Workshop 1 ： Clinical Research Introduction

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PART 1 Reaserch Overview

1.1 回顾性研究

Development and Validation of a Postprocedural Model to Predict Outcome After Endovascular Treatment for Ischemic Strok

三表一图

基线表

Table 1. Overview of Derivation Cohort and Validation Cohort[a]

Characteristic	Derivation cohort HERMES (n = 781)	Validation cohort MR CLEAN registry (n = 3260)
Age, median (IQR), y	67 (57-76)	72 (61-80)
Sex, No./total No. (%)		
Men	414/781 (53)	1684/3260 (52)
Women	367/781 (47)	1576/3260 (48)
NIHSS score, median (IQR)	17 (14-21)	16 (11-19)
Systolic blood pressure, median (IQR), mm Hg	144 (130-159)	150 (131-165)
Serum glucose level, median (IQR), mmol/L	6.7 (5.9-7.8)	6.8 (5.9-8.1)
Previous stroke, No./total No. (%)	89/777 (11)	544/3233 (17)
Hypertension, No./total No. (%)	426/779 (55)	1676/3194 (52)
Atrial fibrillation, No./total No. (%)	217/640 (34)	770/3217 (24)
Diabetes, No./total No. (%)	120/780 (15)	524/3236 (16)
Prestroke mRS score, No./total No. (%)		
0	501/605 (83)	2160/3188 (68)
1	76/605 (13)	421/31888 (13)
2	19/605 (3.1)	239/3188 (7.5)
≥3	9/605 (1.5)	368/3188 (12)
Occlusion location, No./total No. (%)		
ICA(-T)	198/733 (27)	818/3121 (26)
M1	473/733 (65)	1804/3121 (58)
M2 or other[b]	62/733 (8.5)	499/3121 (16)
ASPECTS scale, median (IQR)	8 (7-9)	9 (7-10)
Collateral score, No./total No. (%)		
0	5/602 (0.8)	187/3053 (6.1)
1	81/602 (14)	1094/3053 (36)
2	268/602 (45)	1181/3053 (39)
3	248/602 (41)	591/3053 (19)
Treatment with IV alteplase, No./total No. (%)	678/781 (87)	2445/3248 (75)
Time from stroke onset to arterial puncture, median (IQR), min	240 (185-299)	195 (150-255)
General anesthesia, No./total No. (%)	227/776 (29)	775/3063 (25)
Duration of the procedure, median (IQR), min	64 (40-91)	59 (38-83)
Outcome measures		
Reperfusion grade (mTICI), No./total No. (%)		
0	54/715 (7.6)	531/3173 (17)
1	19/715 (2.7)	94/3173 (3.0)
2A	98/715 (14)	592/3173 (19)
2B	483/715 (68)	715/3173 (23)[c]
2C	NA	339/3173 (11)[c]
3	61/715 (8.5)	902/3173 (28)

单 + 多 因素分析表--- 建模

Table 2. Main Effects in Derivation Cohort (HERMES, n = 781) Presented as Common Odds Ratios (ORs) With 95% CI[a]

Characteristic	Univariable models, OR (95% CI)	Multivariable model, OR (95% CI)
Age, per y		
<65 y	0.99 (0.97-1.01)	1.00 (0.98-1.02)
≥65 y	0.94 (0.92-0.96)	0.94 (0.91-0.96)
Sex		
Men	1.12 (0.87-1.44)	NA
Women	1 [Reference]	NA
Baseline NIHSS score, per point	0.91 (0.88-0.93)	1.03 (1.00-1.06)
Systolic blood pressure, per 10 mm Hg	0.87 (0.82-0.91)	0.97 (0.91-1.03)
Glucose, per 30 mmol/L		
<120 mmol/L	0.55 (0.39-0.79)	0.95 (0.68-1.34)
≥120 mmol/L	0.89 (0.81-0.98)	0.97 (0.89-1.07)
Treatment with IV alteplase	1.07 (0.72-1.60)	NA
Previous stroke	0.84 (0.57-1.25)	NA
Hypertension	0.76 (0.59-0.98)	0.95 (0.71-1.38)
Atrial fibrillation	0.75 (0.56-0.99)	1.04 (0.76-1.43)
Diabetes	0.47 (0.33-0.67)	0.50 (0.33-0.75)
Prestroke mRS score, per point	0.52 (0.40-0.68)	0.61 (0.46-0.82)
Occlusion location		
ICA(-T)	1.0 [Reference]	1.0 [Reference]
M1	1.58 (1.19-2.11)	1.26 (0.91-1.74)
M2 or other	2.37 (1.42-3.94)	2.04 (1.16-3.60)
Collateral score, per point	1.78 (1.46-2.17)	1.24 (0.93-1.65)
ASPECTS	1.35 (1.18-1.53)	1.00 (0.92-1.10)
Time from stroke onset to arterial puncture, per 30 min	0.95 (0.91-0.99)	0.97 (0.93-1.01)
General anesthesia	0.71 (0.53-0.95)	0.98 (0.70-1.37)
Postprocedural reperfusion grade (mTICI), per point	1.73 (1.48-2.01)	1.20 (1.02-1.41)
NIHSS score at 24 h, per point		
<12 points	0.72 (0.68-0.75)	0.71 (0.68-0.75)
≥12 points	0.85 (0.82-0.89)	0.86 (0.83-0.90)
sICH at 24 h	0.11 (0.05-0.24)	0.29 (0.11-0.79)

（**JAMA Neurology**）Development and Validation of a Postprocedural Model to Predict Outcome After Endovascular Treatment for Ischemic Stroke
https://pubmed.ncbi.nlm.nih.gov/37523199/

