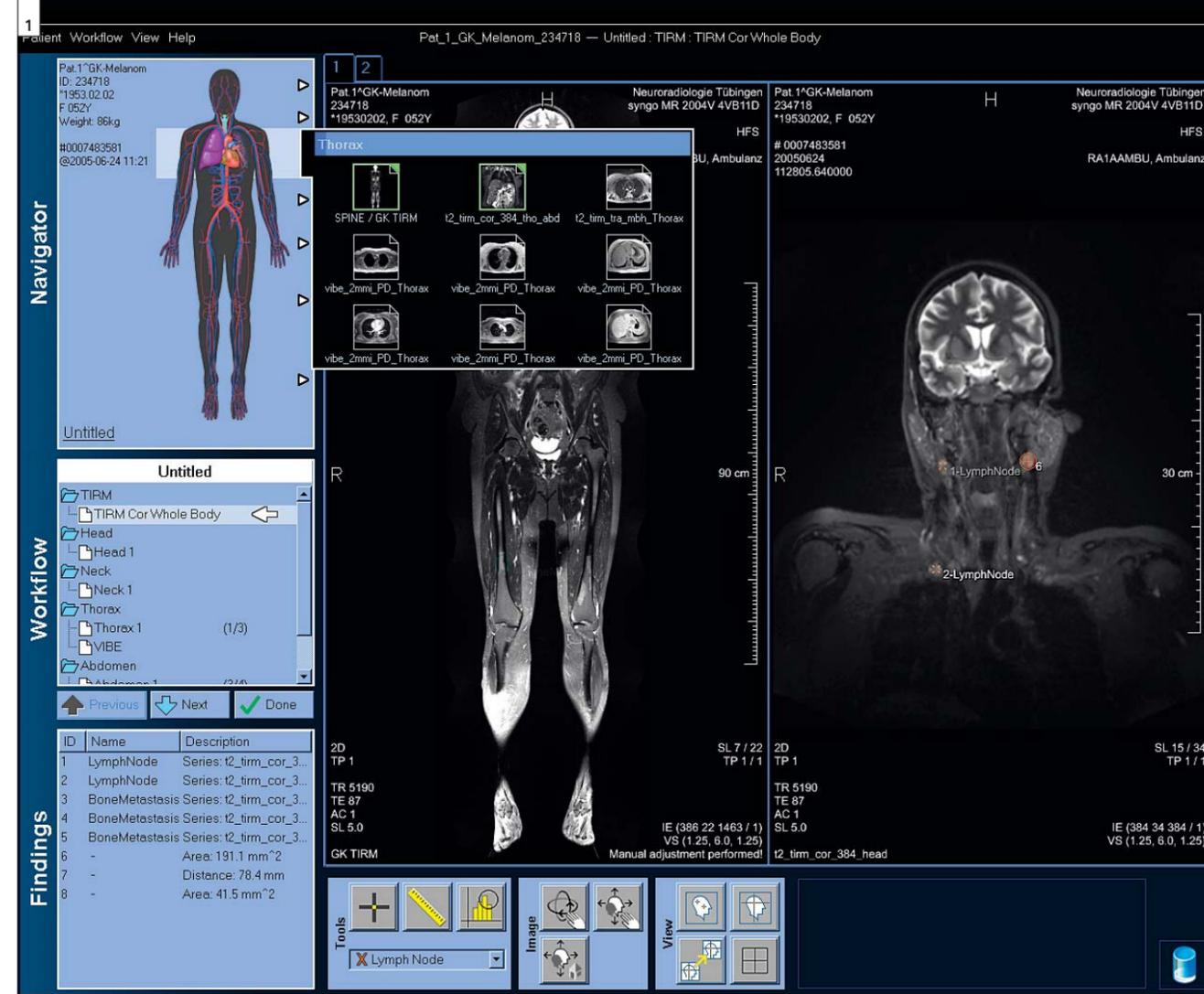
Purpose

The aim of the presented work was therefore to create and evaluate a new software tool to assist and automate the process of reading whole-body / multi-region data sets.

