

## Researchers Develop AI Model to Automatically Segment MRI Images

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OAK BROOK, Ill. — Research scientists in Switzerland have developed and tested a robust AI model that automatically segments major anatomic structures in MRI images, independent of sequence, according to a new study published today in *Radiology*, a journal of the Radiological Society of North America (RSNA). In the study, the model outperformed other publicly available tools.

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Jakob Wasserthal, Ph.D.

MRI provides detailed images of the human body and is essential for diagnosing various medical conditions, from neurological disorders to musculoskeletal injuries. For in-depth interpretation of MRI images, the organs, muscles and bones in the images are outlined or marked, which is known as segmenting.

“MRI images have traditionally been manually segmented, which is a time-consuming process that requires intensive effort by radiologists and is subject to inter-reader variability,” said Jakob Wasserthal, Ph.D., Radiology Department research scientist at University Hospital Basel in Basel, Switzerland. “Automated systems can potentially reduce radiologist’s workload, minimize human errors and provide more consistent and reproducible results.”

Dr. Wasserthal and colleagues built an open-source automated segmentation tool called the TotalSegmentator MRI based on nnU-Net, a self-configuring framework that has set new standards in medical image segmentation. It adapts to any new dataset with minimal user intervention, automatically adjusting its architecture, preprocessing, and training strategies to optimize performance. A similar model for CT (TotalSegmentator CT) is being used by over 300,000 users worldwide to process over 100,000 CT images daily.

In the retrospective study, the researchers trained TotalSegmentator MRI to provide sequence-independent segmentations of major anatomic structures using a randomly sampled dataset of 616 MRI and 527 CT exams.

The training set included segmentations of 80 anatomic structures typically used for measuring volume, characterizing disease, surgical planning and opportunistic screening.

“Our innovation was creating a large data set,” Dr. Wasserthal said. “We used a lot more data and segmented many more organs, bones and muscles than has been previously done. Our model also works across different MRI scanners and image acquisition settings.”

To evaluate the model’s performance, Dice scores—which measure how similar two sets of data are—were calculated between predicted segmentations and radiologist reference standards for segmentations. The model performed well across the 80 structures with a Dice score of 0.839 on an internal MRI test set. It also significantly outperformed two publicly available segmentation models (0.862 versus 0.838 and 0.560) and matched the performance of TotalSegmentator CT.

“To our knowledge, our model is the only one that can automatically segment the highest number of structures on MRIs of any sequence,” he said. “It’s a tool that helps improve radiologists’ work, makes measurements more precise and enables other measurements to be done that would have taken too much time to do manually.”

In addition to research and AI product development, Dr. Wasserthal said the model could potentially be used clinically for treatment planning, monitoring disease progression, and opportunistic screening.

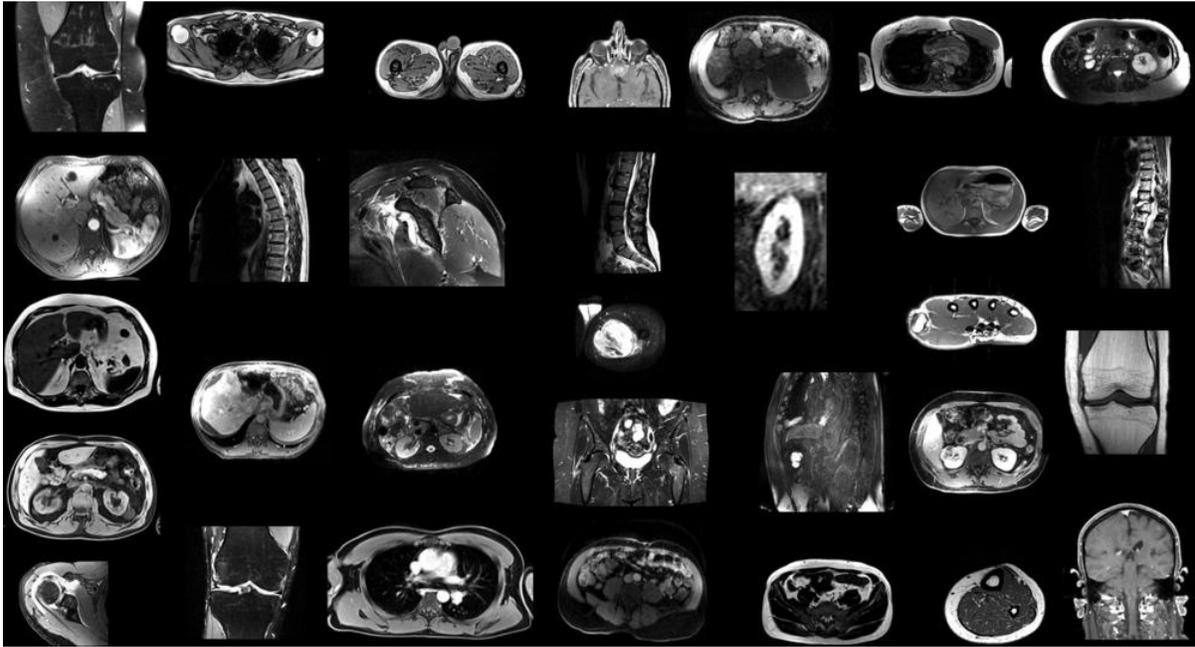
“TotalSegmentator MRI: Robust Sequence-independent Segmentation of Multiple Anatomic Structures in MRI.” Collaborating with Dr. Wasserthal were Tugba Akinci D’Antonoli, M.D., Lucas K. Berger, Ashraya K. Indrakanti, M.D., Nathan Vishwanathan, M.D., Jakob Weiss, M.D., Matthias Jung, M.D., Zeynep Berkarda, M.D., Alexander Rau, M.D., Marco Reiser, Ph.D., Thomas Küstner, Ph.D., Alexandra Walter, Elmar M. Merkle, M.D., Daniel T. Boll, M.D., Hanns-Christian Breit, M.D., Andrew Phillip Nicoli, M.D., Martin Segeroth, M.D., Joshy Cyriac, M.Sc., and Shan Yang, Ph.D.