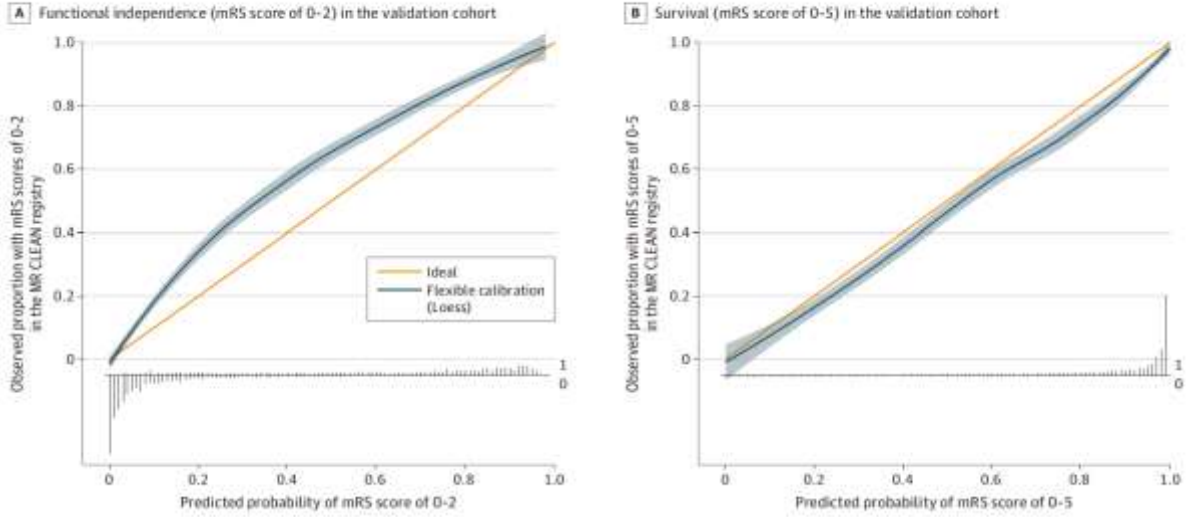
三表一图

模型评估 ——— 表 & 图

Table 3. Performance Measures With 95% CI in Derivation Cohort (N = 781) and Validation Cohort (n = 3260)[a]

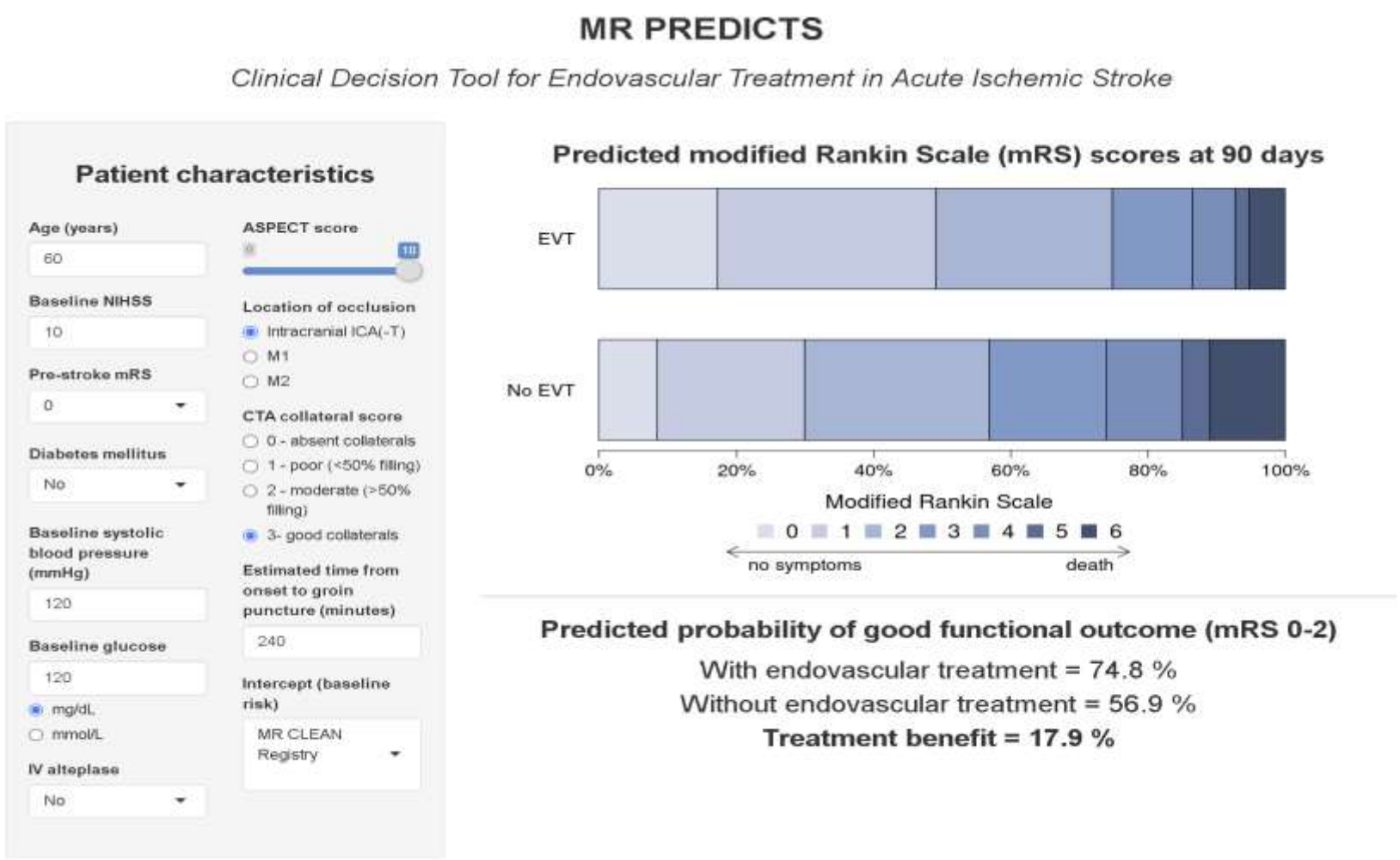
Measure	Ordinal mRS	Functional independence (mRS 0-2)	Survival (mRS 0-5)
Internal validation			
C statistic	0.84 (0.84-0.85)	0.92 (0.91-0.92)	0.87 (0.85-0.88)
External validation			
C statistic	0.84 (0.83 to 0.84)	0.91 (0.90 to 0.92)	0.89 (0.88 to 0.90)
Calibration intercept	NA	0.61 (0.50 to 0.74)	−0.25 (−0.37 to −0.13)
Calibration slope	NA	0.98 (0.92 to 1.05)	0.86 (0.80 to 0.94)

