Table S1. Summary of model agreement and imaging parameters for all participants

Pt	Whole V_0 [cm^3]	Cystic V_0 [cm^3]	FLAIR mean slice thickness (SD) [mm]	FLAIR mean slice spacing (SD) [mm]	2D nRMSE	Whole nRMSE	2D/ Whole nRMSE ratio	PR-SD agree	SD-PD agree
1	41.1	5.8	4.9 (0.4)	3.9 (0.4)	2.48	2.23	1.11	Yes	Yes
3	55.7	2.3	5.0 (0.0)	4.0 (0.0)	6.27	1.32	4.74	No	Yes
4	52.2	0.0	4.5 (0.6)	4.3 (0.5)	7.48	2.97	2.52	Yes	No
5	18.6	1.1	4.5 (1.2)	4.5 (1.2)	4.62	0.79	5.83	Yes	No
8	146.0	11.4	5.0 (0.0)	4.5 (0.7)	N/A	N/A	N/A	N/A	N/A
11	0.9	0.0	3.4 (0.9)	3.2 (0.5)	6.44	1.81	3.56	Yes	No
12	11.4	0.4	4.0 (0.0)	4.0 (0.0)	5.98	1.05	5.70	No	N/A
13	14.7	1.3	4.0 (0.0)	4.0 (0.0)	1.05	0.41	2.55	Yes	N/A
14	41.0	0.0	4.0 (0.0)	4.0 (0.0)	6.30	1.98	3.18	Yes	No
15	5.9	0.0	1.2 (2.3)	2.0 (1.7)	13.88	1.72	8.08	Yes	Yes
16	8.6	1.2	0.2 (1.1)	1.3 (0.9)	N/A	N/A	N/A	N/A	N/A
17	63.7	21.5	4.1 (0.2)	4.0 (0.4)	14.72	2.83	5.21	Yes	N/A
18	12.9	0.0	3.8 (0.5)	3.6 (0.5)	6.61	0.87	7.58	Yes	Yes
19	47.9	0.5	0.0 (0.0)	1.0 (0.0)	6.57	2.94	2.23	Yes	No
20	29.6	0.0	4.0 (0.2)	4.0 (0.0)	18.80	1.51	12.43	No	No
21	85.5	1.3	4.2 (0.4)	4.1 (0.3)	17.78	1.41	12.58	Yes	Yes
22	10.5	1.4	0.0 (0.0)	1.0 (0.0)	7.10	1.10	6.47	Yes	N/A
24	34.5	5.0	4.9 (0.4)	4.9 (0.3)	4.95	1.12	4.41	Yes	Yes
25	26.8	0.6	5.0 (0.0)	4.0 (0.0)	3.86	0.82	4.73	Yes	N/A
26	7.1	0.7	5.9 (0.5)	4.9 (0.3)	3.42	0.44	7.78	No	N/A
27	10.4	1.7	4.0 (0.0)	4.0 (0.0)	5.92	1.40	4.24	Yes	N/A
28	37.7	6.6	6.0 (0.0)	5.0 (0.0)	2.61	0.63	4.16	Yes	N/A
29	19.0	1.7	4.8 (0.4)	4.5 (0.5)	6.08	0.87	6.97	No	Yes
30	32.8	0.0	5.7 (0.7)	4.8 (0.4)	11.46	2.04	5.62	No	N/A
31	42.2	0.0	5.0 (1.7)	4.2 (1.3)	18.08	1.67	10.81	No	No
32	12.8	0.0	0.6 (1.8)	1.5 (1.4)	6.55	2.50	2.62	Yes	Yes
33	44.0	0.0	5.0 (0.0)	5.0 (0.0)	N/A	N/A	N/A	N/A	N/A
35	65.8	1.3	4.0 (0.0)	4.0 (0.0)	N/A	N/A	N/A	N/A	N/A
36	21.4	0.8	3.0 (0.0)	3.0 (0.0)	N/A	N/A	N/A	N/A	N/A
37	10.0	4.1	5.7 (0.8)	4.8 (0.4)	2.75	0.33	8.38	No	No
38	26.6	8.3	6.0 (0.0)	5.0 (0.0)	N/A	N/A	N/A	N/A	N/A

Pt = participant; V_0 = initial volume; SD = standard deviation; nRMSE = normalized root mean squared error; PR-SD = transition from PR to SD; SD-PD = transition from SD to PD, *N/A indicates absence of definitive tumor regrowth or insufficient data points for model fit

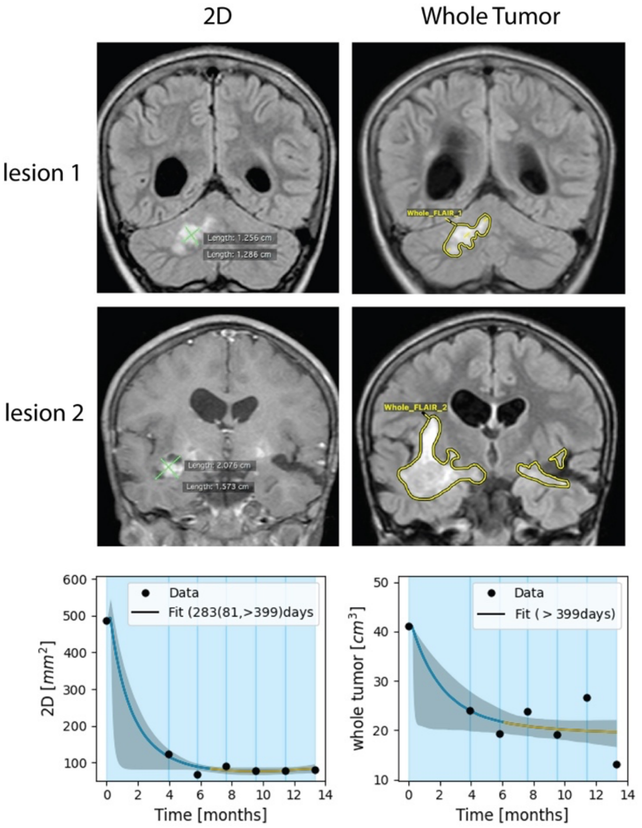
Table S2. Summary of all Wilcoxon Rank sum test p-values

	PR-SD agree	**SD-PD agree**
Whole V_0 [cm^3]	0.727	0.916
Cystic V_0 [cm^3]	0.727	0.189
FLAIR mean slice thickness	0.041	0.600
FLAIR SD slice thickness	0.930	0.637
FLAIR mean slice spacing	0.020	0.916
FLAIR SD slice spacing	0.600	1.000
2D/Whole nRMSE ratio	0.010	0.916

V_0 = initial volume; SD = standard deviation; nRMSE = normalized root mean squared error; PR-SD = transition from PR to SD; SD-PD = transition from SD to PD