The prototype

In close cooperation between the Department of Diagnostic and Interventional Radiology of the University of Tübingen, Germany, and Siemens Healthcare a novel prototype for workflow optimized reading of multi-region MRI data was developed. This software was based on the research and developer platform MeVislab (MeVis, Center for Medical Imaging Computing, Bremen, Germany). In contrast to a conventional reading software, the user interface of the prototype included

- an anatomical navigator (series are sorted in an automated processing step according to their anatomical coverage)
- a workflow navigator (series are sorted and presented according to their logical assignment e.g. scanning for brain or bone metastases)
- a findings navigator (marked findings are stored in an interactive list). These three elements can be easily identified on the screenshot of the user interface provided in figure 1. The measurement tools implemented in this prototype focus on oncologic reading (e.g. 3D MPR, distance line etc.). In contrast to image interpretation with a traditional reading software, the acquired images are directly transferred from the PACS archive to the prototype system and the images are then prepared by automated pre-processing steps by the software. For this prototype this step includes the preparation / calculation of 3D data sets, image / series sorting and generation of a multi-image TIFF file including preview image stamps. The premise behind this automated pre-processing step is that the radiologist profits both during start-up as well as during the whole reading process. The radiolo-



1 A screenshot of the prototype is shown. In contrast to a conventional image reading software user interface, there are three unique sections labelled “Navigator”, “Workflow” and “Findings”. A whole-body MR exam is loaded and all images defined within a dedicated workflow task are displayed (here: coronal TIRM images). All images are also sorted according to their anatomical relationship (“Navigator” section). Marked findings are listed in the “Findings” section and can easily be retrieved by a single click action. At the bottom, some basic reading tool icons are shown.

gist can start immediately with its real work and has immediate access to all relevant data for precise and accurate interpretation of MRI; image sorting, loading and layout adaption during reading are eliminated ideally in this scenario. Despite the clear time advantage (mainly introduced by the elimination of manually loading and image sorting steps), the main differences / advantages of such a prepared reading workflow compared to a traditional reading procedure are as follows:

1. Reading: at the same time as a suspicious lesion is marked by the radiologist, all available images with the same location (but different contrasts and orienta-

tions) can be displayed via cross reference.

2. Finding documentation: all findings are listed in a dedicated template; cross-linking with dedicated text, finding tables and reference images are available at any time and can be shared between different users.

3. Reproducibility of findings: as a consequence of the above two advantages, all lesions marked in a previous reading can be easily displayed and all images are displayed for follow-up exams and also for conferences; this eliminates the need to locate once again all findings based on a written report.

Materials and methods

To evaluate the clinical potential of this prototype, a multi-reader study was conducted. Thirteen whole-body datasets of patients with advanced malignant melanoma were evaluated by three radiologists: 3 / 13 were female (mean age 65 +/- 14 years), 10 / 13 male (mean age 56 +/- 9 years). All patients were also examined with an 18F FDG PET/CT whole-body scan as reference scan (metastases of malignant melanoma are characterized by high glucose uptake). In all patients, a stage IV was present; this tumor stage is characterized by ubiquitous multiple metastases without preferences to an organ system and therefore rises a big



2A Screenshot of a whole-body reading with a prototype of the newly developed reading software platform (*syngo.via*) is shown in this figure, which is also evaluated at our institution. Most important principles of the prototype tested in this article are preserved and can easily be recognized: the former "Workflow" section is shown on the left hand side. In the upper section, by simply clicking on the desired area of interest, all images are loaded in a predefined layout (here for screening the head and neck section). Findings are listed in the lower row ("Findings Navigator"). Additional images which cannot be assigned to either a dedicated anatomical region or to a workflow are allocated to the "MR Remaining images" task. Different colour layouts and icons enable the radiologist to easily grasp matters such as uncompleted tasks or the presence of unassigned images. At the bottom, a set of tools for changing the screen layout and modifying display options e.g. synchronisation between different image series are available. The full range of reading tools including post-processing tools e.g. image fusion can be easily accessed from any image via corner menus (not shown in this screenshot).

challenge to any cross-section imaging modality in the accurate evaluation of tumor load.