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RSNA is an association of radiologists, radiation oncologists, medical physicists and related scientists promoting excellence in patient care and health care delivery through education, research and technology innovation. The Society is based in Oak Brook, Illinois. ([RSNA.org](https://www.rsna.org))

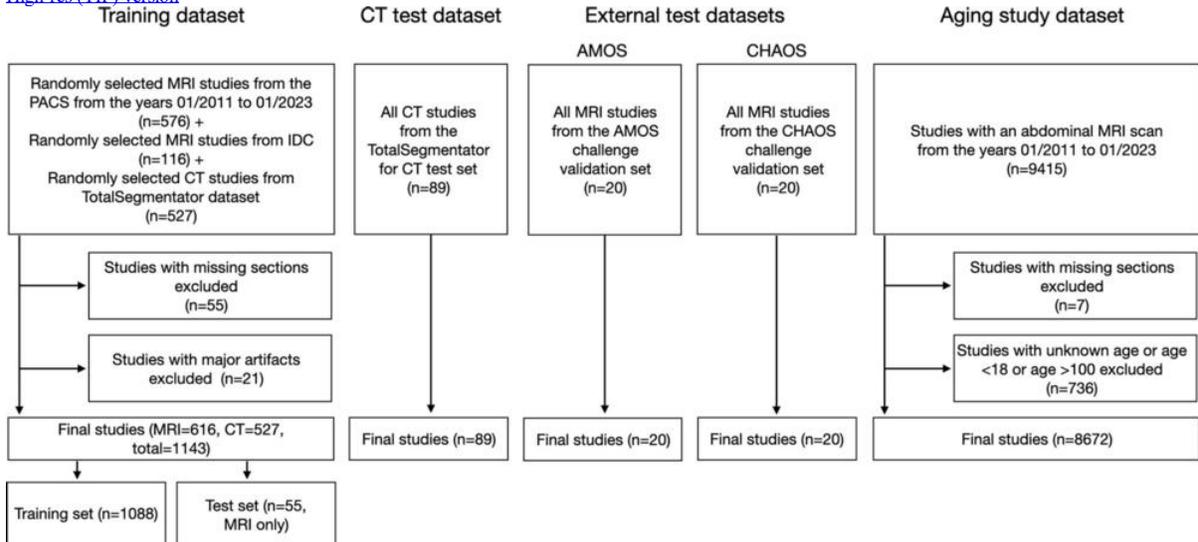
For patient-friendly information on MRI, visit [RadiologyInfo.org](https://www.rsna.org).

