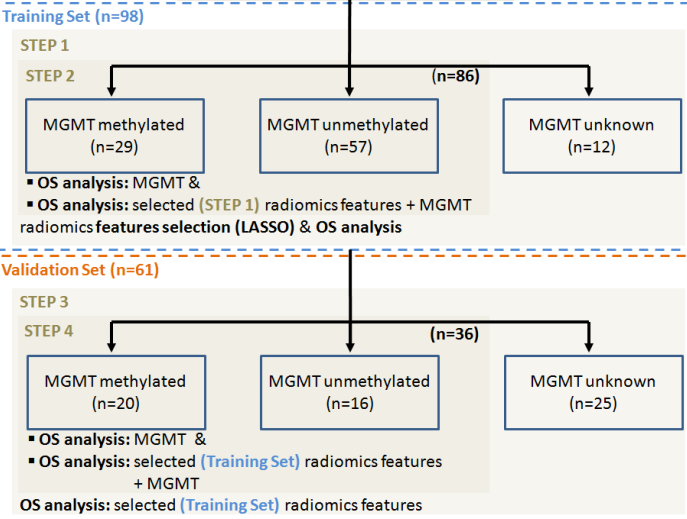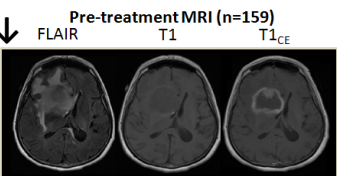# Complementary Value of MRI-Radiomics Features and Molecular Biomarkers in Glioblastoma to Predict Overall Survival

Florent Tixier[1], Hyemin Um[1], Dalton Bermudez[2], Aditi Iyer[1], Aditya Apte[1], Joseph O. Deasy[1], Ingo K. Mellinghoff[3], Robert J Young[2], Harini Veeraraghavan[1]

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PURPOSE: The aim of this study was to evaluate the complementary value of the **molecular biomarker MGMT** and the **radiomics features** derived from MRI images for improving the overall survival (OS) prognosis in glioblastoma patients.

METHODS ↓

Pre-treatment MRI (n=159)
FLAIR   T1   T1CE

Training Set (n=98)

STEP 1
STEP 2   (n=86)

| MGMT methylated (n=29) | MGMT unmethylated (n=57) | MGMT unknown (n=12) |

- OS analysis: MGMT &
- OS analysis: selected (STEP 1) radiomics features + MGMT
radiomics features selection (LASSO) & OS analysis

Validation Set (n=61)

STEP 3
STEP 4   (n=36)

| MGMT methylated (n=20) | MGMT unmethylated (n=16) | MGMT unknown (n=25) |

- OS analysis: MGMT &
- OS analysis: selected (Training Set) radiomics features + MGMT
OS analysis: selected (Training Set) radiomics features

RESULTS →

OS analysis of radiomics features (left) and combination of radiomics with MGMT (right) on **training** and the **validation** cohort.

← Flow chart of the study describing analyses that was performed on the **training** and the **validation** cohort.

CONCLUSION

A subgroup of patients with a methylated MGMT promoter and a low value on the selected radiomics feature has been shown to be able to identify a group of patients with lower risks on the **training** and **validation** cohort.

*p-value adjusted for multiple comparisons (Bonferroni)

p=0.02*

p=0.0005

p=0.02

p=0.01
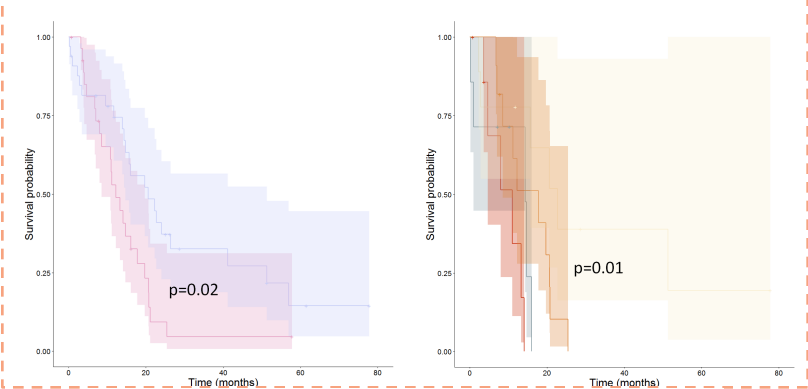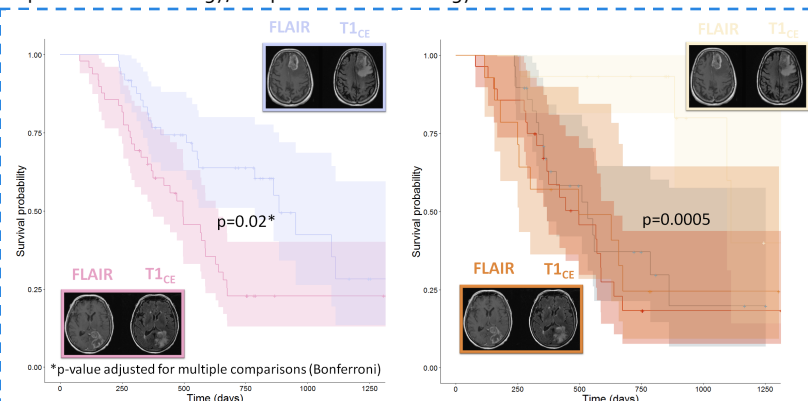
Radiomics (T1CE: $G_{\theta=0, f=2}$ Skewness)

≥ median
< median

MGMT + Radiomics

Unmethylated and < median
Unmethylated and ≥ median
Methylated and < median
Methylated and ≥ median

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