Quantitative measurements for evaluation of the prototype included the required time for loading and opening of an exam, time required for reporting including the comparison of reference series. Documentation was separated also for different body regions (head, neck, thorax, abdomen, pelvis). Also the time required for retrieving a defined lesion was documented. For qualitative evaluation of this prototype, the level of

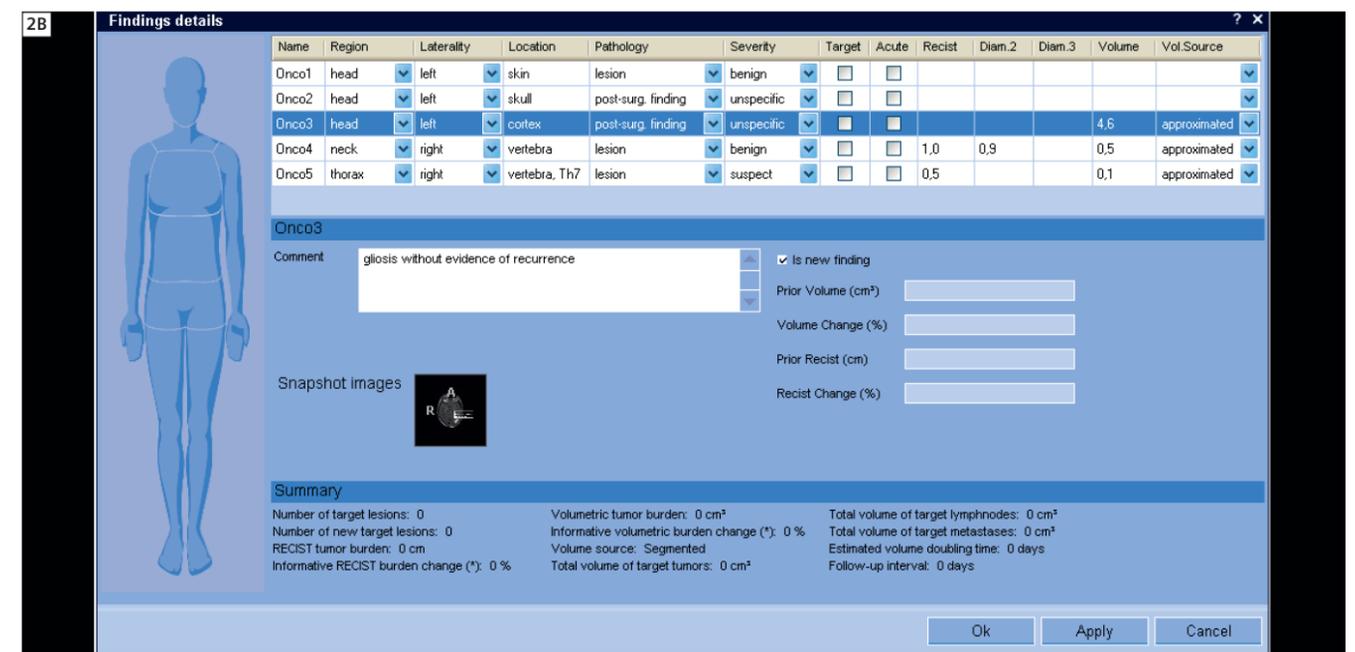
comfort for loading of images, help provided for retrieving a lesion and usability was rated on a 5-point scale (from 0 = poor to 4 = excellent).

All data sets were read by 3 radiologists independently and blinded to any patient data with different levels of clinical experiences (two readers with high experience in all cross section modalities including PET/CT, one with less than six months experience with MR whole-body exams). Statistical analysis included Student-t-tests and calculation of kappa-values for inter-observer variability.