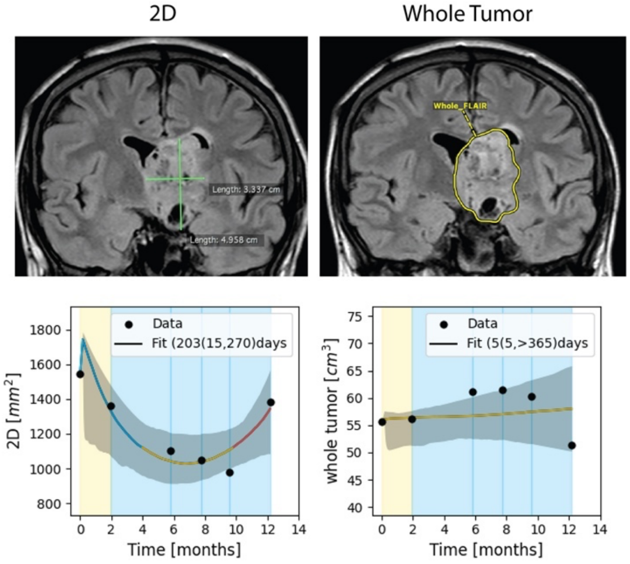
Figure S1. 2D measurements and whole tumor segmentations with model-based treatment response curves. Line colors indicate the model-based assignment to either PR (blue), SD (yellow) or PD (red), and background colors reflect BT-RADS labels relative to the pre-treatment scan. Model fits are shown with 95% confidence interval, and the legend shows the obtained distribution for $t_{V_{\min}}$ as medians with 95% confidence intervals.

PARTICIPANT #1: Low-grade astrocytoma (not otherwise specified)

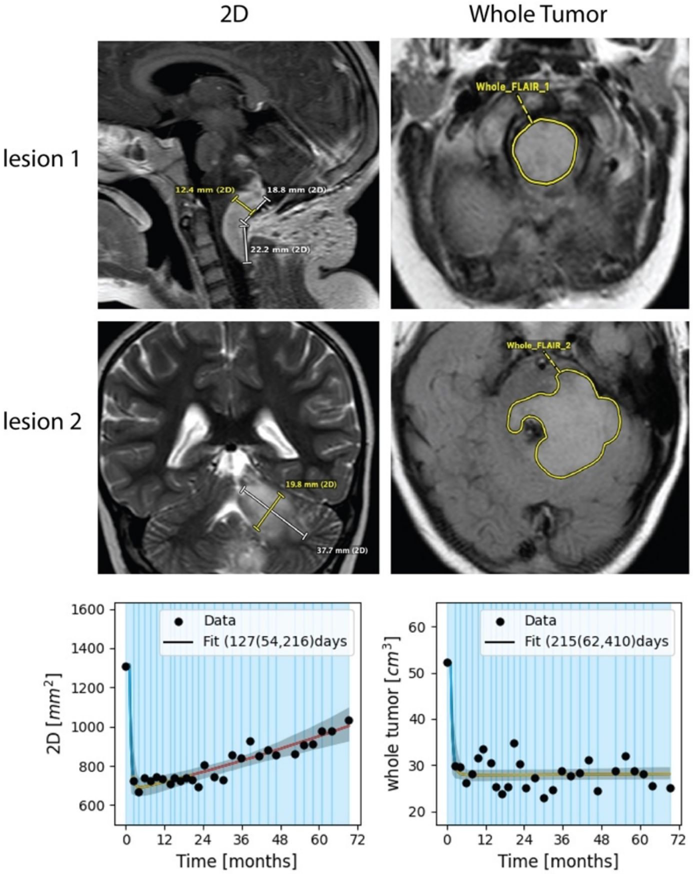


*In the 2D trajectory, the model-based SD to PD transition occurred at the last timepoint of evaluation. This transition is represented by a small red portion at the end of the trajectory line, which in this figure is masked by the overlying point that represents the 2D measurement at the last timepoint of evaluation.