Images (JPG, TIF):



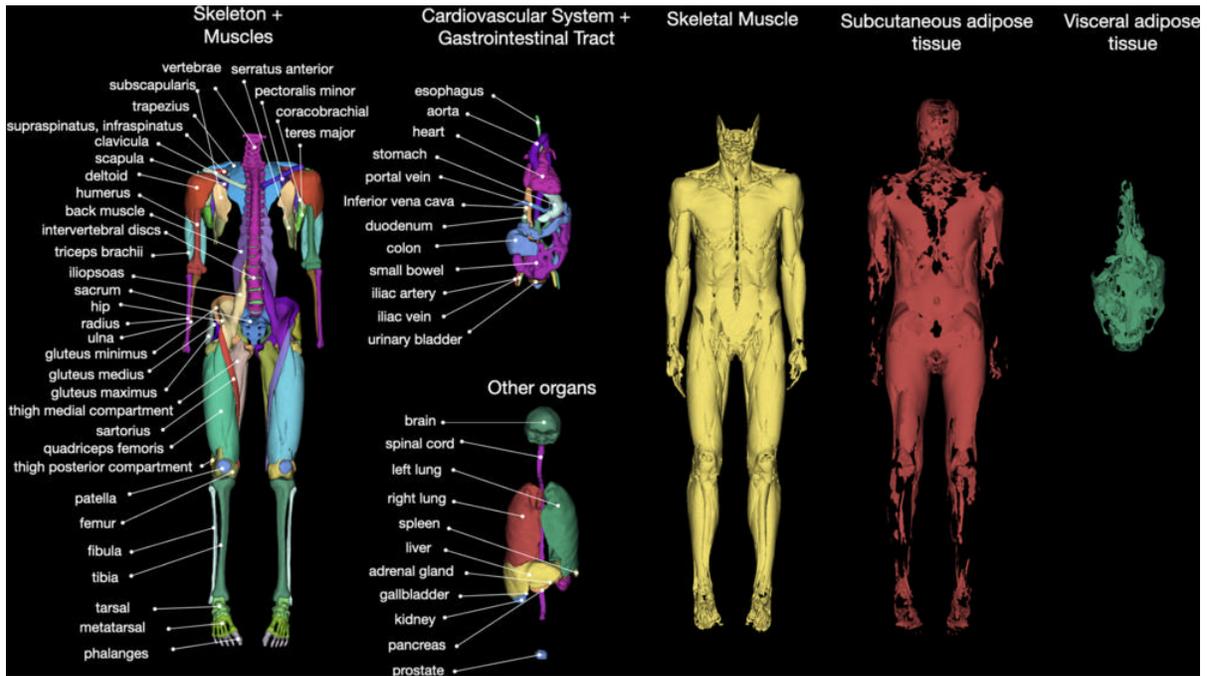
**Figure 1.** Example MRI scans in the training dataset. Since images were randomly sampled from clinical routine, the dataset (n = 561) contains a wide variety of different contrasts, pathologies, and image types.

[High-res \(TIF\) version](#)



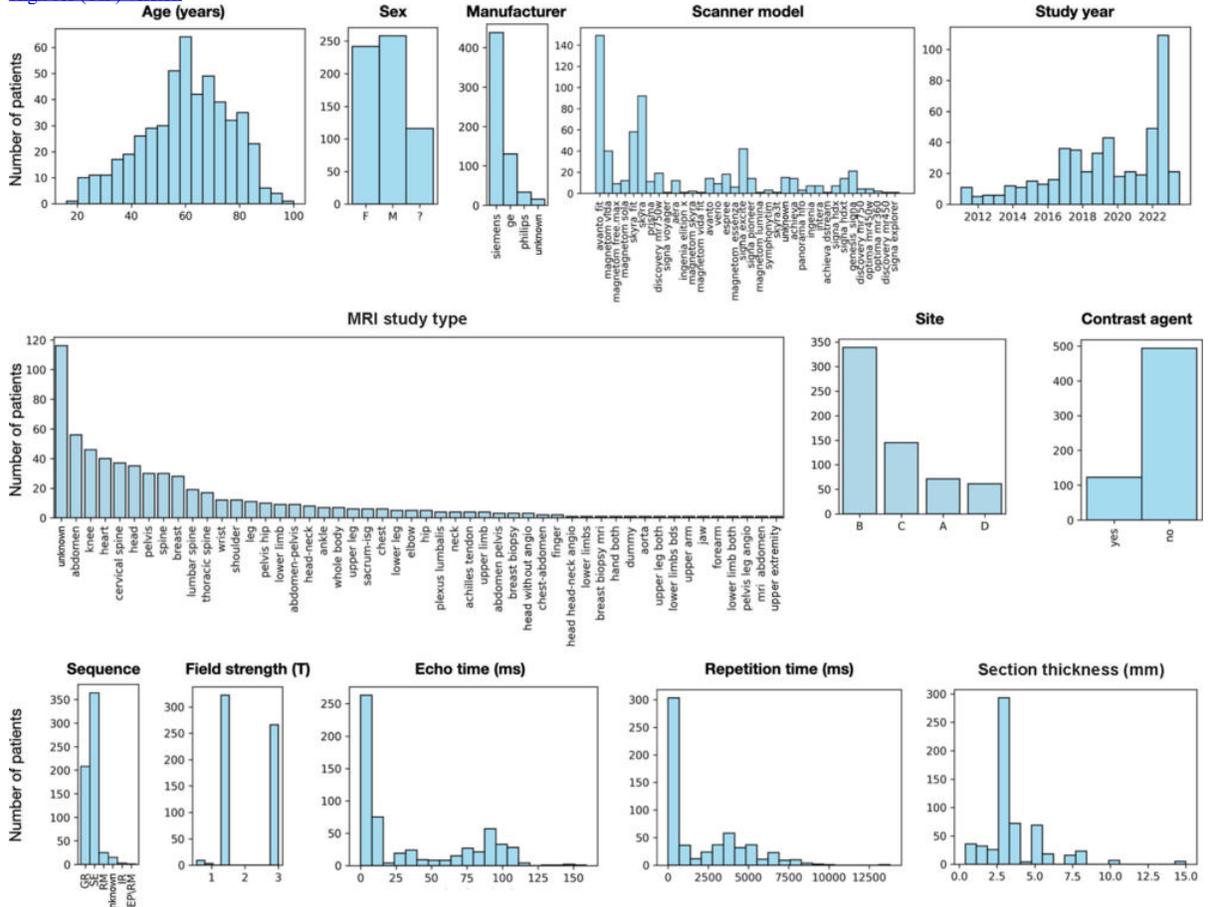
**Figure 2.** Flow diagram showing the inclusion of images into the study. IDC = Imaging Data Commons, PACS = picture archiving and communication system.