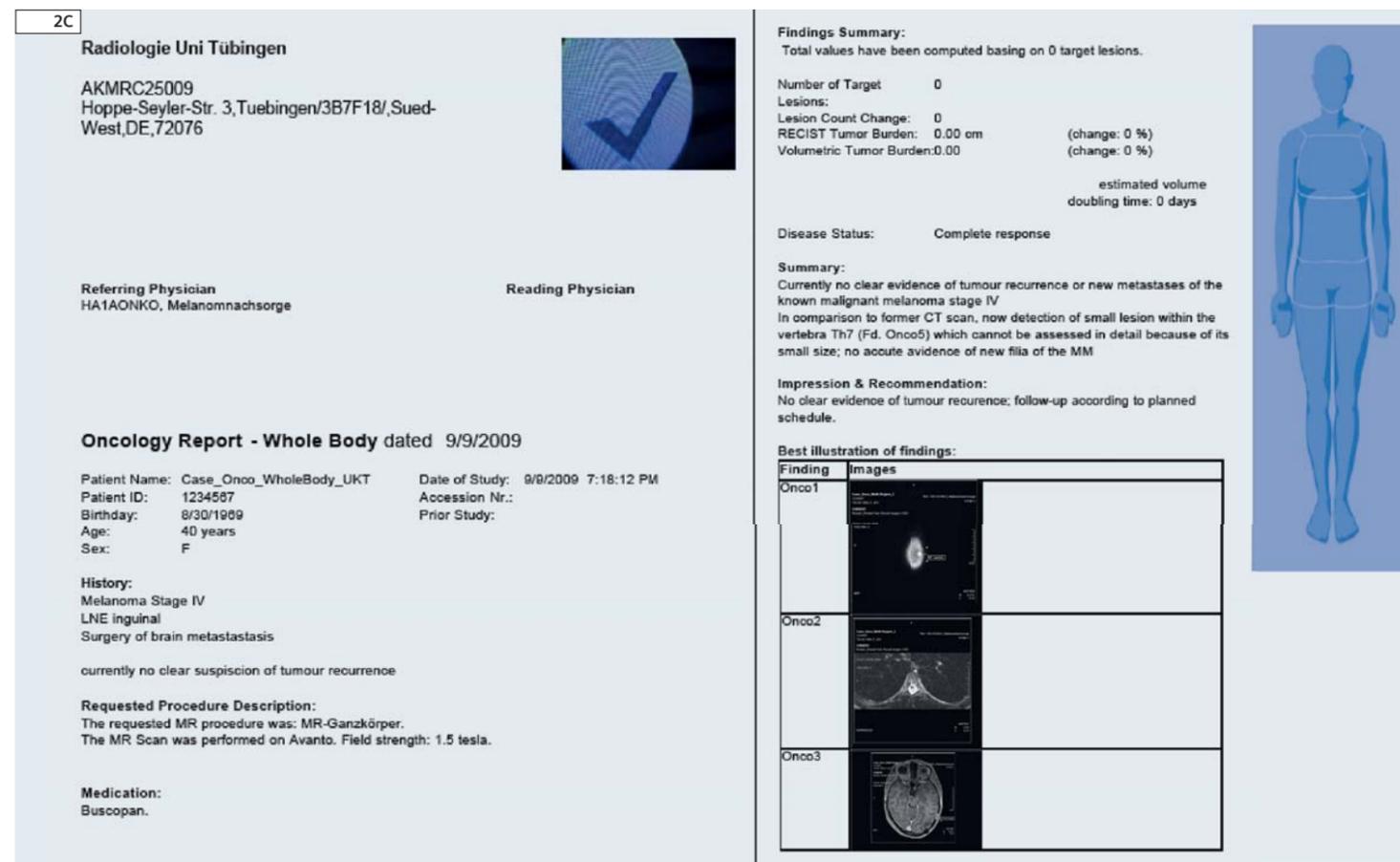
A short comparison between the hardware used for the two evaluated programs is given in table 1.