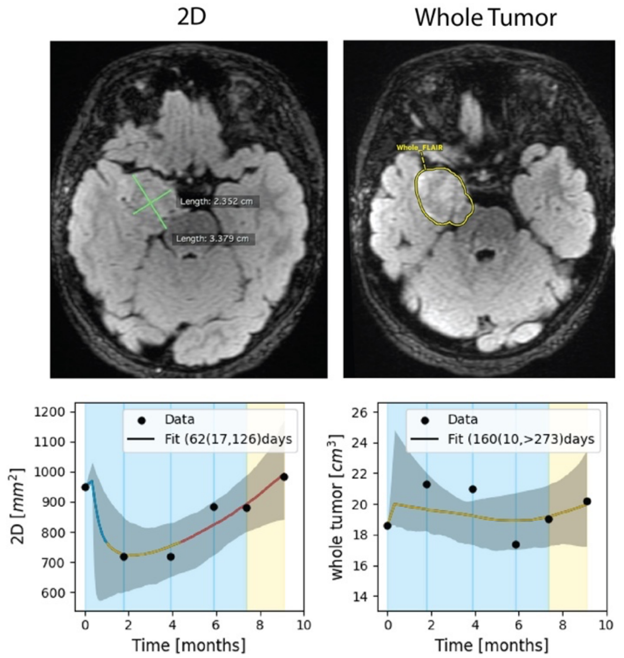
PARTICIPANT #3: Pilocytic astrocytoma



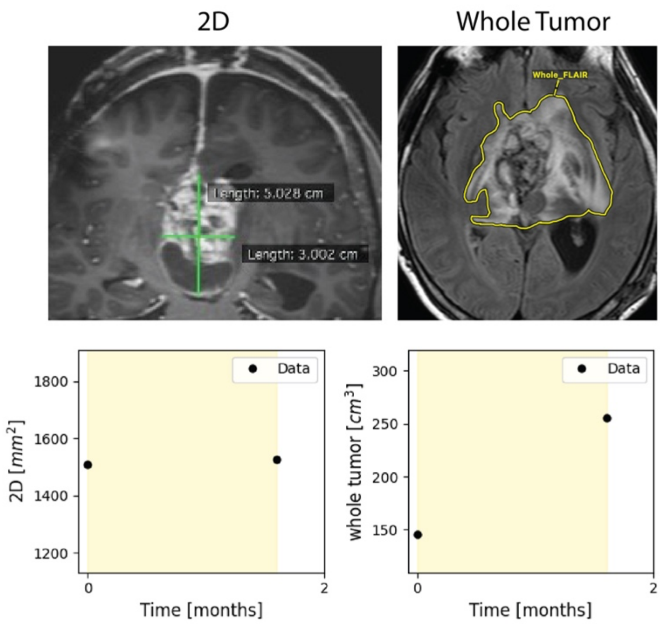
PARTICIPANT #4: Pilocytic astrocytoma



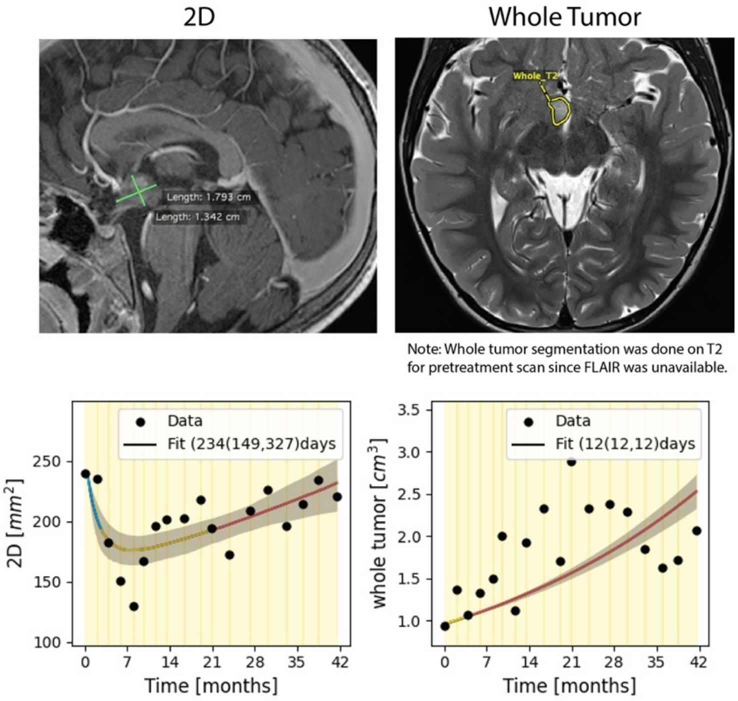
PARTICIPANT #5: Pleomorphic xanthoastrocytoma



PARTICIPANT #8: Pilocytic astrocytoma

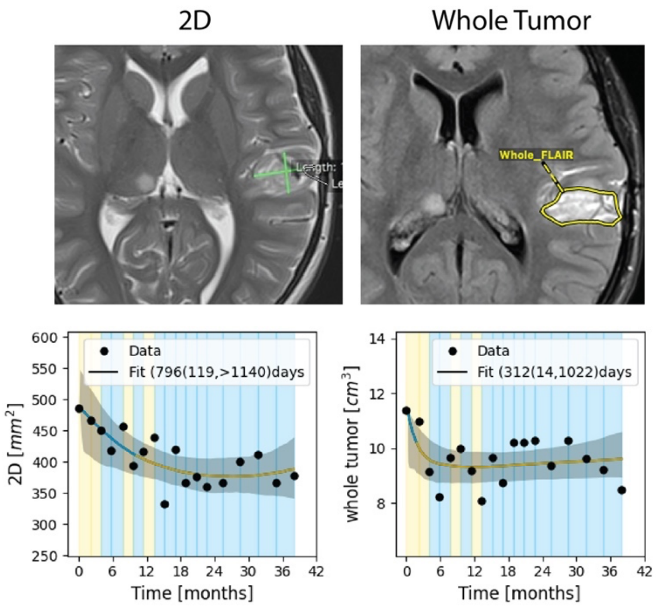


PARTICIPANT #11: Pilocytic astrocytoma



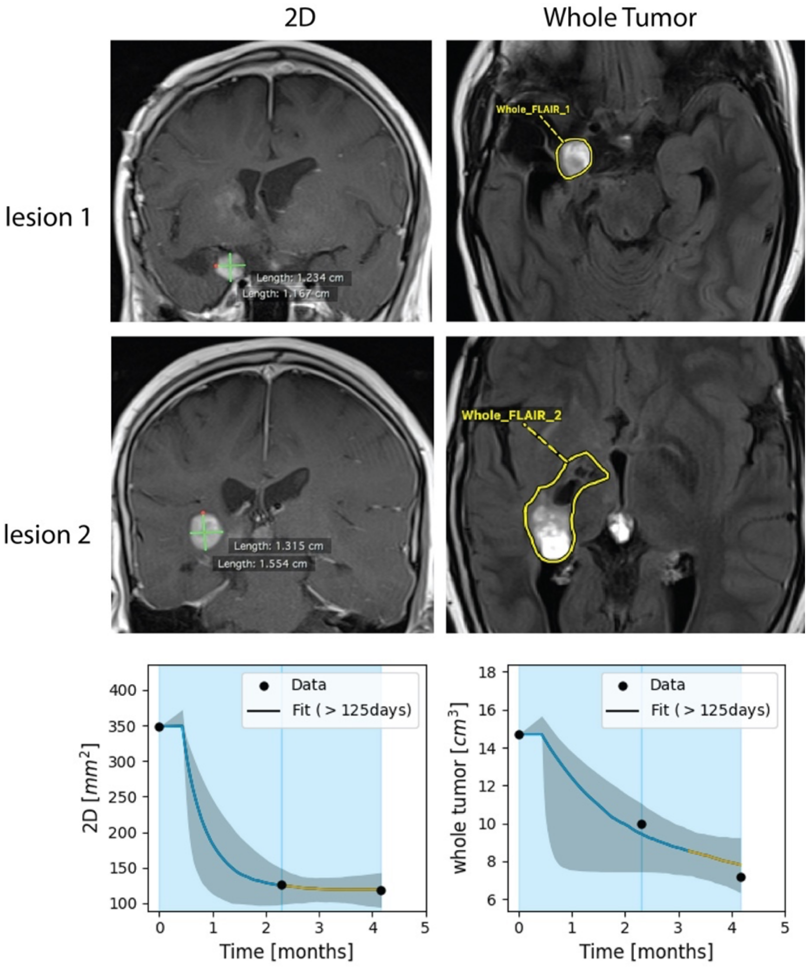
Note: Whole tumor segmentation was done on T2 for pretreatment scan since FLAIR was unavailable.

PARTICIPANT #12: Ganglioglioma

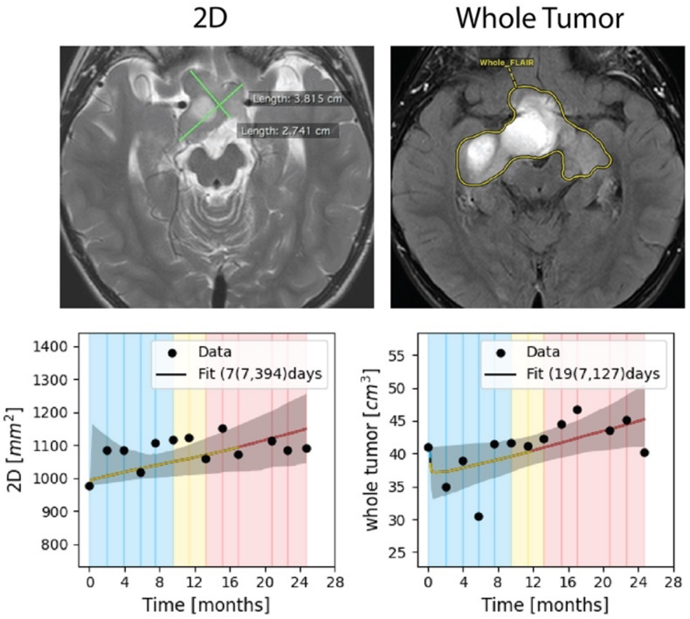


*The right thalamic lesion did not meet minimal size criteria to be included in 2D or volumetric measurements.

