Multi-Consortium International Pediatric Brain Tumor Segmentation Challenge (BraTS-PEDs) 2026: Design and Results

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Abstract. Automated segmentation of pediatric high-grade brain tumors on multiparametric magnetic resonance imaging (MRI) remains challenging because tumor appearance varies across diagnoses, institutions, and treatment stages. This paper presents the design and official results of the 2026 Multi-Consortium International Pediatric Brain Tumor Segmentation (BraTS-PEDs) Challenge. The retrospective, multi-institutional dataset includes treatment-naive and post-treatment imaging, with expert-reviewed reference standard annotations for six tumor regions. The cohort was divided into 294 training cases with released annotations, 91 validation cases with withheld annotations, and 109 hidden test cases. Seventeen containerized algorithms submitted by participants were evaluated using the Dice similarity coefficient (DSC) and normalized surface distance (NSD) across six tumor regions. Final rankings were determined using PermRanker, which aggregates case-wise metric ranks and performs pairwise permutation testing for statistical significance. The team ranked first achieved the highest mean DSC (0.930 ± 0.112) and NSD (0.849 ± 0.197) on the whole tumor. These results establish a standardized benchmark for developing and comparing clinically relevant pediatric brain tumor segmentation methods. Future work will provide deeper insights into these methods and assess the potential of AI-based segmentation for pediatric brain tumors through an extensive post-challenge analysis.

Keywords: Artificial Intelligence · Brain Tumor Segmentation · BraTS-PEDs · Deep Learning · Multiparametric MRI · Pediatric High-Grade Glioma

1 Introduction

Brain tumors are among the deadliest forms of cancer. The Brain Tumor Segmentation (BraTS) Challenge of the Medical Image Computing and Computer Assisted Intervention (MICCAI) Society [3,4] has a long history of providing benchmark datasets and standardized evaluation frameworks for the segmentation and analysis of aggressive primary brain tumors. Although relatively rare, pediatric brain and central nervous system tumors are the leading cause of cancer-related mortality in children and exhibit biological, clinical, and imaging characteristics that differ from those of adult tumors [23]. Pediatric diffuse midline gliomas (DMGs), for example, are high-grade tumors that typically arise in the pons during early childhood, carry a poor prognosis, and often lack classic imaging features observed in adult glioblastoma (GBM), such as well-defined contrast enhancement and necrosis. These distinctions underscore the need for

pediatric-specific imaging datasets and artificial intelligence (AI) methods tailored to this population [21].

Building on the inclusion of pediatric DMGs in the BraTS 2022 test set and the success of the 2023–2025 Multi-Consortium International Pediatric Brain Tumor Segmentation (BraTS-PEDs) challenges, the BraTS-PEDs initiative continues to expand in both scope and scale. The BraTS-PEDs 2026 challenge includes treatment-naive and post-treatment pediatric brain tumor data. The treatment-naive cohort comprises 457 pediatric subjects whose data have been publicly released through The Cancer Imaging Archive (TCIA BraTS-PEDs) [14]. In addition, the 2026 challenge introduces a longitudinal post-treatment cohort of 35 patients, each with at least three magnetic resonance imaging (MRI) timepoints, yielding 105 post-treatment cases in total. This longitudinal cohort enables the development and evaluation of AI-based segmentation methods in the presence of therapy-related changes.

The BraTS-PEDs challenge is made possible through extensive support from multidisciplinary national and international societies and consortia. Imaging data from high-grade pediatric brain tumors were collected through leading pediatric neuro-oncology consortia, including the Children's Brain Tumor Network (CBTN) (`https://cbtn.org`) and the International DIPG/DMG Registry (IDIPGR) (`https://www.dipgregistry.org`). The cohort also includes data from the participating pediatric institutions listed in Section 2.1. Reference standard annotations were generated with participation from the American Society of Neuroradiology (ASNR) (`https://www.asnr.org`). The multiparametric MRI dataset underwent standardized preprocessing and neuroradiologist-reviewed reference standard annotations, with tumor subregions defined in accordance with the Response Assessment in Pediatric Neuro-Oncology (RAPNO) recommendations [9,12].

Participants developed and submitted their containerized algorithms via the Synapse platform (`https://challenges.synapse.org/Challenges/DetailsPage/Task2?id=syn74274097`). Models were evaluated on the leaderboard using validation cases for which the reference standard annotations were withheld. Final evaluation of the submitted algorithms was performed on a completely unseen test cohort using a standardized and reproducible framework. By incorporating both cross-sectional treatment-naive data and longitudinal post-treatment data, BraTS-PEDs 2026 aims to advance robust, clinically relevant pediatric brain tumor segmentation methods while better reflecting real-world scenarios encountered in pediatric neuro-oncology.