Figure 1. Calibration Plots



（**JAMA Neurology**）Development and Validation of a Postprocedural Model to Predict Outcome After Endovascular Treatment for Ischemic Stroke
https://pubmed.ncbi.nlm.nih.gov/37523199/

Model – shiny app --- 增加临床实用性



https://mdmtest.shinyapps.io/RRRR_2/

Development and Validation of a Novel Acute Myeloid Leukemia–Composite Model to Estimate Risks of Mortality

三表一图

基线表 + 单 + 多 因素分析表--- 建模

eTable 4. Patient Characteristics at Diagnosis of Acute Myeloid Leukemia for All Patients as well as and per Institution

eTable 5. Distribution and Classification of HCT-CI and Other Comorbidities

eTable 6. Distribution and Classification of Other Covariates

eTable 7. Univariate Analysis of Associations between Individual Comorbidities and Other Covariates with Post-Initial Therapy Mortality (288 Deaths Over 1 Year)

Table 1. Multivariate Analysis of Associations Between Individual Comorbidities and Other Covariates With Post-Initial Therapy Mortality (288 Deaths Over 1 Year): Hazard Ratios (HRs) and Corresponding Scores for the AML-CI

Comorbidities	HR (95% CI)	Assigned Score for AML-CI	*P* Value
Cardiac	1.6 (1.2-2.3)	1	.05
Diabetes	1.1 (0.9-2.8)	0	.71
Hepatic	1.3 (1.0-1.8)	1	.04
Infection	1.3 (0.9-1.8)	1	.12
Peptic ulcer	1.6 (0.9-2.7)	1	.11
Renal			
Mild	1.1 (0.7-1.6)	0	.71
Moderate/severe	1.0 (0.6-1.5)	0	.84
Prior malignant neoplasm	1.2 (0.9-1.6)	0	.20
Heart valve disease	1.5 (0.9-2.8)	1	.16
Hyperlipidemia	0.9 (0.7-1.2)	0	.58
Hypertension	1.1 (0.8-1.4)	0	.66
Albumin level, g/dL			
<4.0-3.5	1.2 (0.8-1.6)	0	.43
<3.5-3.0	1.3 (0.9-1.8)	1	.20
<3.0	1.6 (1.0-2.4)		.04
Platelet count, $\times 10^3$ µL			
<100-50	1.1 (0.8-1.5)	0	.75
<50-20	1.0 (0.8-1.5)	0	.78
<20	1.3 (0.9-2.0)	1	.15
LDH level, U/L			
>200-500	1.7 (1.2-2.5)	1	.004
>500-1000	1.8 (1.1-2.7)	1	.01
>1000	2.2 (1.4-3.5)	2	.001
Sex			
Male	1.1 (0.8-1.4)	0	.68
Female	1 [Reference]	0	NA

(2017 JAMA Oncology)Development and Validation of a Novel Acute Myeloid Leukemia–Composite Model to Estimate Risks of Mortality

模型评估 ——— 表

Table 2. Comparisons of the Performance of Risk Factors and Indices in Validation Set of 367 (148 Deaths)

Risk Factor	Components	C Statistic[a] (SD[d]) for 1-y Mortality		True AUC[b] (SD) for 1-y Mortality		True AUC[c] (SD) for 8-wk Mortality	
		No.	(SD)	No.	(SD)	No.	(SD)
AML-CI	Cardiac, hepatic dysfunction, infection, peptic ulcer, heart valve disease, albumin level <3.5 g/dL, platelet count <20 × 10^3 cells/μL, LDH level 200-1000 U/L, LDH level >1000 U/L	314	0.596 (0.019)	297	0.606 (0.039)	305	0.659 (0.043)
Original HCT-CI	17 covariates as previously described[10,18]	352	0.649 (0.025)	326	0.674 (0.028)	339	0.684 (0.042)
Augmented HCT-CI	Original HCT-CI + albumin level <3.5 g/dL, platelet count <20 × 10^3 cells/μL, LDH level 200-1000 U/L, and LDH level >1000 U/L	305	0.664 (0.023)	289	0.687 (0.035)	296	0.721 (0.046)
Age (groups)	0-49 (score 0) vs 50-59 (score 1) vs ≥60 y (score 2)	367	0.640 (0.020)	340	0.682 (0.029)	354	0.640 (0.040)
Cytogenetic/molecular risks (groups)	ELN Favorable (score 0) vs intermediate (score 1) vs adverse (score 2)	350	0.614 (0.020)	324	0.654 (0.023)	337	0.597 (0.042)
AML-CM	Augmented HCT-CI + age + cytogenetic/ molecular risks	292	0.719 (0.022)	277	0.758 (0.030)	283	0.776 (0.035)
KPS (groups)	100%-85%vs80%-75%vs≤70%-20%	291	0.619 (0.027)	266	0.646 (0.035)	279	0.676 (0.048)

