Breast MRI Tumor Segmentation Using the Segment Anything Model (SAM) and FMRIB's Automated Segmentation Tool (FAST)

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Background

- In 2025, the American Cancer Society estimates 316,950 new cases of invasive breast cancer in women, 2,800 cases in men, and an additional 59,080 cases of DCIS with 42,680 deaths attributed to breast cancer.[1]
- Changes in tumor volume quantified from tumor segmentations of Breast MRI can predict response to neoadjuvant therapy (NAT)[2]
- As manual tumor segmentation is often impractical, we investigated the performance of the Segment Anything Model (SAM) by Meta AI, and FMRIB's Automated Segmentation Tool (FAST) on pretreatment breast MRIs acquired at two academic medical centers[3,4]

Methods

- Two datasets containing patients with invasive breast cancer were obtained from a retrospective review of our institution's tumor registry (2005-2022) (dataset 1 (DS1); N=91), and a public data set from another institution (dataset 2 (DS2); N = 81)
- A representative slice containing the tumor was selected and classified as mass or non-mass enhancement (NME) by a breast radiologist
- SAM and FAST segmentations were computed from the first post-contrast series for both data sets, and from second post-contrast and subtraction series for DS1 to account for variation in imaging protocols over time
- Segmentation accuracy relative to manual segmentation using the DICE coefficient and group differences were assessed using t-tests of the logit-transformed DICE
- We hypothesized that SAM would outperform FAST overall and for masses, but that FAST (developed for medical image segmentation) would outperform SAM on NME

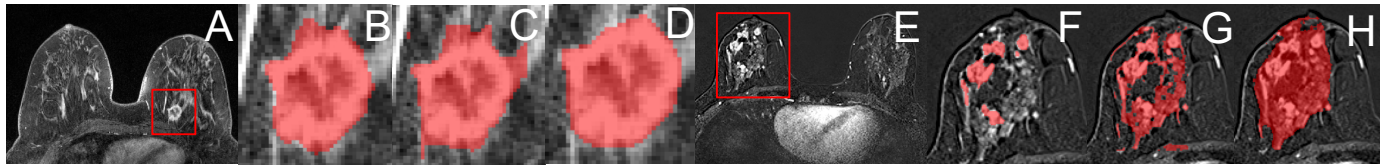


Figure 1. Two representative subjects with biopsy-proven invasive breast cancer from the external data (DS2) with segmentation results shown in red. (A) First post-contrast image showing a mass in the left breast (B) manual segmentation by a breast radiologist, (C) FSL FAST segmentation and (D) SAM segmentation. (E) Subtraction showing NME in the right breast (F) manual segmentation by a breast radiologist, (G) FSL FAST segmentation and (H) SAM segmentation.

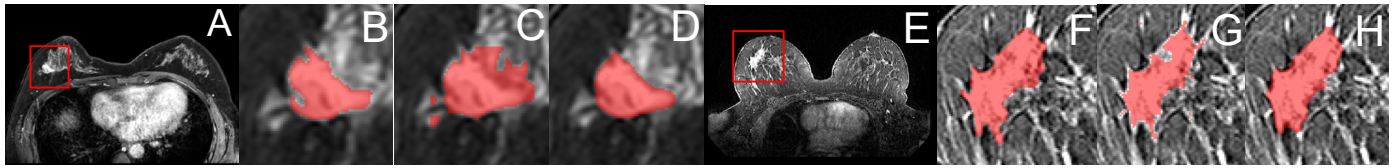


Figure 2. Two representative subjects with biopsy-proven invasive breast cancer from the internal data (DS1) with segmentation results shown in red. (A) First post-contrast image showing a mass in the right breast (B) manual segmentation by a breast radiologist, (C) FSL FAST segmentation and (D) SAM segmentation. (E) First post-contrast image showing NME in the right breast (F) manual segmentation by a breast radiologist, (G) FSL FAST segmentation and (H) SAM segmentation.

Results

- Representative subjects from DS2 with a mass and NME are shown in Fig 1a-d and Fig1e-h, respectively. For the tumor presenting as a mass, FSL overestimated the tumor size relative to the manual segmentation, while SAM showed better agreement. For the tumor presenting as NME, both FSL and SAM overestimate the extent of NME relative to manual segmentation.
- Representative subjects from DS1 with a mass and NME are shown in Fig2a-d and Fig2e-h, respectively. For the tumor presenting as a mass, FSL overestimated the tumor size relative to the manual segmentation, while SAM showed better agreement. For the tumor presenting as NME, FSL underestimated while SAM overestimated tumor size relative to manual segmentation.
- Results of the statistical analysis demonstrated (Table 1):
  - SAM outperformed FAST overall and on tumors presenting as masses
  - In both datasets, there was no statistically significant difference inthe performance of SAM and FAST on segmentation of NME

	Segmentation Method		
	SAM	FAST	p-value
DS1			
All tumors (n=91)	0.83	0.75	**0.0001**
Mass (n=66)	0.88	0.78	**< 0.0001**
NME (n=25)	0.70	0.68	0.4859
p-value	**< 0.0001**	**0.0168**	
DS2			
All tumors (n=81)	0.78	0.73	**0.0039**
Mass (n=51)	0.86	0.80	**0.0012**
NME (n=30)	0.66	0.62	0.2312
p-value	**< 0.0001**	**0.0002**	

Table 1. The mean DICE coefficient is shown above for both data sets (DS1, DS2) and segmentation methods (SAM, FAST). Two-tailed t-tests of the logit-transformed DICE were performed to assess for group differences with a p-value <0.05 considered statistically significant (bold). SAM and FAST show overall good agreement with manual segmentations (mean DICE > 0.70). Both methods show higher accuracy segmenting masses compared to non-mass enhancement (NME). SAM is more accurate than FAST overall, and for tumors presenting as masses. For segmentation of NME, there is no statistically significant difference between the methods.

Conclusion

- SAM is a promising tool for quantifying tumor volume of masses in breast MRI as it outperforms FAST
- Application of such a tool to pre- and post-treatment MRI will allow more accurate assessment of response to chemotherapy in patient undergoing treatment for locally advanced breast cancer

[1]American Cancer Society. Cancer Facts & Figures 2025. Atlanta: American Cancer Society; 2025. [2]Hayashi Y, Takei H, Nozu S, et al. Analysis of complete response by MRI following neoadjuvant chemotherapy predicts pathological tumor responses differently for molecular subtypes of breast cancer [published correction appears in Oncol Lett. 2013 Apr;5(4):1433. doi: 10.3892/ol.2013.1141.]. Oncol Lett. 2013;5(1):83-89. doi:10.3892/ol.2012.1004 [3]Kirillov A,et al.Segment Anything.2023.https://arxiv.org/abs/2304.02643. [4]Zhang Y,et al.IEEE Trans Med Imaging.20(1):45-57,2001. [5]Saha A,et al.Br J Cancer.119(4):508-16,2018 [6]U.S. Cancer Statistics Working Group. U.S. Cancer Statistics Data Visualizations Tool. U.S. Department of Health and Human Services, Centers for Disease Control and Prevention and National Cancer Institute; https://www.cdc.gov/cancer/dataviz, released in June 2024.