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A Web-Based Risk Calculator for Machine Learning–Derived Risk Scores in Multiple Myeloma

Carlos Pérez Míguez[1], Adrián Mosquera Orgueira[1,2], MD, PhD, Marta Sonia González Pérez[2], and Maria-Victoria Mateos [3], MD, PhD

[1] Computational Hematology and Genomics Group, IDIS, Santiago de Compostela, Spain
[2] Department of Hematology and Hemotherapy, University Hospital of Santiago, Santiago de Compostela, Spain
[3] University Hospital of Salamanca, IBSAL, CIC, and CIBERONC, Salamanca, Spain

BACKGROUND

Risk stratification in multiple myeloma (MM) has traditionally relied on clinical and cytogenetic parameters, often with limited predictive accuracy. Machine learning enables more precise risk models by analyzing large datasets and complex variable interactions. A machine learning–based classifier was recently developed using data from the Harmony project.

METHODS

The calculator, developed as a Shiny web application, includes three models—Baseline Risk, Treatment-related, and Dynamic—plus a Help window. The server processes inputs, runs calculations, and generates percentile-based risk graphs.

Risk scores for Overall Survival (OS) and Progression-Free Survival (PFS) are derived from:

- **Baseline Risk Model** (with/without Cytogenetics): Uses age, hemoglobin, β2-microglobulin, and albumin, with optional inputs for 1q Gain and 17p Deletion.
- **Treatment-related Model** (with/without Cytogenetics): Adds treatment type (PI-based, IMID-based, PI-IMID-based).
- **Dynamic Risk Model**: Includes all previous variables (except treatment) plus Best Response to Treatment (Complete Response, Very Good Partial Response, Partial Response, Stable Disease, Progressive Disease).

Scores are further stratified by transplant eligibility, comparing patient risk percentiles within eligible and non-eligible cohorts.

Figure 1. *Workflow of model development and validation using the HARMONY cohort (N = 14,345). The dataset was split into a training set (N = 7,072) for model development—including baseline-risk, treatment-based, and dynamic-risk models (OS and PFS)—and a test set (N = 3,771) for validation. The QR code links to the Risk Calculator.*

RESULTS

Users select a model and enter values for age, hemoglobin, β2-microglobulin, and albumin, optionally adding cytogenetic data in the Baseline and Treatment-related models. The calculator generates percentile-based risk scores for OS and PFS.

Results appear as intuitive risk graphs (0–100), showing the patient's relative risk within the training cohort. The tool also stratifies OS and PFS by transplant eligibility, refining risk assessment and supporting clinical decision-making.