(2017 JAMA Oncology)Development and Validation of a Novel Acute Myeloid Leukemia–Composite Model to Estimate Risks of Mortality

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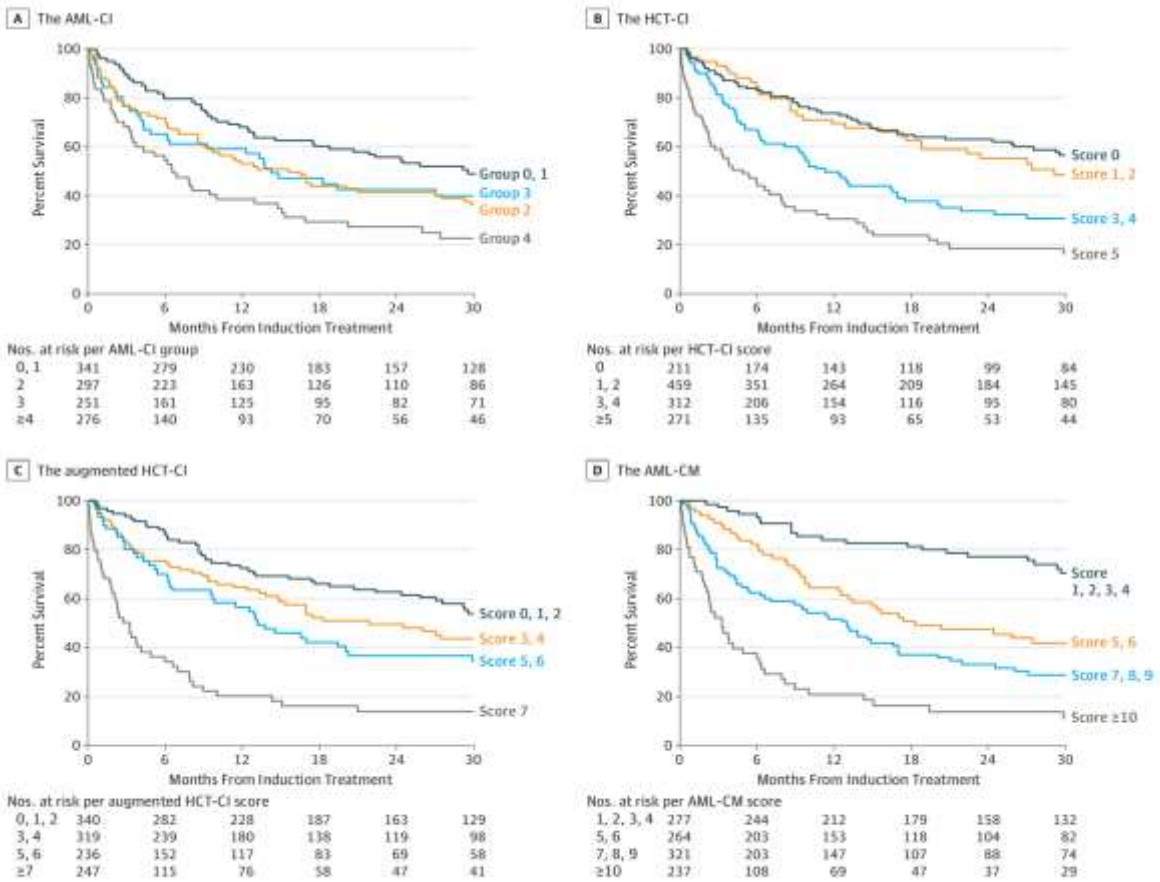
Figure. Kaplan-Meier Estimates of Survival



Kaplan Meier Estimates of Survival. A, Estimated survival stratified according to the acute myeloid leukemia-comorbidity index (AML-CI). B, Estimated survival stratified according to the hematopoietic cell transplantation-comorbidity index (HCT-CI). C, Estimated survival stratified according to the augmented HCT-CI. D, Estimated survival stratified according to the AML-composite model (AML-CM).

(2017 JAMA Oncology)Development and Validation of a Novel Acute Myeloid Leukemia–Composite Model to Estimate Risks of Mortality

1.2 RCT

JAMA Oncology

RCT: Allogeneic HCT vs Standard Consolidation Chemotherapy in Patients With Intermediate-Risk Acute Myeloid Leukemia

POPULATION

81 Men, 62 Women

Adults aged 18-60 y with acute myeloid leukemia in first complete remission with an available donor

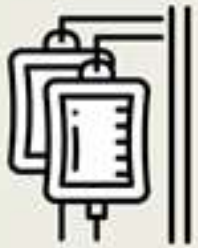
Mean age: 51 y

SETTINGS / LOCATIONS

16 Hospitals in Germany

INTERVENTION

143 Patients randomized



67 Chemo-consolidation
1 To 3 cycles of high-dose cytarabine and transplantation in case of relapse only

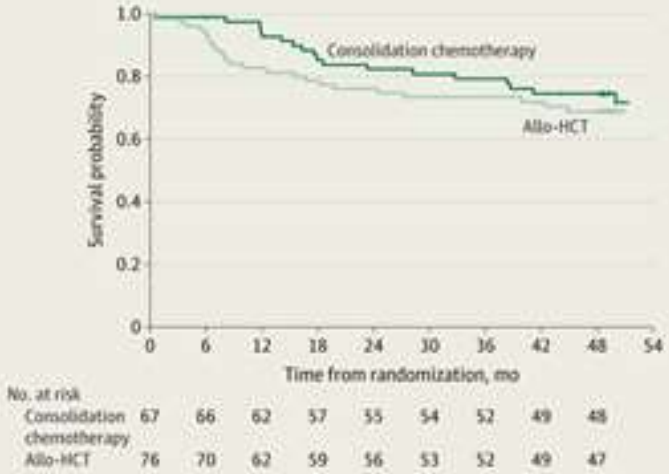
76 Allogeneic HCT
Direct allogeneic hematopoietic cell transplantation (HCT) as consolidation therapy