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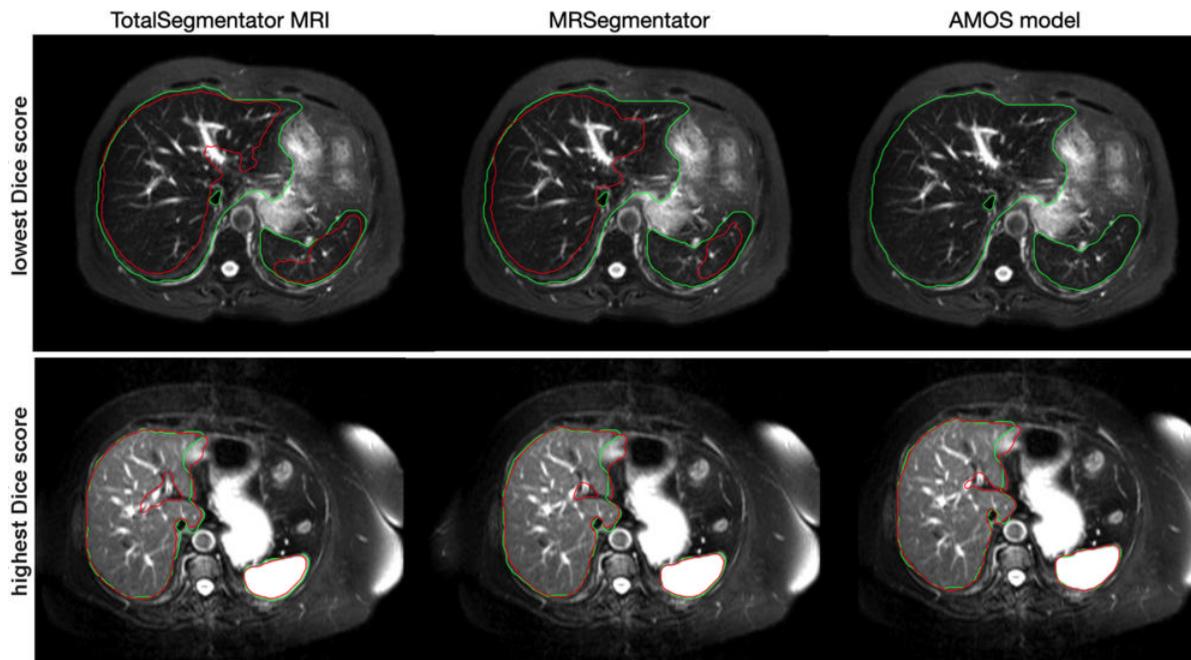
**Figure 3.** Overview of segmented anatomic structures.

