# EpiGe

EpiGe-App https://www.epige.irsjd.org/

Gómez-González et al. present a machine learning decision support system (DSS) that enables the classification of the principal molecular groups WNT, SHH, and non-WNT/non-SHH directly from quantitative PCR (qPCR) data. We propose a framework where the developed DSS appears as a user-friendly web-application-EpiGe-App that enables automated interpretation of qPCR methylation data and subsequent molecular group prediction. The basis of our classification strategy is a previously validated six-cytosine signature with subgroup-specific methylation profiles. This reduced set of markers enabled us to develop a methyl-genotyping assay capable of determining the methylation status of cytosines using qPCR instruments. This study provides a comprehensive approach for the rapid classification of clinically relevant medulloblastoma groups, using readily accessible equipment and an easy-to-use web application 1).

1)
Gómez-González S, Llano J, Garcia M, Garrido-Garcia A, Suñol M, Lemos I, Perez-Jaume S, Salvador N, Gene-Olaciregui N, Galán RA, Santa-María V, Perez-Somarriba M, Castañeda A, Hinojosa J, Winter U, Moreira FB, Lubieniecki F, Vazquez V, Mora J, Cruz O, La Madrid AM, Perera A, Lavarino C. EpiGe: A machine-learning strategy for rapid classification of medulloblastoma using PCR-based methyl-genotyping. iScience. 2023 Aug 12;26(9):107598. doi: 10.1016/j.isci.2023.107598. PMID: 37664618; PMCID: PMC10470382.