PRIMARY OUTCOME

The primary end point was overall survival (OS), calculated from the date of randomization until date of death or censored on date of last follow-up, if no death occurred

FINDINGS

There was no significant difference in OS between the allogeneic HCT group and chemo-consolidation group



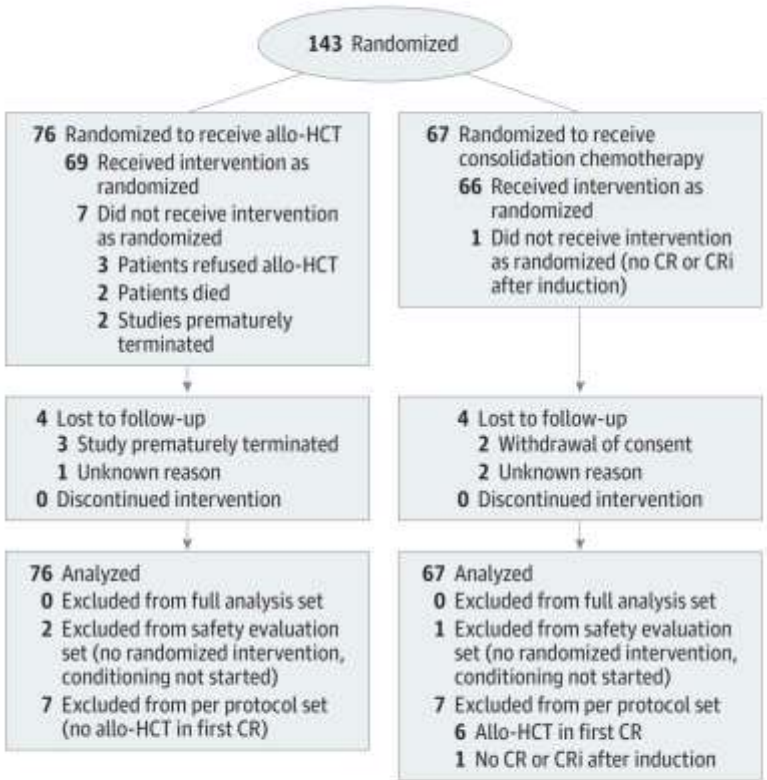
Overall survival at 2 y:
Chemo-consolidation: 84% (95% CI, 73%-92%)
Allogenic HCT: 74% (95% CI, 62%-83%)
P = .22

Bornhäuser M, Schliemann C, Schetelig J, et al. Allogeneic hematopoietic cell transplantation vs standard consolidation chemotherapy in patients with acute myeloid leukemia with intermediate risk: a randomized clinical trial. *JAMA Oncol*. Published online February 9, 2023. doi:10.1001/jamaoncol.2022.7605

详细设计方案： coi220096supp1_prod_1681755656.40592.pdf (jamanetwork.com)

Allogeneic Hematopoietic Cell Transplantation vs Standard Consolidation Chemotherapy in Patients With Intermediate-Risk Acute Myeloid Leukemia A Randomized Clinical Tria

Figure 1. CONSORT Flow Diagram



Allo-HCT indicates allogeneic hematopoietic stem cell transplant; CR, complete remission; and CRi, complete remission with incomplete blood cell count recovery.

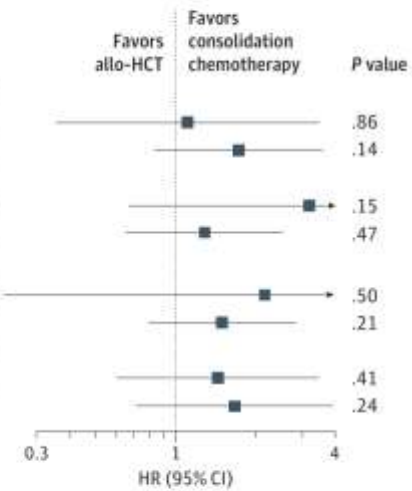
Table. Patient and Treatment Characteristics[a]

Characteristic	Allo-HCT (n = 76)	Consolidation therapy (n = 67)
Age, median (range), y	50.5 (19.0-60.0)	51.0 (24.0-60.0)
Age group, y		
18-40	16 (21)	11 (16)
41-60	60 (79)	56 (84)
Sex		
Female	31 (41)	31 (46)
Male	45 (59)	36 (54)
Cytogenetics		
Normal karyotype	54 (71)	55 (82)
Other intermediate abnormalities	16 (29)	12 (18)
CEBPA status		
Biallelic variant	4 (5)	1 (1)
NPM1 status/*FLT3*-ITD status		
Variant/variant	12 (17)	13 (20)
Variant/wild type	17 (25)	14 (22)
Wild type/variant	5 (7)	3 (5)
Wild type/wild type	35 (51)	34 (53)
Missing	7 (9)	3 (4)
FLT3-ITD ratio, median (range)	0.57 (0.36-1.00)	0.54 (0.22-0.63)
ELN 2017 category		
Favorable	24 (32)	19 (28)
Intermediate	50 (66)	46 (69)
Adverse	2 (2)	2 (3)
Available donor		
Matched sibling	18 (24)	23 (34)
Matched unrelated (10/10)	51 (67)	35 (52)
1 Allele mismatched unrelated (9/10)	7 (9)	9 (13)