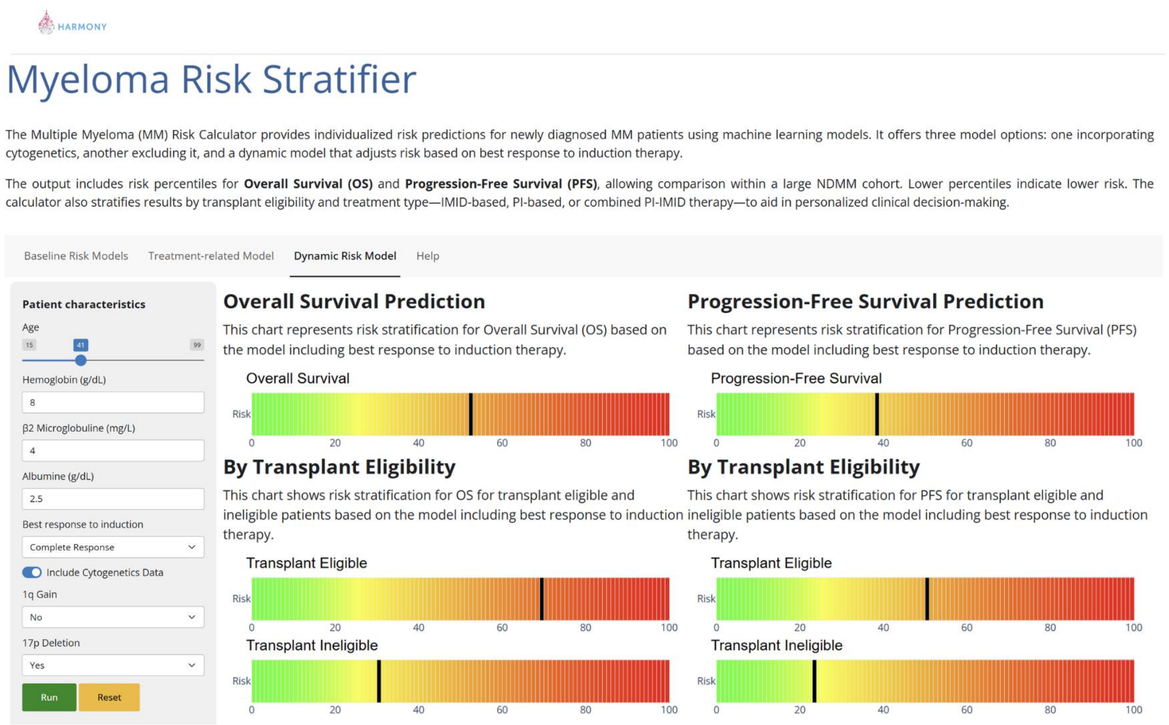

Figure 2A. *Interface of the Dynamic Risk Model in the Myeloma Risk Stratifier. The tool allows input of patient-specific characteristics to generate individualized risk predictions for Overall Survival (OS) and Progression-Free Survival (PFS), including stratification by transplant eligibility. Results are displayed as percentiles, with lower values indicating lower risk.*

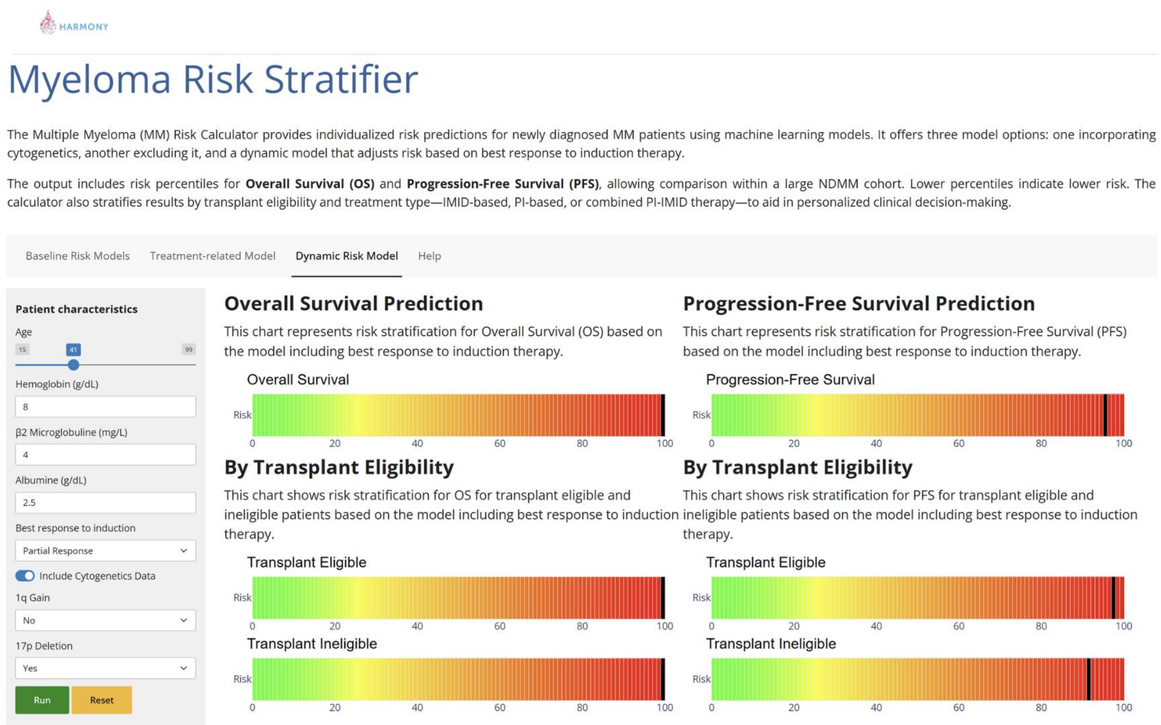

Figure 2B. *Example output of the Dynamic Risk Model in the Myeloma Risk Stratifier with updated patient inputs. Risk percentiles for Overall Survival (OS) and Progression-Free Survival (PFS) are displayed, including subgroup stratification by transplant eligibility. Higher percentiles indicate greater risk, assisting in individualized treatment planning.*

CONCLUSIONS

This web-based calculator provides automated risk assessment integrating clinical, cytogenetic, and treatment response data. Its intuitive design supports personalized decision-making.

Access: https://taxonomy.harmony-platform.eu/riskcalculator/

CONTACT

Carlos Pérez Míguez
GrHeCo-Xen (IDIS)
Bioinformatician
carlos.perez@grheco.com

https://comylive.cme-congresses.com