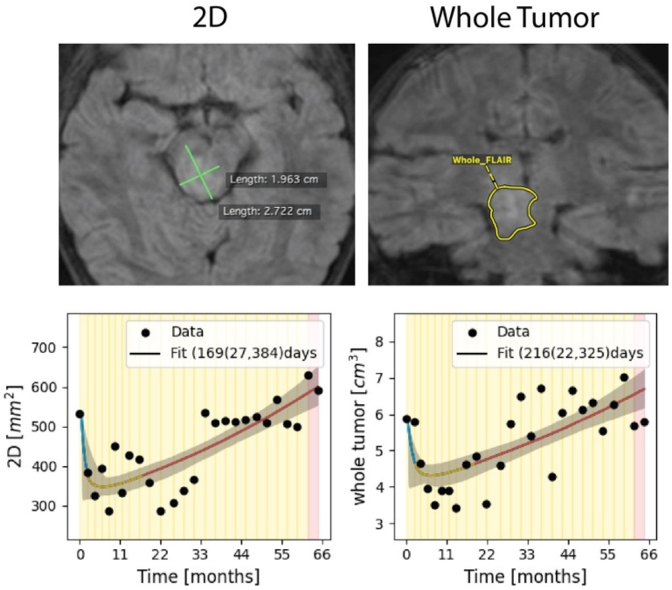
PARTICIPANT #13: Pilocytic astrocytoma



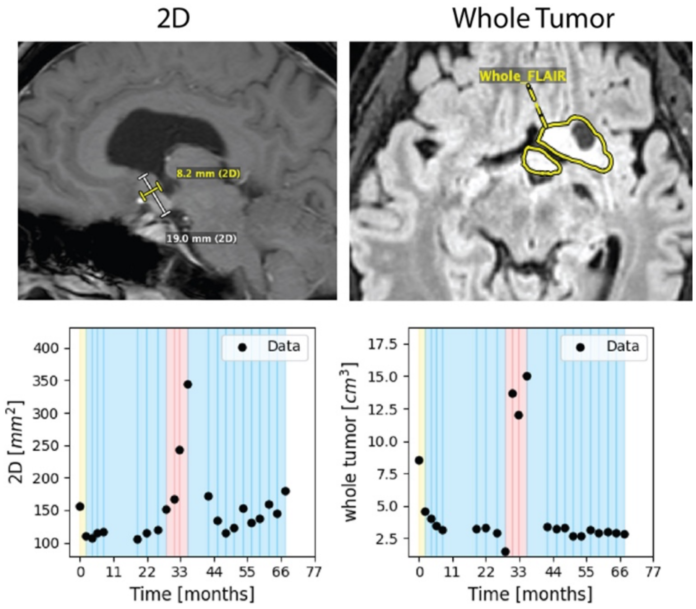
PARTICIPANT #14: Pilocytic astrocytoma



PARTICIPANT #15: Ganglioglioma

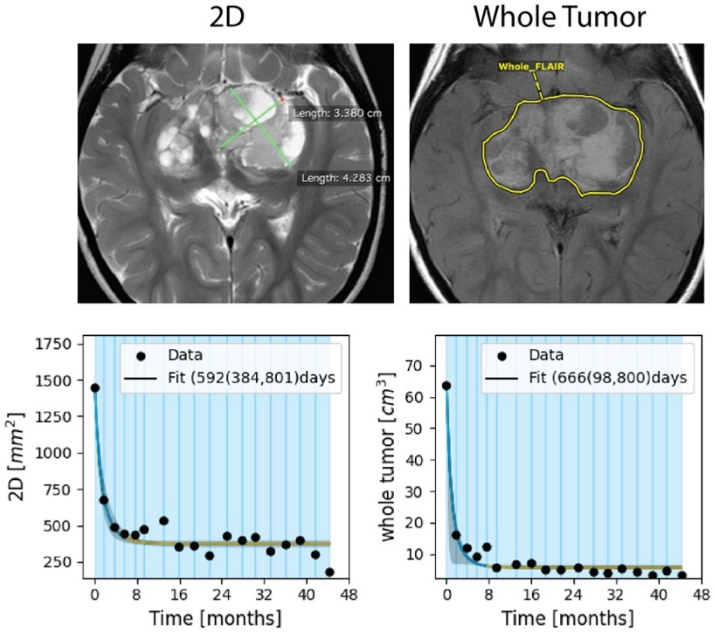


PARTICIPANT #16: Ganglioglioma

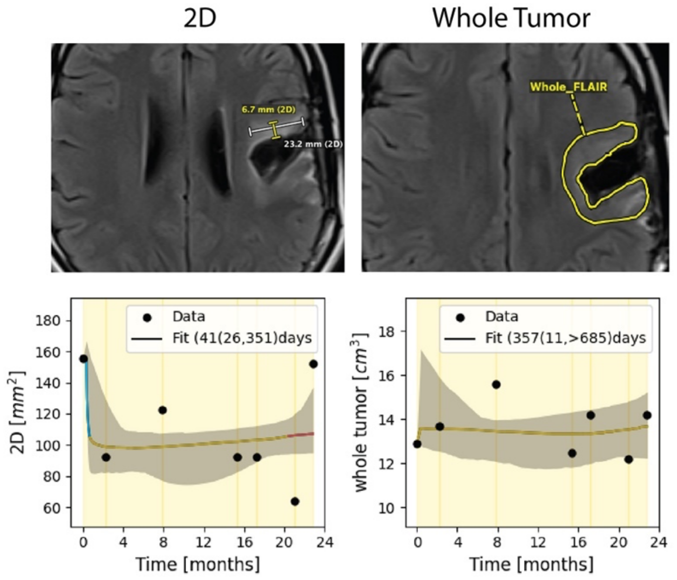


*No trend line was drawn as participant #16 had a trajectory that did not comply with model intended dynamics.