Results

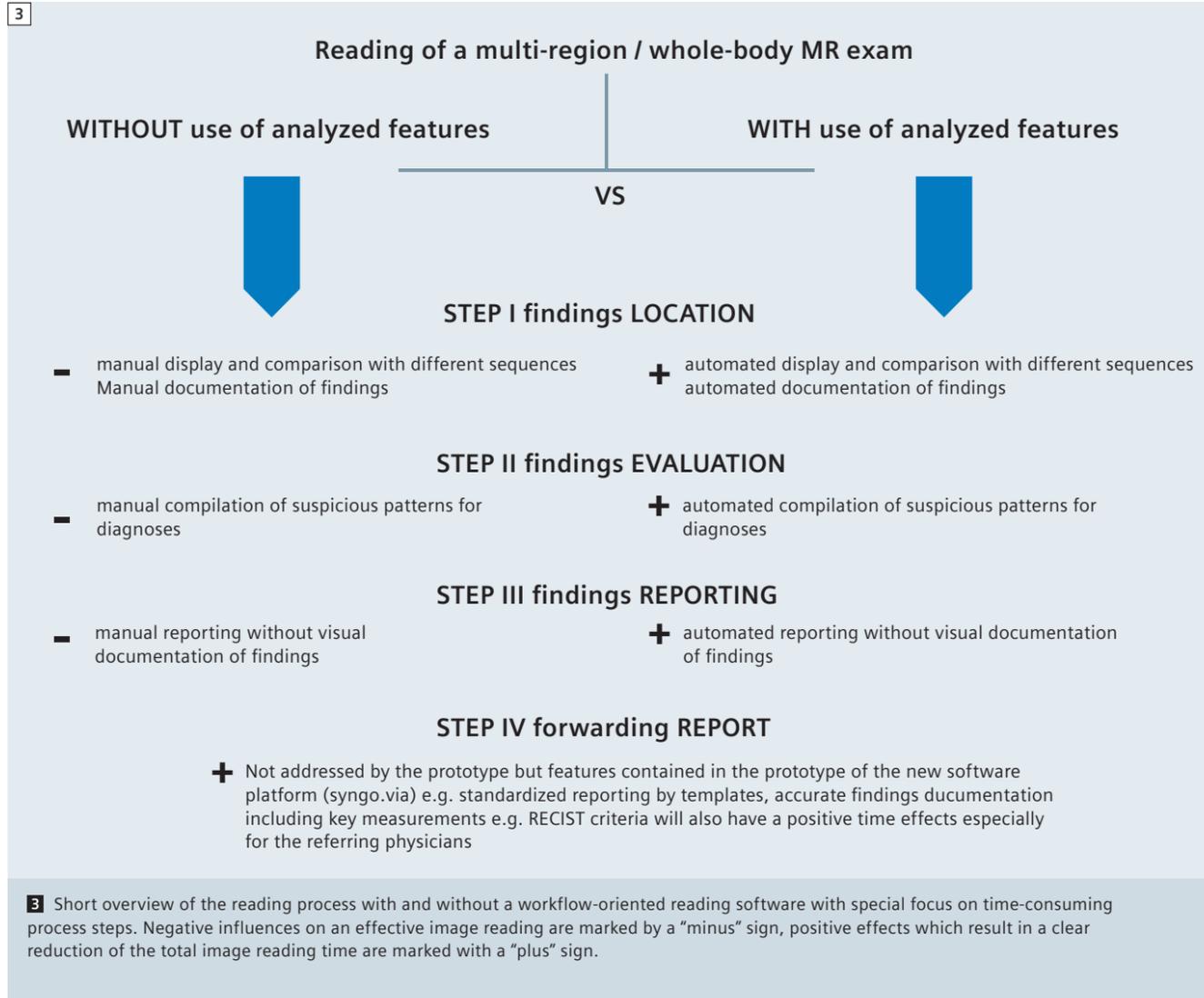
For one MR exam, an average of 1141 images were read by each reader. The average loading time was 39.7 (+/- 5.5) seconds with the conventional reading software and with the prototype 6.5 (+/- 1.4) seconds ($p < 0.01$). To display the different regions, the achieved time reductions by the prototype for readers 1 / 2 / 3 were as follows:



2B In a next step, the new software platform provides a fast and precise definition of all image findings via drop-down menus and input boxes. If a malignancy is present and the data assigned, all relevant information for the referring physician is summarized in the lower section. For an oncology study as performed in this example, this also includes the tumor burden according to RECIST criteria.



2C The results can also be transferred into a standardized report form which can also include images for a better visualization of the findings for the referring physician and the patient. This screenshot shows an example of how such a report can look.



head region 36 / 50 / 54%,
 thorax region 59 / 56 / 62%,
 abdominal region 62 / 63 / 48%,
 pelvic region 73 / 64 / 55%.
 To retrieve a previously described finding, an average of 148 (+/- 95) seconds were required with the standard reading software whereas this finding was displayed after 2.5 (+/- 0.5) with the prototype (up to 98% time saved).
 In total, 629 lesions were classified as potentially malignant by the three readers (301 with the conventional reading software, 328 with the prototype).
 Based on reference exams, the same number of metastases was detected with both systems and there was no sta-

tistically significant difference between the three readers ($p < 0.01$, $k > 0.9$).

