

Challenge Data 2025 : Overall Survival Prediction of Patients with Myeloid Leukemia

Winning solution

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<https://github.com/arthurdrk/QRT-Challenge-2025>



ChAllengeData
By MathA



This year's challenge was about a subtype of **blood cancer** called myeloid leukemia.

- Accumulation of abnormal immature myeloid cells
- The bone marrow produces dysfunctional blood cells

Goal of the Challenge : Predict risk disease

The risk is measured through the **overall survival** of patients, i.e., the duration of survival from the diagnosis of the blood cancer to the time of death or last follow-up.

Data Overview

Data is divided in two parts : **Clinical Data** and **Molecular Data**
Very large dataset :

- **3,323** patients in train set
- **1,193** patients in test set

	ID	CENTER	BM_BLAST	WBC	ANC	MONOCYTES	HB	PLT	CYTOGENETICS
0	P132697	MSK	14.0	2.8	0.2	0.7	7.6	119.0	46,xy,del(20)(q12)[2]/46,xy[18]
1	P132698	MSK	1.0	7.4	2.4	0.1	11.6	42.0	46,xx
2	P116889	MSK	15.0	3.7	2.1	0.1	14.2	81.0	46,xy,t(3;3)(q25;q27)[8]/46,xy[12]
3	P132699	MSK	1.0	3.9	1.9	0.1	8.9	77.0	46,xy,del(3)(q26q27)[15]/46,xy[5]
4	P132700	MSK	6.0	128.0	9.7	0.9	11.1	195.0	46,xx,t(3;9)(p13;q22)[10]/46,xx[10]

Figure 1 – Head of clinical train set

	ID	CHR	START	END	REF	ALT	GENE	PROTEIN_CHANGE	EFFECT	VAF	DEPTH
0	P100000	11	119149248.0	119149248.0	G	A	CBL	p.C419Y	non_synonymous_codon	0.0830	1308.0
1	P100000	5	131822301.0	131822301.0	G	T	IRF1	p.Y164*	stop_gained	0.0220	532.0
2	P100000	3	77694060.0	77694060.0	G	C	ROBO2	p.?	splice_site_variant	0.4100	876.0
3	P100000	4	106164917.0	106164917.0	G	T	TET2	p.R1262L	non_synonymous_codon	0.4300	826.0
4	P100000	2	25468147.0	25468163.0	ACGAAGAGGGGGTGTTC	A	DNMT3A	p.E505fs*141	frameshift_variant	0.0898	942.0

Figure 2 – Head of molecular train set

Each patient is associated with a unique identifier and detailed clinical information :

- ID : unique identifier per patient
- CENTER : clinical center
- BM_BLAST : bone marrow blasts in % (blasts are abnormal blood cells)
- WBC : white blood cell count in Giga/L
- ANC : absolute Neutrophil count in Giga/L
- MONOCYTES : monocyte count in Giga/L
- HB : hemoglobin in g/dL
- PLT : platelet count in Giga/L
- CYTOGENETICS : description of the karyotype observed in blood cells, measured by a cytogeneticist

One line per patient per somatic mutation :

- ID : Unique identifier per patient
- CHR_START_END : Position of the mutation on the human genome
- REF_ALT : Reference and alternate (mutant) nucleotide
- GENE : Affected gene
- PROTEIN_CHANGE : Consequence of the mutation on the protein expressed by the gene
- EFFECT : Broad categorization of the mutation consequence on the gene
- VAF : Variant Allele Fraction (proportion of cells carrying the deleterious mutation)
- DEPTH : Coverage (total number of reads at the locus)

Target & Evaluation Metric

Target : Overall Survival (OS)

- X_i = time to event (OS_YEARS)
- Δ_i = event indicator (1 = death, 0 = censored) (OS_STATUS)
- Truncation : $\tau = 7$ years

Metric : Concordance Index (C-Index)

- Measures ranking quality (0.5 = random, 1 = perfect)
- Concordant if : earlier death \rightarrow higher predicted risk

IPCW C-Index (handles censoring)

We weight pairs using the probability of being uncensored :

$$\hat{C}_\tau = \frac{\sum_{i,j} \Delta_i \hat{G}(X_i)^{-2} \mathbf{1}\{X_i < X_j\} \mathbf{1}\{\text{Risk}_i > \text{Risk}_j\}}{\sum_{i,j} \Delta_i \hat{G}(X_i)^{-2} \mathbf{1}\{X_i < X_j\}}$$

where $\hat{G}(t)$ is the Kaplan–Meier estimate of $P(\text{not censored at } t)$ (the censoring survival function).