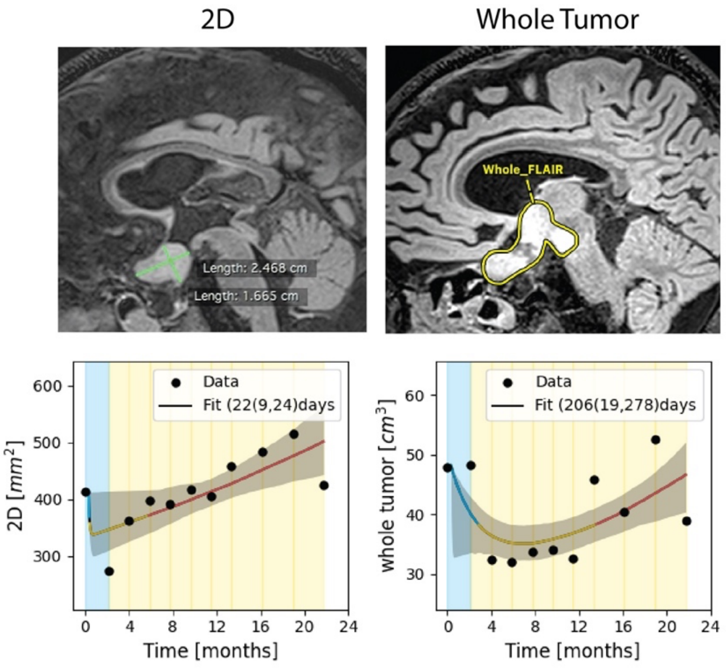
PARTICIPANT #17: Pilocytic astrocytoma



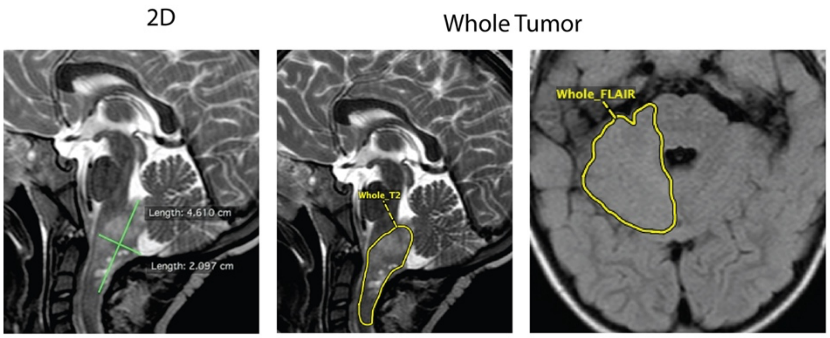
PARTICIPANT #18: Pleomorphic xanthoastrocytoma



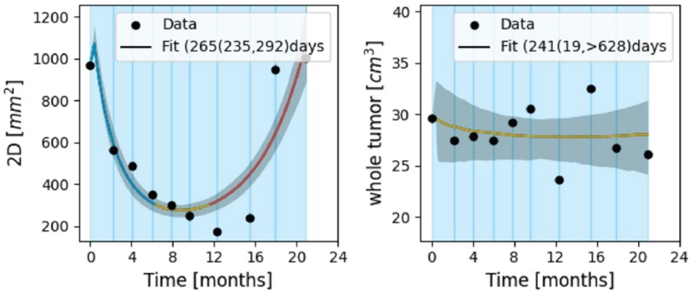
PARTICIPANT #19: Pilocytic astrocytoma



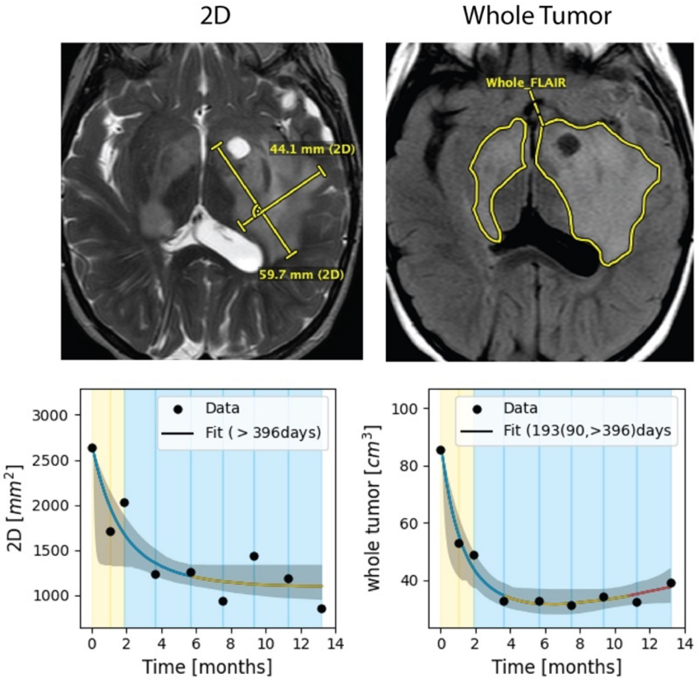
PARTICIPANT #20: Pilocytic astrocytoma



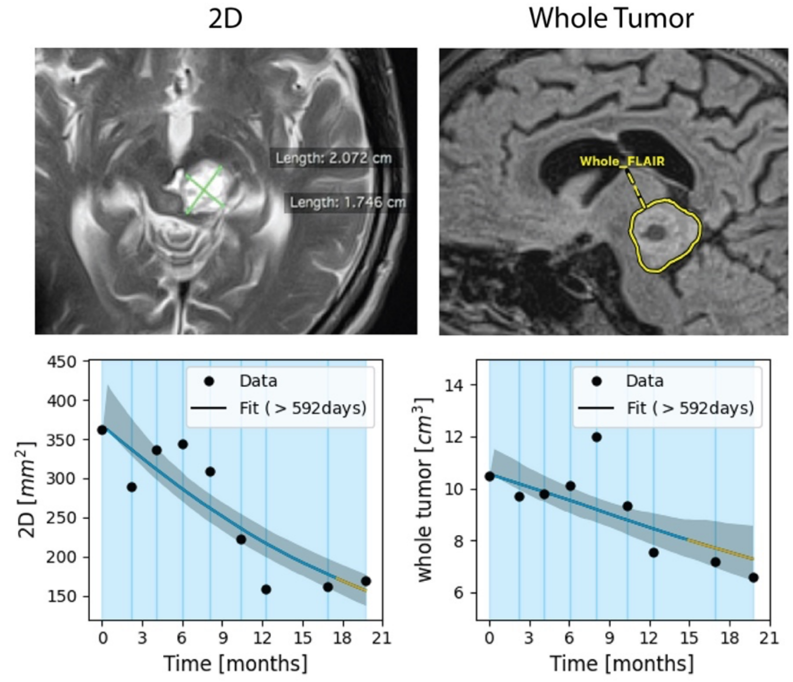
Note: Tumor extended from foramen magnum into cerebellum. Cerebellar portion was best segmented on axial FLAIR while foramen magnum portion was best segmented on sagittal T2. Both volumes were added to obtain whole tumor volume. As RAPNO stipulates only one set of 2D measurements per lesion, it was not possible to choose a plane that captured the full extent of disease in both cerebellum and foramen magnum to include in 2D measurements.



