

Multimodal MRI radiomic models to predict genomic mutations in DIPG with missing imaging modalities

DIPG : poor prognosis median survival
less than 1 year

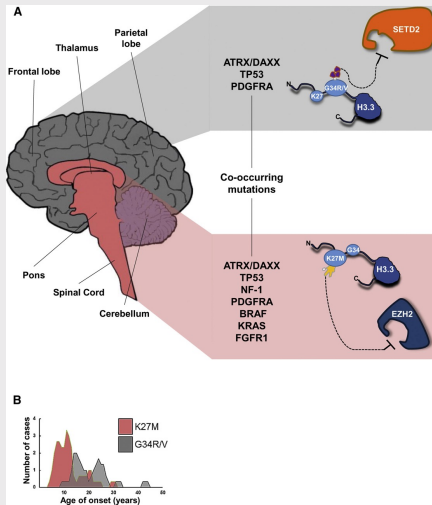
BIOMEDE study : three drugs according to genomic profiles

→ No significant changes in OS.

→ (BIOMEDE 2.0) ONC-201

→ compassionnal use of ONC-201

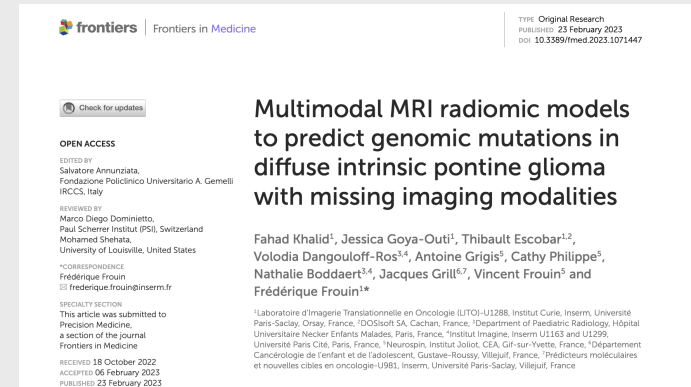
→ Protocol HGG CSI



Yuen BTK et al Cancer Cell 2013

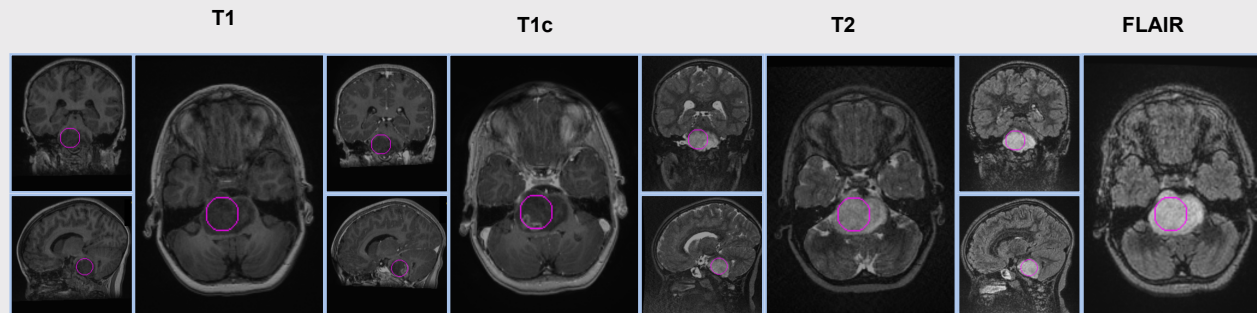
Molecular studies

- H3.1 -> longer OS than H3.3 & WT
Cohen et al Neuro-Oncology 2017
- ACVR1 mutation -> specific therapy?
Carvalho et al, Cancer Discovery 2022
- TP53 mutation -> radio-resistance
Werbrouck et al, Clin Cancer Res, 2019

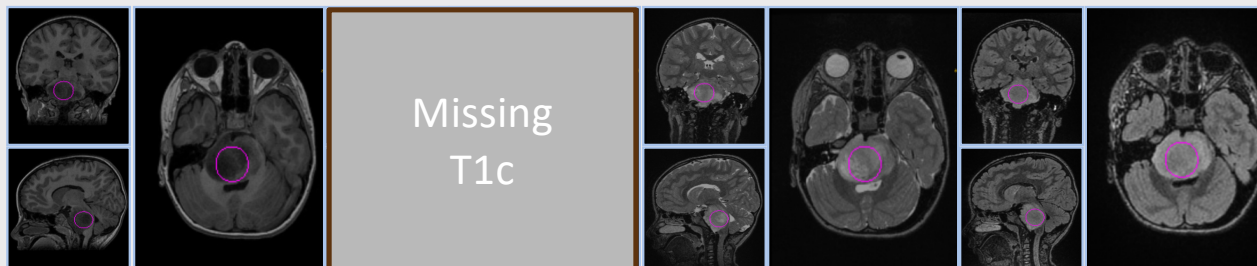


Multi-modal MR data with missing modalities

Patient 1



Patient 2



To predict genomic mutations
The multi model approach
dealing with missing modalities
gives the best results

whatever the prediction

Important to validate and increase the interest of the approach...

External validation of the diffuse intrinsic pontine glioma survival prediction model: a collaborative report from the International DIPG Registry and the SIOPE DIPG Registry

Sophie E. M. Veldhuijzen van Zanten^{1,9} · Adam Lane^{2,3} · Martijn W. Heymans⁴ · Joshua Baugh³ · Brooklyn Chaney³ · Lindsey M. Hoffman³ · Renee Doughman³ · Marc H. A. Jansen¹ · Esther Sanchez⁵ · William P. Vandertop⁶ · Gertjan J. L. Kaspers^{1,7} · Dannis G. van Vuurden¹ · Maryam Fouladi⁴ · Blaise V. Jones⁸ · James Leach⁸

The prognostic variables in the DIPG survival prediction model were age (age ≥ 3 years = 1/age < 3 years = 0) and symptom duration at time of diagnosis (as continuous variable), presence of ring enhancement on diagnostic MR-imaging (yes = 1/no = 0), and the use of oral or intensive (i.v.) chemotherapy at any time during the disease course (yes = 1/no = 0). This model was converted into the following clinical prediction rule: (age ≥ 3 years $\times 7$) + (symptom duration in months $\times -1$) + (ring enhancement $\times 4$) + (oral chemotherapy and/or intensive chemotherapy $\times -4$). With

- MR Data from SIOPE BTG (3D or multi slice – diagnosis time - outside BIOMEDE trial)
- Code ?