Data visualisation

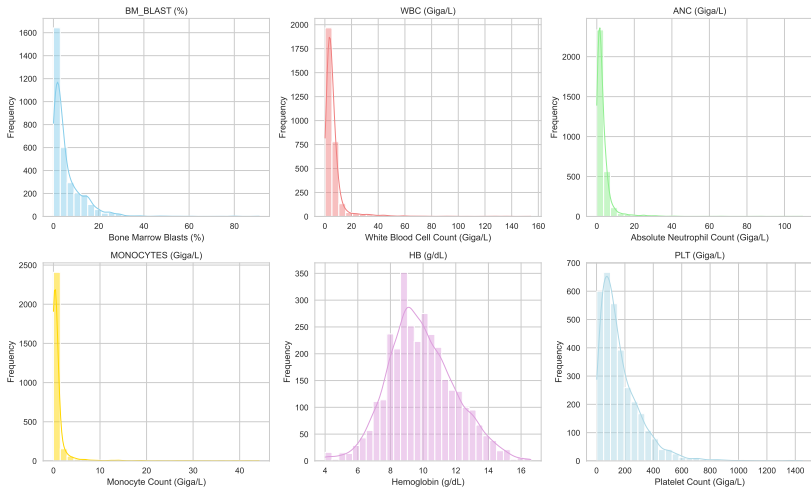


Figure 3 – Clinical variables distributions

Data visualisation

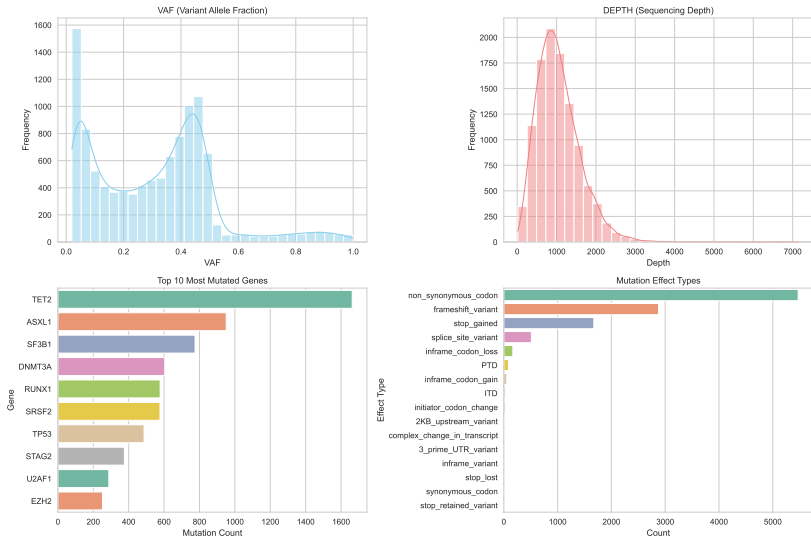


Figure 4 – Molecular variables distributions

Data Preprocessing

- Missing clinical values imputed using optimized XGBoost models (trained on the training set and applied to validation data)
- Continuous variables scaled using RobustScaler (median and IQR) to reduce the influence of outliers
- $\text{Log}(1+p)$ transformation applied to highly skewed variables to stabilize variance and reduce asymmetry

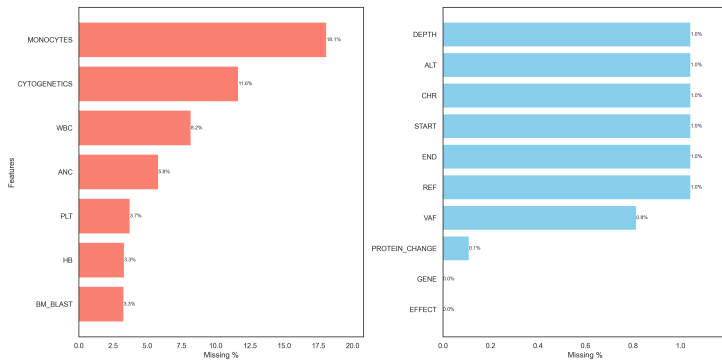


Figure 5 – Missing values in Clinical train and Molecular train

Prognostic Standard (ELN 2017)

Cytogenetic abnormalities and gene mutations are the primary determinants of prognosis in **Acute Myeloid Leukemia** (Döhner et al., 2017).