In this article, we present the challenge design, data, evaluation methods, as well as for the first time the official ranking results of all the participating teams prior to the time of the conference.

2 Materials and Methods

2.1 Data

The BraTS-PEDs dataset is a retrospective, multi-institutional collection of MRI scans from pediatric patients with high-grade gliomas. Diagnoses include DMGs and high-grade anaplastic astrocytoma. The dataset combines preoperative treatment-naive examinations and longitudinal post-treatment imaging. Data were contributed by the CBTN, the IDIPGR, the DFCI-BCH-BWH-PEDs-HGG collection available through TCIA [35], Yale University, Duke University, and Children's Hospital of Philadelphia. CBTN and IDIPGR are multi-institutional repositories that aggregate imaging data from pediatric centers internationally. All data were collected under institutional review board approval or waiver and transferred under formal data-sharing agreements. The assembled cohort includes 457 treatment-naive patients with one imaging timepoint each and 35 post-treatment patients with three longitudinal timepoints each. Table 1 summarizes the contributing sources and corresponding patient counts. A detailed description of the BraTS-PEDs dataset is provided in the associated data description [18].

Table 1. Contributing data sources and corresponding patient counts.

#	Source	Patients
1	CBTN	116
2	IDIPGR	227
3	DFCI-BCH-BWH-PEDs-HGG	61
4	Yale University	27
5	Duke University	26
6	Children's Hospital of Philadelphia	35

The overall cohort was partitioned into three subject-wise nonoverlapping subsets: (i) 294 training cases released with reference standard annotations, (ii) 91 validation cases released without annotations, and (iii) 109 cases retained as a hidden hold-out test set. The test cases were inaccessible to participants, thereby supporting an unbiased evaluation of the submitted algorithms. Each case represents a single imaging timepoint.

2.2 Annotation Protocol

Reference standard annotations were established using a staged workflow [18] that integrated automated initialization, manual correction, and expert review. Preliminary segmentations were first generated using an automated model (`https://github.com/d3b-center/peds-brain-auto-seg-public`). Trained annotators then reviewed and corrected these segmentations in ITK-SNAP (`https://www.itksnap.org/pmwiki/pmwiki.php`) [34], following detailed annotation

guidelines. Three board-certified neuroradiologists reached consensus on a common segmentation approach. They subsequently evaluated every annotation and iteratively approved or refined the segmentations as needed.

MRI Sequences The BraTS-PEDs 2026 Challenge dataset comprises multiparametric MRI scans including the following sequences:

- pre-contrast native T1-weighted (T1N)
- contrast-enhanced T1-weighted (T1C)
- T2-weighted (T2W)
- T2-weighted Fluid Attenuated Inversion Recovery (T2F)

Tumor Sub-Regions The segmentation of pediatric brain tumors into four main subregions was recommended by RAPNO working group for evaluation of the treatment response in high-grade gliomas and DMGs. The individual and combined subregions used as evaluation labels are defined as follows:

- **Enhancing tumor (ET; label 1):** Areas with enhancement (brightness) on T1C sequences as compared to T1N. In case of mild enhancement, checking the signal intensity of normal brain structure can be helpful.
- **Nonenhancing tumor (NET; label 2):** Any other abnormal signal intensity within the tumorous region that cannot be defined as enhancing or cystic. For example, the abnormal signal intensity on T1N, T2F, and T2W sequences that is not enhancing on T1C sequences should be considered as nonenhancing portion.
- **Cystic component (CC; label 3):** Typically appearing with hyperintense signal (very bright) on T2W sequences and hypointense signal (dark) on T1C sequences. The cystic portion should be within the tumor, either centrally or peripherally (as compared to ED which is peritumoral). The brightness of CC is here defined as comparable or close to cerebrospinal fluid (CSF).
- **Peritumoral edema (ED; label 4):** Abnormal hyperintense signal (very bright) on T2F sequences. ED is finger-like spreading that preserves underlying brain structure and surrounds the tumor.
- **Tumor core (TC; label 1,2,3):** Including the part of the tumor that is typically resected (ET, NET, and CC).
- **Whole tumor (WT; label 1,2,3,4):** Including all tumor subregions (TC and ED).

Figure 1 illustrates an example of the four MRI sequences and the corresponding reference standard annotations for a single training case.