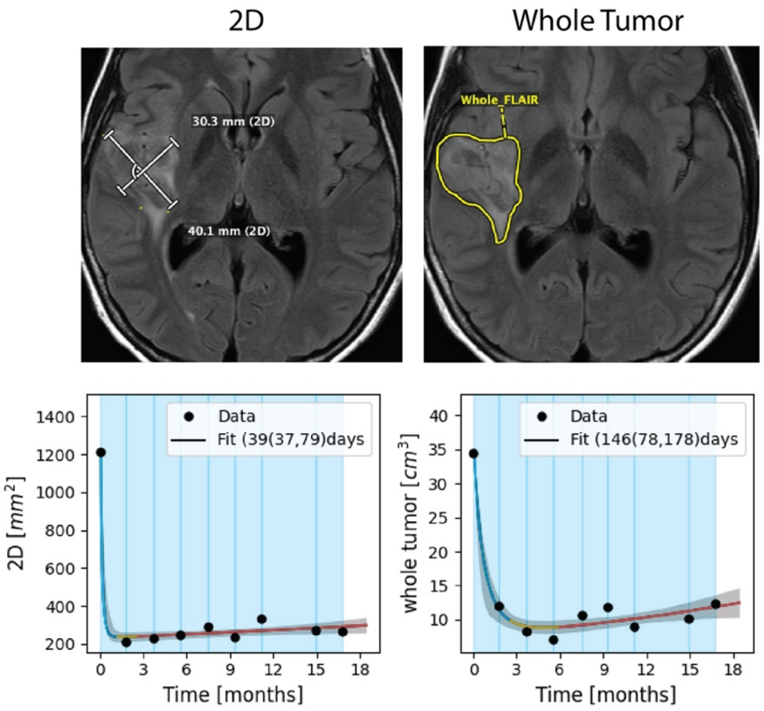
PARTICIPANT #21: Pilocytic astrocytoma



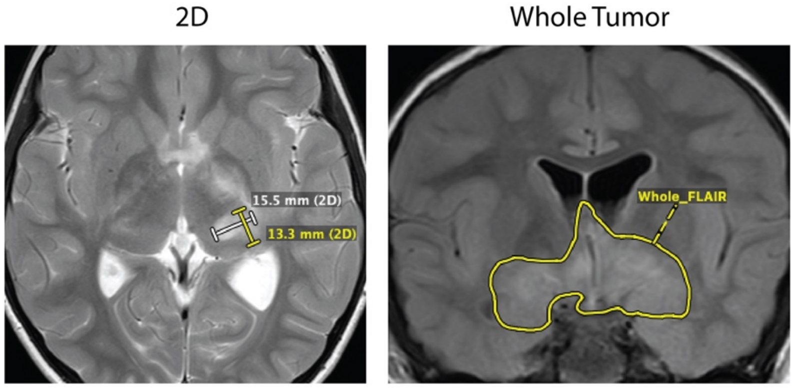
PARTICIPANT #22: Ganglioglioma

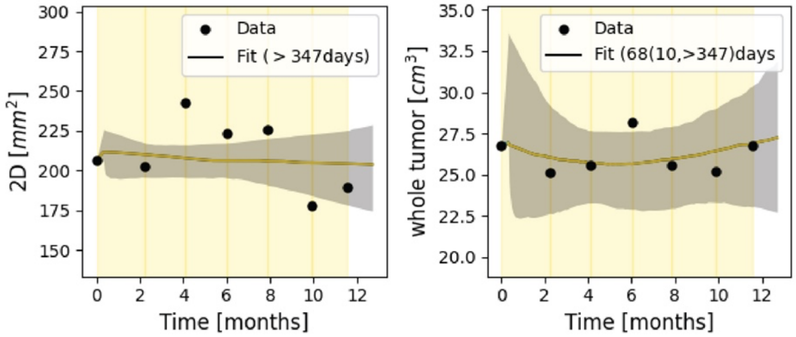


PARTICIPANT #24: Anaplastic astrocytoma (Grade 3)

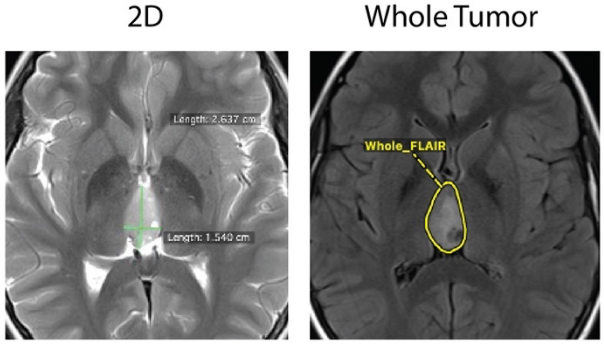


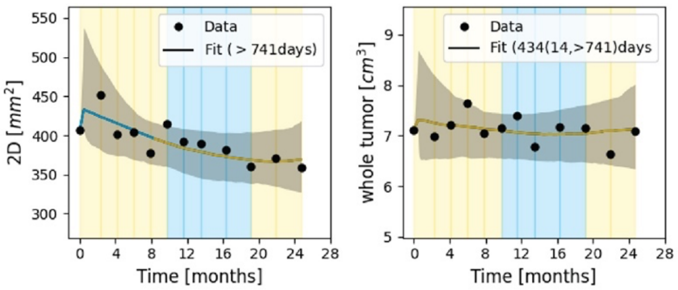
PARTICIPANT #25: Pilocytic astrocytoma



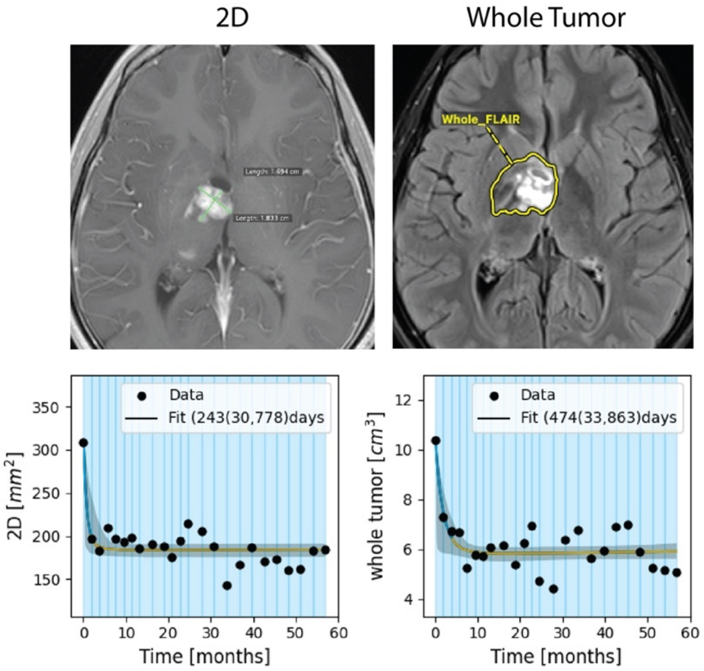


PARTICIPANT #26: Pilocytic astrocytoma

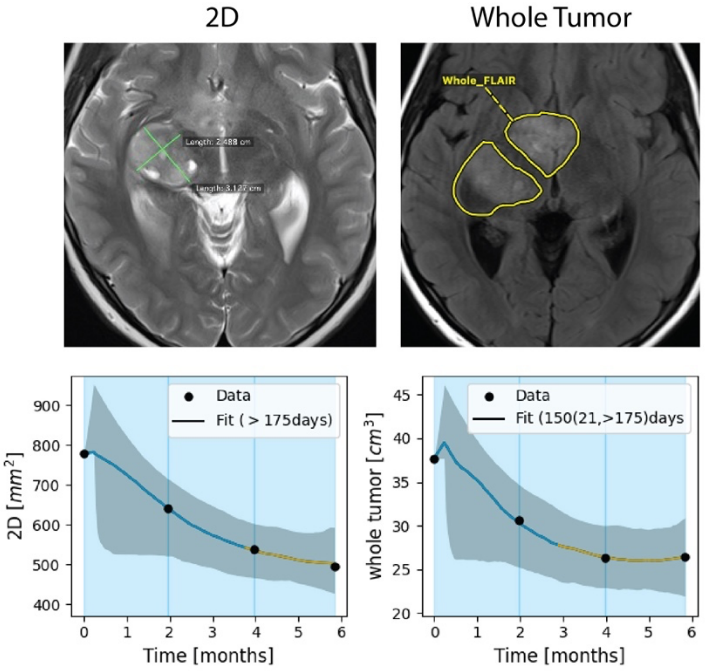




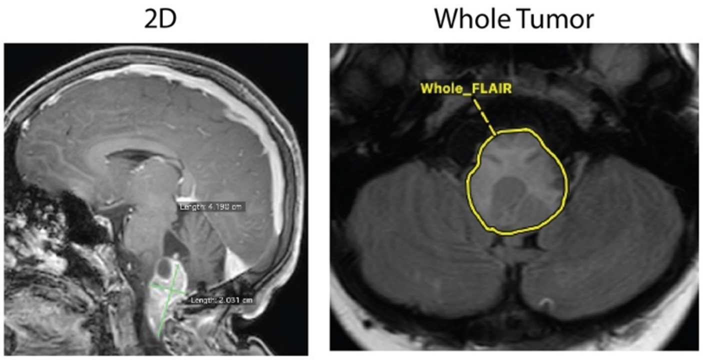
PARTICIPANT #27: Diffuse astrocytoma (Grade 2)