1. Cytogenetics (ISCN)

- **Normal** : $46,XX$ (F) or $46,XY$ (M). 23 standard pairs.
- **Abnormal** : Structural or numerical changes.
- *Example* : **-7** (Monosomy 7) indicates a high-risk profile.

$46,XY,-7$ = Male + Monosomy 7

2. Gene Mutations

- Comprehensive list of **mutated genes** per patient.
- Detailed descriptions of each mutation variant.
- Integrated with cytogenetics to define final ELN risk groups.

→ **Goal** : Transform these complex raw strings (ISCN/Mutations) into numerical features for XGBoost and Neural-MTLR.

Converting ISCN descriptions into structured features :

1. Abnormality Burden

- Total number of events
- Affected chromosomes
- Ploidy status (Hypo/Hyper)

2. Clinical Lesions

- Deletions ($-5/7$, $5q/7q$)
- Rearrangements (CBF, APL)
- Specific mutations (17p, inv3)

3. Risk Summary

- Monosomal/Complex karyotype
- ELN risk class
- Binary score (Adverse / Non-adverse)

4. Clonal Structure

- % of abnormal metaphases
- Size of the dominant clone
- Severity of the worst clone

Feature engineering

Added prognostic value of cytogenetics

Setup

- Models :
 - 1 Clinical + Molecular only
 - 2 Clinical + Molecular + Cytogenetics
- Cox elastic-net, fully nested CV (5-fold outer, 3-fold inner)

Performance (outer CV mean \pm SD)

Metric	No cytogenetics	With cytogenetics
C-index	0.741 \pm 0.004	0.742 \pm 0.004
IBS	0.161 \pm 0.009	0.161 \pm 0.009
AUC (1 year)	0.795 \pm 0.010	0.796 \pm 0.010

Interpretation

- Cytogenetics provide a *small but consistent* improvement
- Gains are stable across folds (nested CV \rightarrow low overfitting risk)
- Directionally aligned across all metrics (C-index, IBS, AUC)

Feature engineering

Gene Survival Analysis - Summary

Global statistics

- 124 genes analyzed
- 27 significant genes ($\text{FDR} < 0.05$)
- 26 higher-risk genes ($\text{HR} > 1$)
- 1 protective gene ($\text{HR} < 1$)

Gene	HR [95% CI]	FDR	Effect
TP53	2.74 [2.41–3.13]	4.91×10^{-49}	Higher risk
RUNX1	2.14 [1.89–2.43]	5.19×10^{-31}	Higher risk
ASXL1	1.67 [1.50–1.85]	2.18×10^{-20}	Higher risk
STAG2	1.96 [1.69–2.28]	2.33×10^{-17}	Higher risk
SF3B1	0.64 [0.56–0.72]	1.12×10^{-11}	Protective

Methods

- Log-Rank test (comparison of survival curves)
- Univariate Cox model (Hazard Ratios)
- Benjamini-Hochberg FDR correction
- Bootstrap (200 iterations) for stability assessment

Feature engineering

Extracting Signal from High-Dimensional Genomic Data

1. High-Dimensional Input & Filtering

Representing patient i as a binary sparse vector : $\mathbf{x}_i \in \{0, 1\}^p$

- **Noise Reduction** : Retain genes with prevalence $\in [1\%, 99\%]$.
- **Rationale** : Eliminates "uninformative constants" to maximize the **signal-to-noise ratio**.

2. Survival Modeling : The Cox Framework

Modeling the **Hazard Rate** to quantify death risk over time.

- **Flexibility** : Semi-parametric (no baseline hazard assumption).
- **Censoring** : Robust handling of non-uniform follow-up periods.

Objective : Molecular Risk Score

Consolidate the sparse mutational landscape into a single, continuous metric to forecast survival and stratify risk.

Feature engineering

Quantifying Mutational Impact on Survival

Model Specification

For patient i , the instantaneous risk of death (Hazard) is modeled as :

$$h(t \mid \mathbf{x}_i) = h_0(t) \exp(\mathbf{x}_i^\top \boldsymbol{\beta})$$

Core Assumption

- **Proportional Hazards :**
The Risk Ratio between patients is **time-invariant**.
- **Flexibility :** $h_0(t)$ is unspecified, allowing focus on the **relative alpha** of mutations.

Interpretation

- $\beta > 0$: High-risk mutation.
- $\beta < 0$: Protective effect.
- **Censoring :** Naturally handles "survivors" or lost-to-follow-up data via partial likelihood.

Feature engineering

Elastic Net Cox Model with Nested CV

Elastic Net-Penalized Cox Model

Estimate $\hat{\beta}$ by maximizing the penalized partial log-likelihood :

$$\ell_{\text{partial}}(\beta) - \lambda((1 - \alpha)\|\beta\|_2^2 + \alpha\|\beta\|_1)$$

- `lifelines.CoxPHFitter` (`penalizer = λ` , `l1_ratio = α`)
- **Nested CV** : 5 outer folds, 3 inner folds, 30 Optuna trials
- Hyperparameters selected by maximizing Harrell C-index
- Final $(\lambda^*, \alpha^*) = (\text{median}(\lambda^{(k)}), \text{median}(\alpha^{(k)}))$

Molecular Risk Score (MRS)

$$\text{MRS}_i = \mathbf{x}_i^\top \hat{\beta}$$

Higher MRS \Rightarrow higher mortality risk (used for patient stratification).

Feature engineering

Evaluation of the Composite Risk Score

- **Harrell's C-index (5-fold CV) : 0.70**
- **Bootstrap (1000 resamples) : mean C-index = 0.700, 95% CI [0.686; 0.713]**

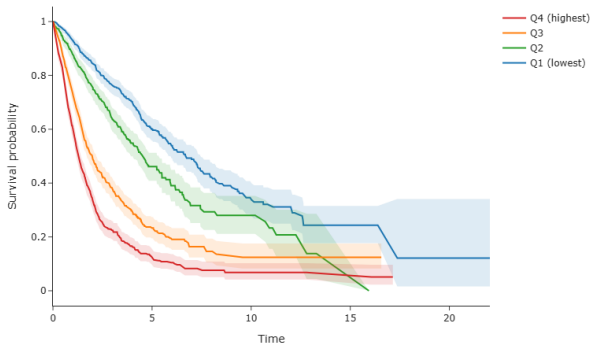
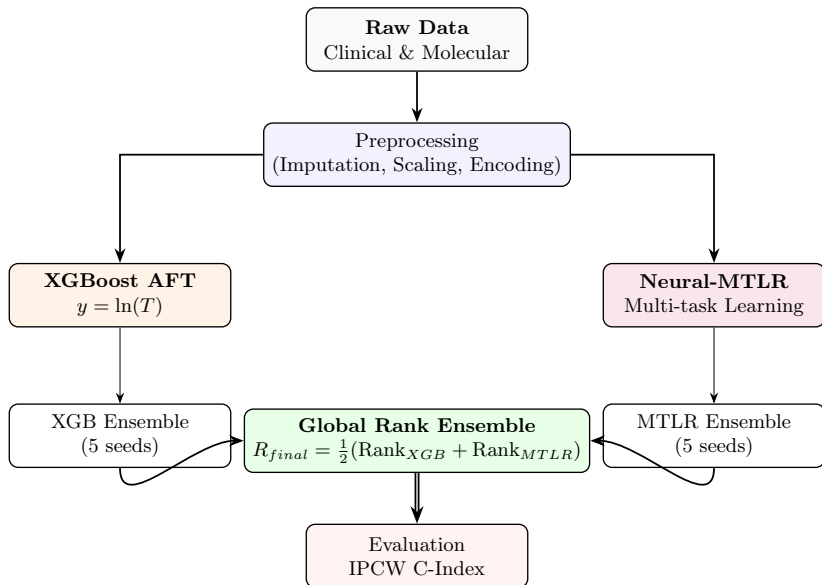


Figure 6 – Kaplan–Meier survival curves by molecular risk quartile

- **Clear monotone pattern : higher risk quartiles are associated with poorer survival.**

Model Architecture Overview



The **Accelerated Failure Time (AFT)** model is a robust alternative to Cox models, focusing on the survival time scale.

Acceleration Assumption

Covariates x act as a multiplicative factor $\exp(\eta(x))$ on survival time :

$$T = e^{\eta(x)} \cdot T_0 \quad \implies \quad \ln(T) = \eta(x) + \ln(T_0)$$

- $\eta(x) < 0$: The event occurs **earlier** (accelerated time).
- $\eta(x) > 0$: The event is **delayed** (prolonged survival).

The XGBoost Advantage : Instead of a simple linear function, it learns a flexible $\eta(x)$ via tree boosting, capturing **non-linear effects** and complex genomic interactions.

Training is performed by minimizing the **Negative Log-Likelihood** to account for incomplete data.

Likelihood for Patient i

$$\mathcal{L}_i = \delta_i \underbrace{\ln f(z_i)}_{\text{Observed Event}} + (1 - \delta_i) \underbrace{\ln S(z_i)}_{\text{Censoring}}$$

$$\text{where } z_i = \frac{\ln t_i - \eta_i}{\sigma}$$

- **Scale Parameter σ** : Controls log-survival dispersion (lower σ = higher confidence).
- **Numerical Stability** : Uses a second-order Taylor expansion ; gradients depend on the chosen distribution (Weibull, Log-Normal).

Multi-Task Logistic Regression (MTLR) treats survival as a sequence of dependent binary classification tasks.

- **Time Grid** : Defines k time points τ_1, \dots, τ_k (e.g., event quantiles) to partition the time axis.
- **Target Encoding** :
 - Pre-event : Vector of 1s (Survival).
 - Post-event : Vector of 0s (Event occurred).

Key Advantage

No Proportional Hazards Assumption : Allows the impact of a covariate to change or fluctuate over time.

Neural-MTLR

Architecture and Monotonicity

A neural network implemented via `nn.Sequential` extracts non-linear features prior to the MTLR layer.

From Features to Survival Curve

- ➊ **Feature encoding** : Dense layers map clinical data into a latent representation.
- ➋ **Piecewise linear scoring** : The MTLR layer outputs k scores $\{\phi_1, \dots, \phi_k\}$.
- ➌ **Global Softmax** : Ensures

$$\sum_j P(\text{death in interval } j) = 1.$$

Smoothing Regularization :

$$\text{Penalty} = \gamma \sum_{j=1}^{k-1} \|\theta_{j+1} - \theta_j\|_2^2$$

This yields a **monotone and stable** survival curve $S(t)$, avoiding unrealistic discontinuities.

Model Comparison and Ensemble Strategy

XGBoost AFT

Type : Parametric (Flexible η)

Assumption : Log-linearity in time

Strength : Robust to small samples

Output : Scalar log-time

Neural-MTLR

Type : Non-parametric

Assumption : No hazard structure

Strength : Captures non-PH effects

Output : Survival distribution

Rank-Based Ensemble Strategy

Combines complementary strengths by aggregating ranks :

$$\text{Score}_{\text{final}} = \text{mean}(\text{rank}(\hat{y}_{\text{AFT}}) + \text{rank}(P_{\text{MTLR}}))$$

Key Benefits :

- Robust to scale differences
- Reduced variance
- Improved stability

Effect of Ensembling — XGBoost AFT

IPCW C-index (5-fold nested cross-validation)

Model	Mean \pm SD	95% CI
Single model	0.7223 ± 0.0139	[0.7050 ; 0.7395]
Ensemble (5 seeds, rank-avg.)	0.7243 ± 0.0131	[0.7080 ; 0.7406]

Paired comparison (fold-wise) :

$$\Delta C = +0.0021, \quad t = 2.70, \quad p = 0.054$$

Interpretation

- Small but consistent improvement.
- Borderline statistical significance at the 5% level.
- Ensemble reduces variance and stabilises rankings.

Effect of Ensembling — Neural-MTLR

IPCW C-index (5-fold nested cross-validation)

Model	Mean \pm SD	95% CI
Single model	0.6997 ± 0.0163	[0.6795 ; 0.7199]
Ensemble (5 seeds, rank-avg.)	0.7102 ± 0.0151	[0.6914 ; 0.7290]

Paired comparison (fold-wise) :

$$\Delta C = +0.0105, \quad t = 6.56, \quad p = 0.0028$$

Interpretation

- Clear and statistically significant improvement.
- Rank-based ensembling is particularly beneficial here.
- Suggests complementary inductive bias across random seeds.