2.3 Data Preprocessing

All multiparametric MRI scans were processed using the 2026 BraTS-PEDs pipeline [18]. Imaging sequences were first co-registered to the SRI24 common template [30] and resampled to an isotropic resolution of 1 mm^3. Facial features

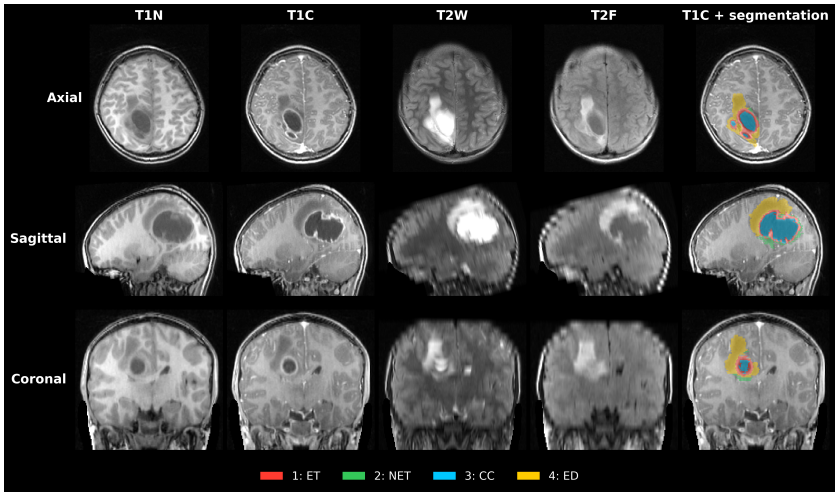

Fig. 1. Training case showing four MRI sequences and reference standard annotations. The four tumor subregions are color-coded: enhancing tumor (ET; red), nonenhancing tumor (NET; green), cystic component (CC; blue), and peritumoral edema (ED; yellow).

were subsequently removed through image defacing [13] to protect patient identity. Skull stripping was intentionally omitted to retain the complete anatomical context. Software used within this workflow included the Cancer Imaging Phenomics Toolkit [11,26] and the Federated Tumor Segmentation platform [25].

2.4 Validation Metrics

We primarily evaluated segmentation performance using two subject-wise metrics [29,22]: the Dice similarity coefficient (DSC) and normalized surface distance (NSD) (`https://metrics-reloaded.dkfz.de/metric?id=normalized_surface_distance`). DSC measures voxel-level overlap between the predicted and reference standard segmentations, whereas NSD measures surface overlap within a boundary threshold of 1.0 mm. Both metrics were calculated separately for each tumor subregion (ET, NET, CC, and ED) and for the combined regions (TC and WT), yielding 12 metric values per case.

Additionally, lesion-wise DSC and NSD were computed for diagnostic reference and post-challenge analyses. In contrast to subject-wise evaluation across the complete image, these scores assess segmentation overlap separately for each individual lesion.

2.5 Ranking Methods

We ranked submitted models using cumulative ranks derived from the 12 segmentation validation metrics. Final rankings were computed with PermRanker [5],

following the DELPHI-based recommendations for image analysis validation [22,29]. This framework combines ranking with statistical significance testing.

Let $r(M_i, C_j, P_k)$ denote the rank of model M_i on test case C_j according to metric P_k. For each case and metric, the performance of M_i was compared with that of every other model, with a lower rank indicating better performance. The ranks across all metrics were then aggregated to obtain the case-level cumulative rank:

$$CR(M_i, C_j) = \sum_{k=1}^{K} r(M_i, C_j, P_k), \tag{1}$$

where $K = 12$ is the number of validation metrics. The case-level cumulative ranks were summed across the test set to obtain the **BraTS-PEDs final cumulative rank (FCR)** for each model:

$$FCR(M_i) = \sum_{j=1}^{J} CR(M_i, C_j), \tag{2}$$

where j indexes the $J = 109$ cases in the test set. Models were ordered in ascending order of this cumulative rank, such that a lower value indicated better overall performance. Statistical significance assessment was performed using PermRanker for each pair of ranked participating models.

3 Challenge Results

During the leaderboard validation phase, 500 valid submissions were received from 34 unique submitters (teams or individuals). During the final testing phase, 17 teams submitted a valid containerized model. All 17 models were evaluated on the same hidden test set of 109 cases and included in the official final ranking. Methodological and implementation details, including links to openly accessible training code, will be available through each team's paper in the published proceedings.