Figure 3. Analyses of Overall and Disease-Free Survival According to Prognostic Baseline Factors

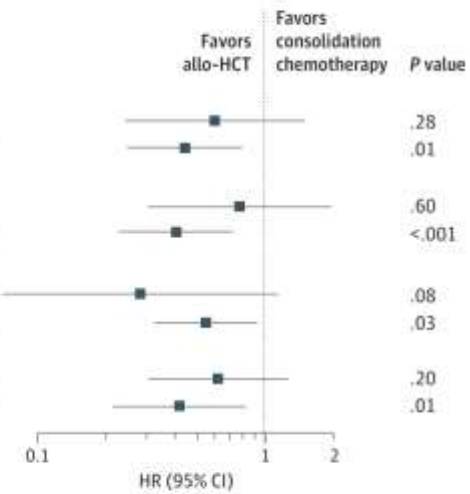
A Overall survival

	HR (95% CI)	P value
ELN		
Favorable	1.13 (0.35-3.51)	.86
Nonfavorable	1.74 (0.83-3.62)	.14
HLA		
Identical sibling donor	3.21 (0.67-15.47)	.15
Compatible UD	1.29 (0.65-2.56)	.47
Age, y		
≤40	2.17 (0.23-20.91)	.50
>40	1.50 (0.79-2.86)	.21
Sex		
Female	1.45 (0.60-3.50)	.41
Male	1.67 (0.71-3.94)	.24



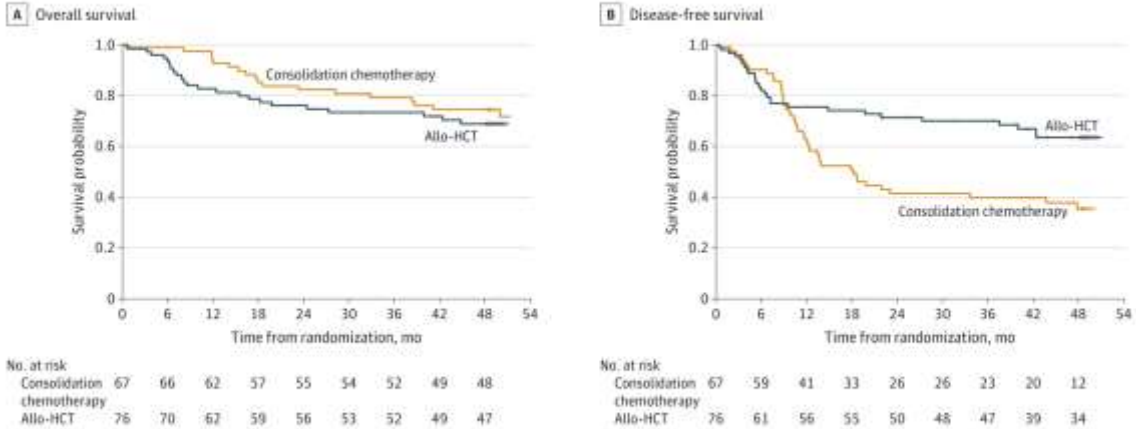
B Disease-free survival

	HR (95% CI)	P value
ELN		
Favorable	0.61 (0.24-1.51)	.28
Nonfavorable	0.45 (0.25-0.80)	.01
HLA		
Identical sibling donor	0.78 (0.31-1.97)	.60
Compatible UD	0.41 (0.23-0.74)	<.001
Age, y		
≤40	0.29 (0.07-1.16)	.08
>40	0.56 (0.33-0.93)	.03
Sex		
Female	0.63 (0.31-1.27)	.20
Male	0.43 (0.22-0.84)	.01



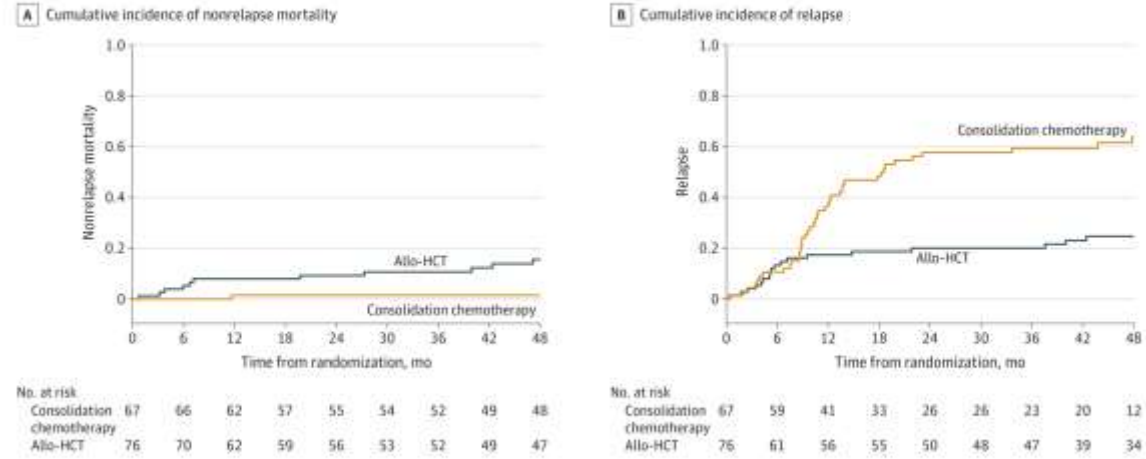
Hazard ratios (HRs) for age of 40 years or younger could not be estimated because of the small number of events. Allo-HCT indicates allogeneic hematopoietic stem cell transplant; ELN, European Leukemia Network; HLA, human leukocyte antigen; UD, unrelated donor.