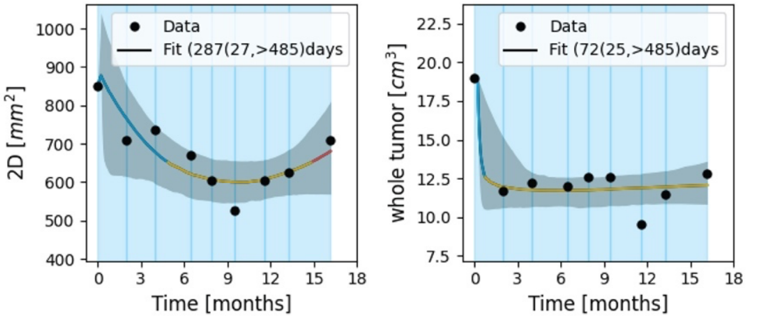


PARTICIPANT #28: Malignant glioma (not otherwise specified)

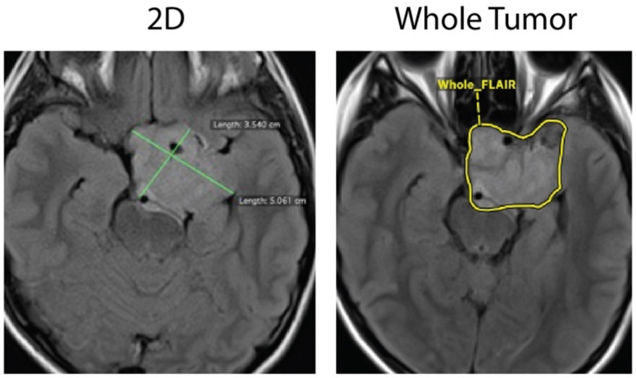


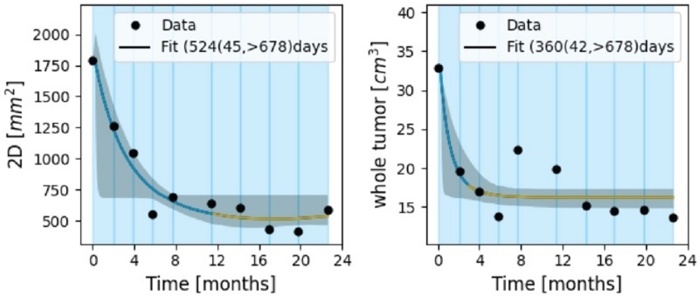
PARTICIPANT #29: Glioneuronal tumor with desmoplasia



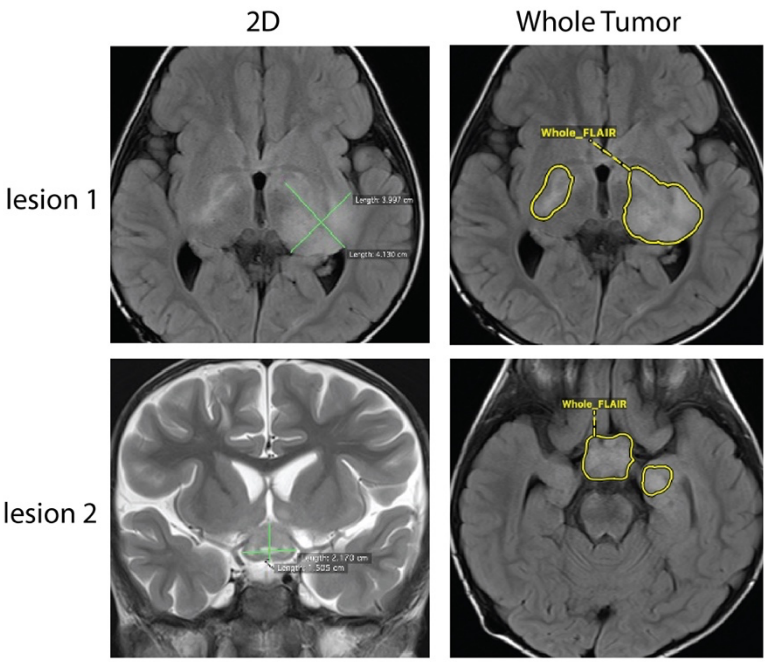


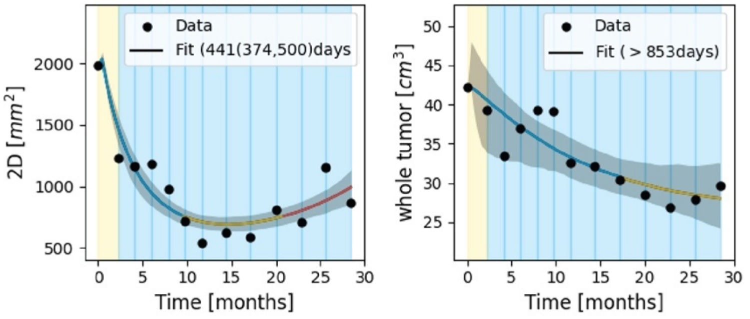
PARTICIPANT #30: Malignant glioma (not otherwise specified)