Table 2 summarizes the official ranking together with the mean DSC and NSD on the whole tumor (WT). FLAIR-Viaevum ranked first with a cumulative rank of 9075.5, followed by IMICS_uoft and Angelus, with a cumulative rank of 9683 and 9913.5, respectively. FLAIR-Viaevum achieved both the highest mean DSC WT (0.93) and the highest mean NSD WT (0.849). Because the final ranking aggregates all challenge metrics across all test cases, the ordering is not determined by either of these two WT metrics alone.

Overall, 16 of the 17 teams achieved a high DSC WT greater than 0.90; only the last-ranked team was below this threshold, with a mean DSC WT of 0.837. Greater variation across teams was observed for NSD WT: the team-level means ranged from 0.582 to 0.849, compared with 0.837 to 0.93 for DSC WT. DSC WT and NSD WT did not always produce consistent relative ordering across teams. These differences indicate that voxel-overlap and surface-overlap metrics capture complementary aspects of segmentation performance.

Table 2. Official BraTS-PEDs 2026 ranking and whole-tumor (WT) segmentation performance across 109 test cases. DSC WT and NSD WT are reported as mean ± standard deviation. FCR refers to the final cumulative rank. Lower cumulative rank is better. The midlines separate tiers of teams.

Final Rank	Team	FCR	DSC WT	NSD WT
1	**FLAIR-Viaevum** [19]	9075.5	0.930 ± 0.112	0.849 ± 0.197
2	**IMICS_uoft** [8]	9683	0.929 ± 0.110	0.845 ± 0.194
3	**Angelus** [24]	9913.5	0.921 ± 0.118	0.822 ± 0.224
4	**NeuroNinjas** [15]	10124	0.920 ± 0.121	0.826 ± 0.223
5	BrainTumorResearch [16]	10859	0.927 ± 0.113	0.833 ± 0.200
6	mist2026 [7]	10896.5	0.920 ± 0.116	0.825 ± 0.211
7	NeuroSapiens [10]	11359	0.925 ± 0.113	0.835 ± 0.198
8	IRE [32]	11517.5	0.907 ± 0.173	0.815 ± 0.237
9	Loriim_Barros [1]	11548.5	0.911 ± 0.152	0.822 ± 0.214
10	Vision_Lab [6]	11797	0.918 ± 0.116	0.803 ± 0.221
11	haohao_li [20]	11909.5	0.925 ± 0.097	0.824 ± 0.196
12	TeamTiger_BraTS [2]	12274.5	0.906 ± 0.151	0.803 ± 0.224
13	HMNUnet [28]	12629.5	0.909 ± 0.130	0.806 ± 0.223
14	SillycatYoon [33]	12816	0.917 ± 0.127	0.817 ± 0.204
15	qiangqiangqiang [17]	12829	0.917 ± 0.119	0.824 ± 0.202
16	AngryFicus [27]	13696.5	0.909 ± 0.109	0.781 ± 0.189
17	Med_Img_Pred_THS [31]	17195.5	0.837 ± 0.151	0.582 ± 0.175

According to the pairwise permutation tests performed with PermRanker, the 17 teams were organized into 7 performance tiers at a significance threshold of $P < 0.05$: rank 1-2; ranks 3–4; ranks 5–8; ranks 9–12; ranks 13–15; rank 16; and rank 17 (Table 2). Within each multi-team tier, the difference across teams was not statistically significant. FLAIR-Viaevum and IMICS_uoft formed the top tier, significantly outperforming all other teams. The teams in the second tier included Angelus and NeuroNinjas, which were not significantly different from each other, but significantly better than the remaining teams. Finally, we consider the teams ranked 1–4 as the top-performing teams in BraTS-PEDs 2026.

4 Discussion

BraTS-PEDs 2026 provides a pediatric-specific benchmark for segmenting high-grade brain tumors on multiparametric MRI, including both treatment-naive and post-treatment training cases. Seventeen containerized models were evaluated on the same hidden test set of 109 cases. The results indicate that current methods can identify the overall tumor extent reliably in most test cases. Nevertheless,

the corresponding standard deviations, which ranged from 0.097 to 0.173, show that performance remained heterogeneous across individual cases.

The DSC WT summaries in Table 2 can obscure failures in smaller or less prevalent subregions such as ET, NET, CC, and ED. The distribution of tumor subregions varies across cases, and a distributional gap exists between the training, validation and test cohort. This paper reports the summary of this year's participation and results. Future extended meta-analysis should therefore investigate case-level and subregion-specific performance in addition to aggregate WT results, method-family comparisons, validation-to-test generalization, and other factors that may influence performance for in-depth insights.

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