Discussion

One of the main problems in the integration of multi-region / whole-body MR exams in our clinical routine is founded on the immense amount of data which has to be handled during the reading process. While the implementation of PACS systems within a department allows a wide and fast contribution of images throughout the institution and beyond, the implemented software for displaying the images and also for post-processing has not disburdened the radiologist significantly. In reality, without

any real assistance e.g. for image sorting, optimal layouts, no standardized reports etc. provided by these systems, the radiologist has to spend a lot of effort in these operative / administrative tasks and as a consequence negative effects on the time efficiency of the reading process as well as his attention for his real task – providing best care to the patient by accurate and error-free reporting – are likely. A potential approach for improving the efficiency of reading large MRI data sets is shown with the evaluated prototype. Previous studies by different working groups already pointed out that the implementation of an automated working lists and

changes within the workflow chain can result in significant time gains [Gale et al., Siegel et al.]. As an example, Gale et al. could reduce the required time for reading by an "autoread-function" by 38%; by automated importing and sorting of the next exam Siegel et al. could reduce the time between the reading of exams by approximately 10%.
 Cross-section exams with large image data are not read immediately in clinical routine (although a few exceptions do exist, such as computed tomography as part of the emergency room procedure) and before starting the reading process, these images are transferred to a PACS archive. With our prototype, the pre-processing step required 2 to 3 minutes for preparing a whole-body MR exam; compared to the required time in a conventional reading process including archiving the images as well as request and delivery of the whole exam to the reading workstation. This one-time step did not have a negative effect on the reading process. It should also be emphasized that the required time for such a preparation step will clearly be reduced since firstly the available computing power is increasing dramatically each year and secondly the status of the software reported in this article is prototype status. This study clearly demonstrated that a workflow-optimized automated reading software has a clear time

benefit compared to conventional ones. Obviously the radiologist's experience has an effect on the speed and accuracy of the reading process. Nevertheless, even for the highly experienced readers in this study, the time benefit as well as the gain in comfort was obvious; this is especially true for retrieving a pre-defined lesion. In conclusion it can be stated that with the demonstrated new software a significant time saving when working with whole-body data sets can be realized without any compromise with regard to diagnostic confidence and with a significant advantage in terms of convenience. As a result, the problem of evaluating examinations with thousands of images can be approached systematically.
 The tested prototype was implemented to demonstrate the key elements of a new workflow-oriented reading software. After proving the advantages of such a technology, the next step would be the integration of such a new approach in image reading within a framework for a real multi-modality reading platform. The requirements for such a software also include further advancements in handling advanced image data and reading tools such as image fusion for reading, for example, PET/CT data. In addition, techniques for linking the image acquisition and reading without any time delays are also

required to meet the demands for image interpretation on the fly, a prerequisite for efficient reading in emergency scenarios. We are currently testing a prototype of a new image reading software platform and within this platform, the evaluated workflow-features in our prototype are now available for all image modalities; we believe that this represents a great step forward in workflow-oriented image reading technology. The radiologist is supported actively in its reading task in an intuitive as well as efficient way and is not hampered by predetermined steps required by most of currently available reading platforms.

References

- 1 Gale DR, Gale ME, Schwartz RK, Muse VV, Walker RE. An automated PACS workstation interface: a timesaving enhancement. AJR Am J Roentgenol. 2000 Jan;174(1):33-6.
- 2 Siegel E, Reiner B. Work flow redesign: the key to success when using PACS. AJR Am J Roentgenol. 2002 Mar;178(3):563-6.

Contact

Prof. Heinz-Peter Schlemmer
 Department of Radiology
 German Cancer Research Center (DKFZ)
 Im Neuenheimer Feld 280
 69120 Heidelberg
 Germany
 h.schlemmer@dkfz.de

Table 1: For the evaluation of the prototype, a standard PC equipped with two 19" TFT displays was used. For reference, a standard reading workstation was used. Both systems were installed within the same subnetwork. The technical specifications were as follows:

	Prototype	reference reading system (MV 1000)
OS	Microsoft Windows XP	Microsoft Windows 2000
CPU	2x 1.7 GHz Intel Xeon	2x 2.8 GHz Intel Xeon
RAM	1 GB	3 GB
GPU	NVIDIA Quadro4 750 XGL	Matrox Millenium 450
Harddisk controller	Ultra ATA system	SCSI system
Network controller	Intel Pro/100 S	Intel Pro/1000 MT