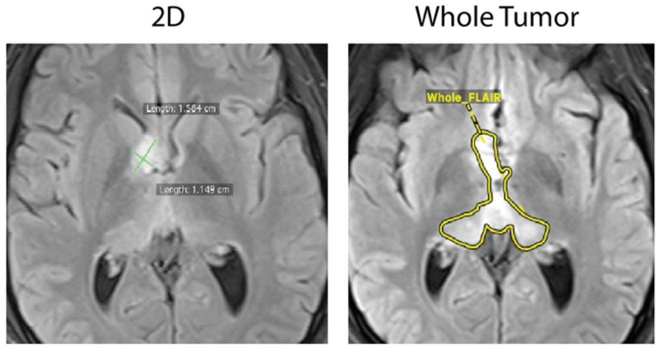


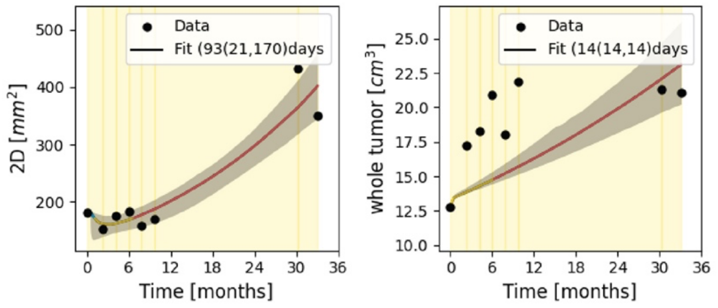
PARTICIPANT #31: Fibrillary astrocytoma



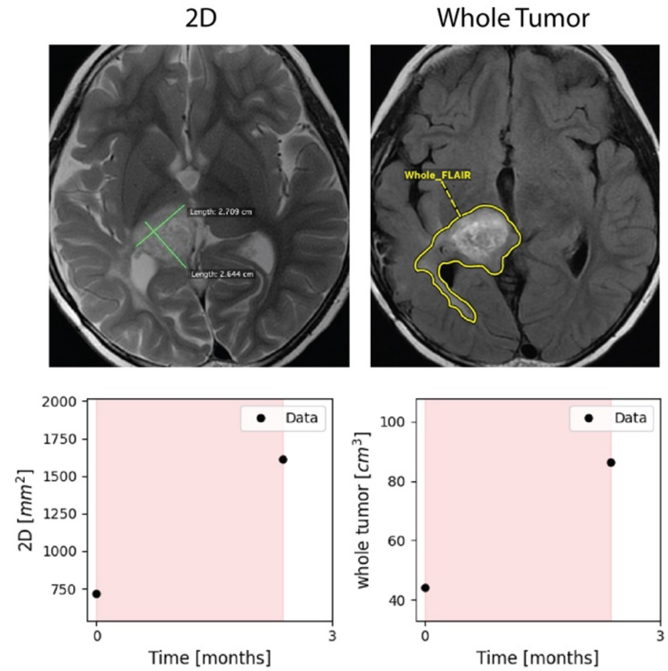


PARTICIPANT #32: Ganglioglioma

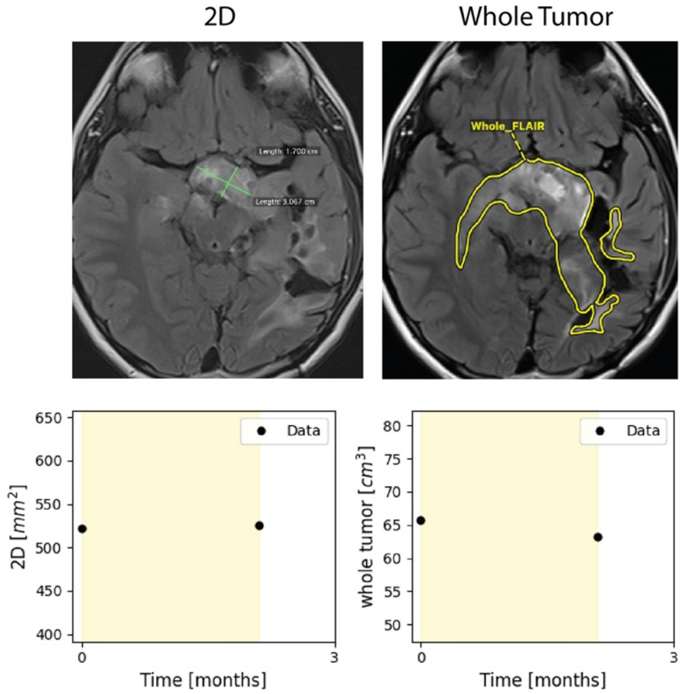




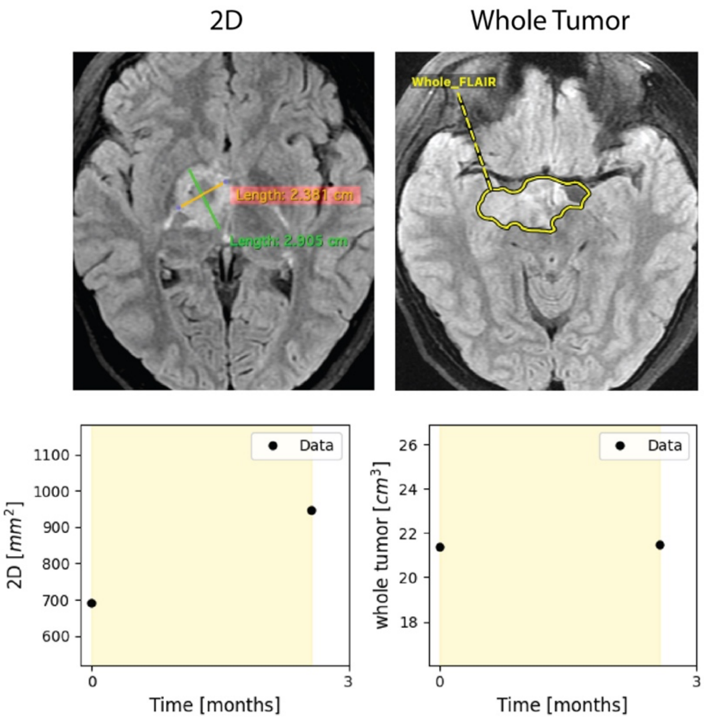
PARTICIPANT #33: Diffuse midline glioma (H3K27M mutant)



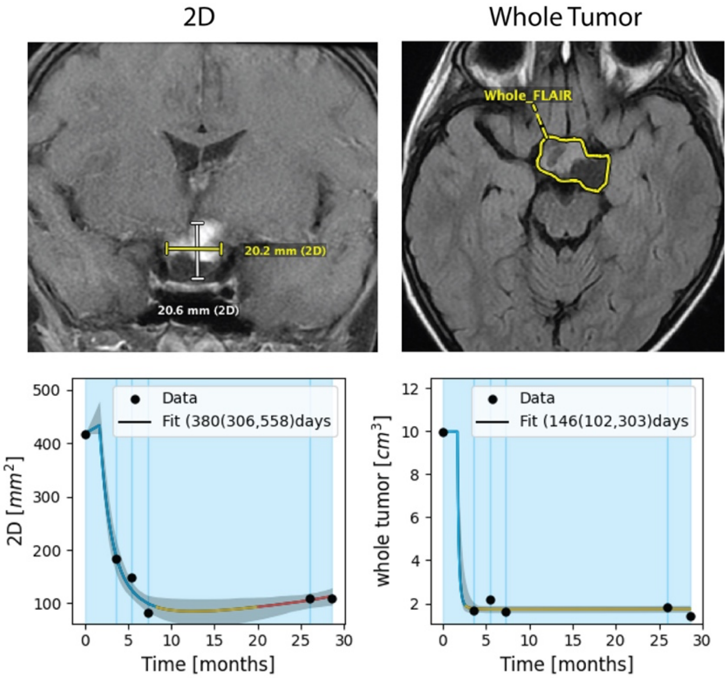
PARTICIPANT #35: Ganglioglioma



PARTICIPANT #36: Glioblastoma (not otherwise specified)



PARTICIPANT #37: Ganglioglioma



PARTICIPANT #38: Pilocytic astrocytoma