Figure 2. Kaplan-Meier Estimates of Overall and Disease-Free Survival According to the Intention-to-Treat Analysis



Allo-HCT indicates allogeneic hematopoietic stem cell transplant.

Figure 4. Cumulative Incidence of Nonrelapse Mortality and Incidence of Relapse



Allo-HCT indicates allogeneic hematopoietic cell transplant.

1.3 AI for life & Medical

FlowChart and Table 1

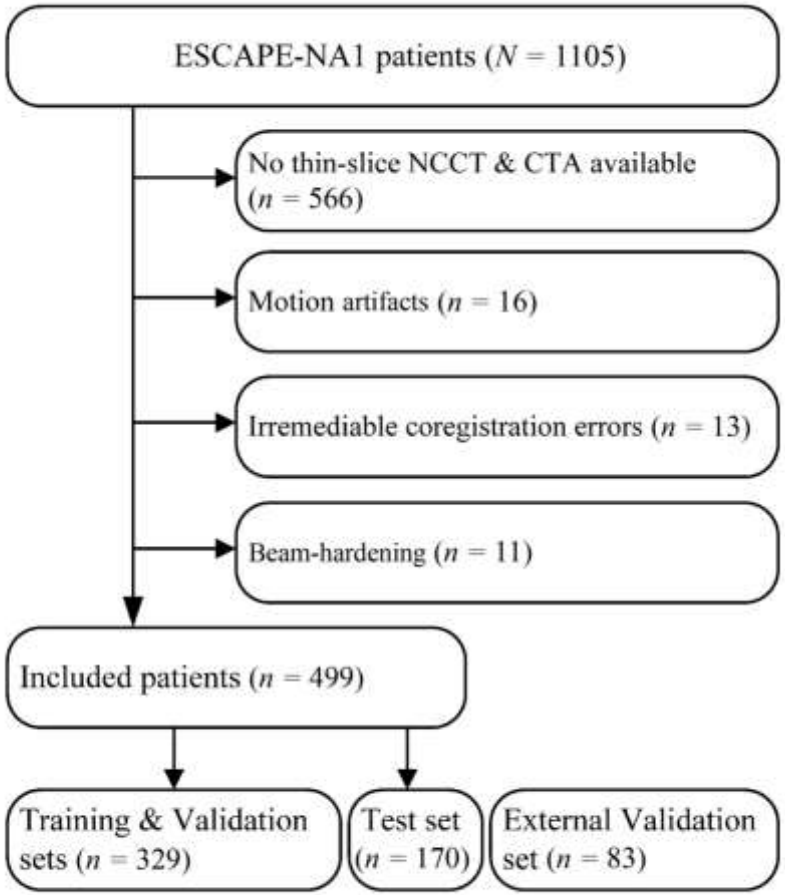


FIG 1. Flowchart of patient inclusion.

Table 1: Patient characteristics in the derivation data and in the internal and external test data[a]

Characteristic	Derivation Set (*n* = 329)	Internal Test Set (*n* = 170)	External Test Set (*n* = 83)
Age (yr)[b]	69 (59–78)	68 (59–79)	71 (63–79)
Male	173 (52.6)	89 (52.4)	43 (51.8)
Race			
White	261 (79.3)	142 (83.5)	NA
Asian	26 (7.9)	10 (5.9)	
African American	35 (10.6)	14 (8.2)	
Other	7 (2.1)	4 (2.4)	
Onset-to-CT time[b]	160 (82–268)	154 (79–284)	120 (89–184)
Baseline NIHSS score[b]	17 (12–21)	16 (13–20)	9 (5–15)
ASPECTS[b]	8 (7–9)	8 (7–9)	10 (8–10)
Hypertension	222 (67.5)	127 (74.7)	49 (59.0)
Hyperlipidemia	140 (42.6)	79 (46.5)	NA
Diabetes	70 (21.3)	36 (21.2)	9 (10.8)
IV alteplase	193 (58.7)	99 (58.2)	66 (79.5)
IV nerinetide	155 (47.1)	87 (51.2)	0
Occlusion site			
ICA	71 (21.6)	39 (23.0)	8 (9.6)
M1, MCA	248 (75.4)	125 (73.5)	26 (31.3)
M2, MCA	10 (3.0)	6 (3.5)	10 (12.1)
M3/M4, MCA	0	0	13 (15.7)
ACA (A2/A3)	0	0	3 (3.6)
PCA (P2)	0	0	2 (2.4)
No occlusion	0	0	21 (25.3)

Note:—ACA indicates anterior cerebral artery; PCA, posterior cerebral artery; NA, not applicable.
[a] Except where indicated, data are number of patients, with percentages in parentheses.
[b] Data are the median with the IQR in parentheses.

Automated Segmentation of Intracranial Thrombus on NCCT and CTA in Patients with Acute Ischemic Stroke Using a Coarse-to-Fine Deep Learning Model

Baseline and Algorithms

Table 1. Baseline Characteristics

Characteristic*	Included patients with stroke
Age, y	78.8 (10.0)
Sex	
Male	183 (47.7)
Female	201 (52.3)
Body mass index, kg/m^2	25.1 (4.3)
TOAST classification	
Large artery artherosclerosis	22 (5.7)
Cardioembolism	106 (27.6)
Small artery occlusion	85 (22.1)
Other determined	2 (0.6)
Undetermined	169 (44.0)
Barthel index	11.8 (7.7)

*Data are presented as number (%) or mean (SD). TOAST indicates Trial of ORG 10172 in Acute Stroke Treatment.