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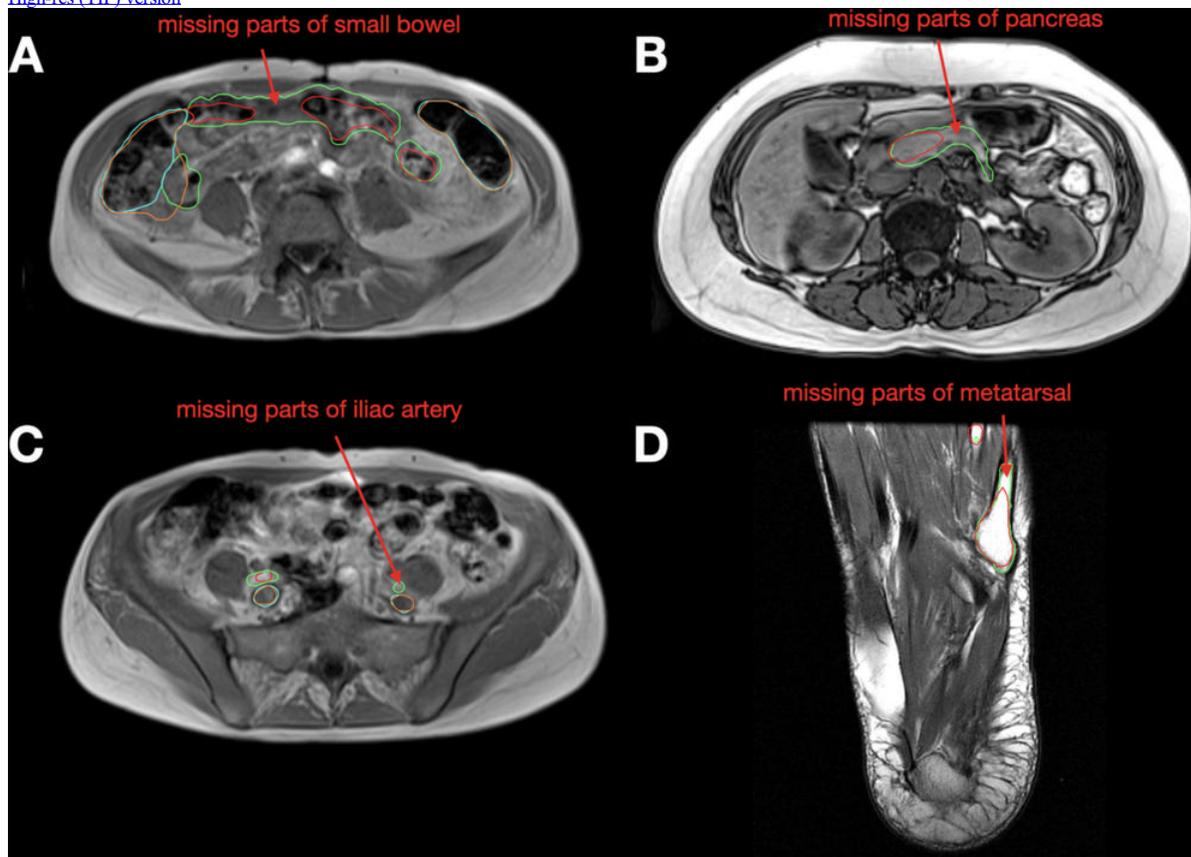
**Figure 4.** Histograms show the distribution of different parameters of the training dataset, demonstrating the dataset's high diversity (561 MRI scans and 527 CT images). angio = angiography, bds = both sides, EP = echo planar, IR = inversion recovery, isg = sacroiliac joint, GR = gradient recalled, RM = respiratory motion, SE = spin echo.

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**Figure 5.** Axial MRI images from the cases with the lowest (top) and highest (bottom) Dice score in the CHAOS external test set for our proposed model, TotalSegmentator MRI, as well as for two publicly available baseline models, MRSegmentator and AMOS. The reference segmentation for liver and spleen is shown in green, and the segmentation of the model is shown in red. The CHAOS dataset was used to show the best and the worst results because this dataset is the most independent from the training data of the three models.

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**Figure 6.** Examples of failure cases on axial MRI scans from the MRI test set. (A) The small bowel model prediction (red) is missing parts compared with the reference segmentation (green). The colon prediction (orange) overreaches the reference segmentation (cyan). (B) The pancreas model prediction (red) is missing parts compared with the reference segmentation (green). The iliac vein prediction (orange) is very similar to the reference segmentation (cyan). (D) The metatarsal model prediction (red) is missing parts compared with the reference segmentation (green).

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Resources:

