[Development and Validation of a Combined Hypoxia and Immune Prognostic Classifier for Head and Neck Cancer](https://aacrjournals.org/clincancerres/article/25/17/5315/81611/Development-and-Validation-of-a-Combined-Hypoxia)

Hypoxia and immune signatures plus additional genes of interest from HT-seq gene count files downloaded from the TCGA HNC dataset

1. normalized by dividing the expression values by the sum of expression values
2. then log2 transformed;
3. z-scores were calculated
4. using Spearman distance and Ward criterion in R
5. plot heatmaps using the z-score values matrix for color intensities
6. a Cox regression multivariate was used to calculate the combined effect of HPV status and heatmap groups, using the Survival package in R
7. Outcome measure was overall survival (OS) from treatment end date to death or last follow up and censure.

A diagram of a test

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identified distinct HNC patient subgroups with coordinate expression of hypoxia- and immune response–related genes

[Performance Comparison of Deep Learning Autoencoders for Cancer Subtype Detection Using Multi-Omics Data](https://www.mdpi.com/2072-6694/13/9/2013)

Glioblastoma multiforme (GBM) for example, 276 patients of this cancer type (male—164, female—112), with 17,814 features for mRNA expression, 470 features for miRNA expression, and 13,000 features for DNA methylation

A diagram of a machine learning

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1. A mathematical equation with black text

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2. chose 100/400/500 number of important features from each dataset based on maximum variance (VAR) using the function FSbyVar from the CancerSubtypes package in R
3. Design Loss for 4 autoencoders:









1. used Euclidean distance and Spearman correlation as a similarity measure between two patients
2. an unsupervised subtypes discovery method combined with k-means [36] and Partitioning around medoids (PAM) [37] as our clustering methods

A diagram of a network

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[Development and validation of a hypoxia-immune-based microenvironment gene signature for risk stratification in gastric cancer](https://translational-medicine.biomedcentral.com/articles/10.1186/s12967-020-02366-0)

1. background correction and quartile normalization were performed for each series by applying the robust multiarray average algorithm
2. t-SNE Hallmark gene sets specific to hypoxia, comprising about 200 genes, are downloaded from the Molecular Signatures Database (MSigDB version 6.0), Analyzing Expression Changes in HIF-1 Pathway
3. limma DEGs
4. Similarly, ESTIMATE (Estimation of STromal and Immune cells in MAlignant Tumor tissues using Expression data) Identifcation of immune status and immune‑related DEGs
5. Cox regression previously identified hypoxia and immune statuses of patients that are combined to a two-dimensional index to identify prognostic DEGs
6. LASSO Cox regression model is employed to select the most prognostic genes from all identified hypoxia-immune-related prognostic DEGs

[Tumour genomic and microenvironmental heterogeneity for integrated prediction of 5-year biochemical recurrence of prostate cancer: a retrospective cohort study](https://www.thelancet.com/journals/lanonc/article/PIIS1470-2045(14)71021-6/fulltext)

1. identified unique genomic subtypes with use of unsupervised hierarchical clustering.
2. used the percentage of a patient’s genome harbouring copy number alterations (percent genome alteration) as a surrogate for genomic instability, and assessed this proportion together with tumour hypoxia.
3. supervised machine learning with a random forest21 to develop a statistical model, resulting in a DNA signature, which classified patients at risk of biochemical relapse on the basis of their copy-number profiles.

[A novel hypoxia- and lactate metabolism-related signature to predict prognosis and immunotherapy responses for breast cancer by integrating machine learning and bioinformatic analyses](https://pubmed.ncbi.nlm.nih.gov/36275774/)

1. edgeR extract differentially expressed genes, including LMRGs and HRGs (hypoxia-lactate metabolism-related)
2. Cox regression analysis
3. divided the prognostic genes into favorable genes, where high RNA expression correlates with longer survival time, and unfavorable genes, where high RNA expression correlates with shorter survival times
4. random survival forest(RSF) algorithm to reduce the dimensions
5. stepwise multivariate Cox regression analysis constructed the HLMRPM [risk score = (0.6139585 ×ESRP1) + (-0.3698120 ×MAFF) + (0.1682696×SLC2A1) + (-0.2963183 × DARS2) + (0.2690044×TH)]
6. Kaplan–Meier survival analysis

[Identification and validation of hypoxia-derived gene signatures to predict clinical outcomes and therapeutic responses in stage I lung adenocarcinoma patients](https://pubmed.ncbi.nlm.nih.gov/33754044/)

1. “Cell cycle progression (CCP)”, “Epithelial-mesenchymal transition (EMT)” and “Hypoxia” in each sample from the training set were quantified using a single-sample gene set enrichment analysis (ssGSEA) algorithm
2. CIBERSORT was used to quantify immune infiltration
3. Z-score scaling was applied to both ssGSEA and immune infiltration scores
4. Weighted gene co-expression network analysis (WGCNA) was used to construct a scale-free co-expression network to identify a gene module which is mostly correlated with hypoxia
5. (LASSO) Cox or logistic regression models and random forest (RF) algorithm were used to further screen for the most robust candidates
6. a hypoxia-related prognostic risk score (HPRS) and a hypoxia-related immunotherapeutic response score (HIRS) for each sample were calculated as follows: A black and white symbol

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[Development and validation of a hypoxia-associated signature for lung adenocarcinoma](https://pubmed.ncbi.nlm.nih.gov/35079065/)

1. The Cancer Genome Atlas (TCGA)-LUAD cohort was split into training (n=252) and test (n=250) datasets. (?? Why this porportion)
2. Cluster by expression similarity
3. Prediction analysis for microarray (PAMR) was applied to the 35 seed genes, selecting 28 genes with the minimum tenfold cross-validation error rate.

[Establishment and External Validation of a Hypoxia-Derived Gene Signature for Robustly Predicting Prognosis and Therapeutic Responses in Glioblastoma Multiforme](https://pubmed.ncbi.nlm.nih.gov/35155681/)

Quantification: Expression profiling of gene sets was done in GBM samples using single-sample gene set enrichment analysis (ssGSEA) and gene set variation analysis (GSVA).

Association Analysis: Univariate Cox regression analysis was performed to evaluate the associations between hallmarks of cancer and GBM prognosis.

Weighted Gene Coexpression Network Analysis (WGCNA):

Network Construction: WGCNA was applied to construct a scale-free coexpression network based on the expression profiling of GBM samples.

Module Selection: Genes in the coexpression module strongly associated with hypoxia were screened for further analysis.

Construction of a Least Absolute Shrinkage and Selection Operator (LASSO) Prognostic Model:

Gene Selection: Prognosis-related genes in the hypoxia-relevant coexpression module were identified using univariate Cox regression.

Model Building: A LASSO prognostic model was established using the glmnet package, and risk scores were determined for GBM patients based on gene expression and LASSO regression coefficients.

[Development and validation of a hypoxia-stemness-based prognostic signature in pancreatic adenocarcinoma](https://pubmed.ncbi.nlm.nih.gov/35935823/)

1. The Pearson correlation coefficient (PCC) between the expression level and mRNAsi value of each hypoxia gene was then calculated using the Cor function in R software
2. univariate Cox regression analysis to identify HSRGs significantly associated with OS
3. least absolute shrinkage and selection operator (LASSO) regression algorithm in the “lars” R package was subsequently applied to acquire the optimal OS-related HSRGs
4. risk score of each sample was calculated as follows
5. A black and white text

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[Immune gene patterns and characterization of the tumor immune microenvironment associated with cancer immunotherapy efficacy](https://pubmed.ncbi.nlm.nih.gov/36950600/)

Although not hypoxia, it looked the hypoxia score and applied simialry methods, also extend features to A blue sign with black text

Description automatically generated

A diagram of a data flow

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[Characterizing the landscape of cervical squamous cell carcinoma immune microenvironment by integrating the single‐cell transcriptomics and RNA‐Seq](https://onlinelibrary.wiley.com/doi/epdf/10.1002/iid3.608)

A diagram of a cell division

Description automatically generated with medium confidence

[Identification and validation of a prognostic signature related to hypoxic tumor microenvironment in cervical cancer](https://pubmed.ncbi.nlm.nih.gov/35657977/)

Univariate Cox Analysis:

Univariate Cox analysis was performed on the TCGA-CESC cohort (n = 289) to identify significant Hypoxia-Related Genes (HRGs) with prognostic value in cervical cancer.

The 'survival' package in R was used, and genes with a P-value < 0.01 were considered significant.

Cohort Splitting:

The 289 patients were randomly assigned to a training cohort (n = 203) and a test cohort (n = 86) at a 7:3 ratio using the 'caret' package.

Model Development - LASSO Method:

The least absolute shrinkage and selection operator (LASSO) method was employed in the TCGA-training cohort using the 'glmnet' package in R.

LASSO helps select a subset of the most informative and parsimonious features (HRGs in this case) by applying a penalty term.

The penalty parameter (λ) for the LASSO model was determined through tenfold cross-validation.

Signature Development:

The identified HRGs from the LASSO model were used to create the Hypoxia-related Prognostic Signature (ccHPS).

The ccHPS assigns a risk score to each tumor sample, combining the coefficients of HRGs and their expression abundance in each sample.

[Establishment of Prognosis Model in Acute Myeloid Leukemia Based on Hypoxia Microenvironment, and Exploration of Hypoxia-Related Mechanisms](https://pubmed.ncbi.nlm.nih.gov/34777463/)

Identification of Hypoxia-Related Signatures:

Univariate Cox proportional hazards regression was used to preliminarily screen AML prognostic genes (p < 0.05).

Cohort 1 was randomly divided into a training set and a test set.

A combination of Cox proportional hazards regression and LASSO was applied to select the most important hypoxia-related signatures. The penalty parameter (λ) was determined by 10-fold cross-validation.

Multivariate Cox Regression and Risk Model Building:

Multivariate Cox regression analysis was performed to estimate independent prognostic factors associated with patient survival.

The stepwise method was employed to select the best subset of predictors.

A hypoxia-related prognostic risk (HRS) score model was built using the regression coefficients (β) weighted by the multivariate Cox proportional hazards regression model in the training set.