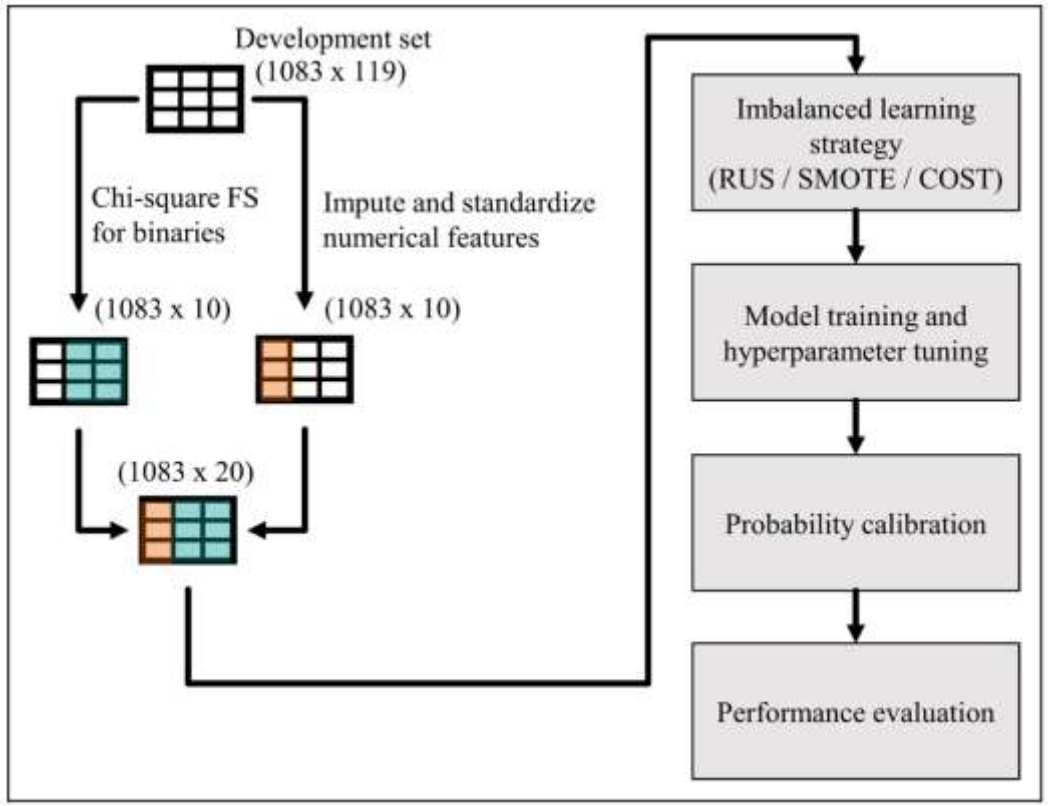
Table 2. Results of Applied Machine Learning Algorithms in Combination With Different Strategies for Treating Class Imbalance

Learning algorithm*	RUS	SMOTE	COST	ADBLA
Most-frequent dummy	0.50 (0.00)	0.50 (0.00)	...	...
Logistic regression	0.58 (0.15)	0.66 (0.09)	0.56 (0.11)	...
Naïve Bayes	0.56 (0.09)	0.63 (0.08)	...	...
Linear SVM	0.59 (0.13)	0.70 (0.07)	0.53 (0.09)	...
Ridge classifier	0.59 (0.14)	0.68 (0.08)	0.64 (0.12)	...
Linear discriminant analysis	0.60 (0.11)	0.67 (0.09)	...	...
Decision tree	0.52 (0.05)	0.59 (0.05)	0.58 (0.05)	...
k-nearest neighbors	0.55 (0.09)	0.58 (0.06)	...	...
Nonlinear SVM	0.57 (0.12)	0.56 (0.06)	0.59 (0.11)	...
Multi-layer perceptron	0.56 (0.08)	0.61 (0.03)	...	...
Gaussian process classifier	0.51 (0.04)	0.52 (0.10)	...	...
Random forest	0.57 (0.08)	0.65 (0.09)	0.64 (0.08)	...
Extra trees	0.60 (0.11)	0.64 (0.09)	0.64 (0.07)	...
AdaBoost	0.54 (0.04)	0.65 (0.07)	...	...
XGBoost	0.50 (0.06)	0.61 (0.05)	0.59 (0.07)	...
Stacking meta-classifier	0.58 (0.13)	0.61 (0.05)	...	...
Voting classifier	0.58 (0.09)	0.64 (0.06)	...	...
SGD classifier	0.55 (0.11)	0.67 (0.04)	0.54 (0.10)	...
Elliptic envelope	...	...	...	0.55 (0.06)
One-class SVM	...	...	...	0.49 (0.11)
Isolation forest	...	...	...	0.57 (0.05)
Balanced bagging	...	...	...	0.57 (0.05)
Balanced random forest	...	...	...	0.62 (0.07)
Easy ensemble	...	...	...	0.64 (0.08)
RUSBoost	...	...	...	0.58 (0.07)

ADBLA indicates Anomaly Detection and Balanced Learning Algorithms; AUROC, area under the receiver operating characteristic curve; COST, cost-sensitive learning; RUS, random undersampling; SGD, stochastic gradient descent; SMOTE, synthetic minority oversampling technique; and SVM, support vector machine.

Prediction of Recurrent Ischemic Stroke Using Registry Data and Machine Learning Methods: The Erlangen Stroke Registry

FlowChart and Main result



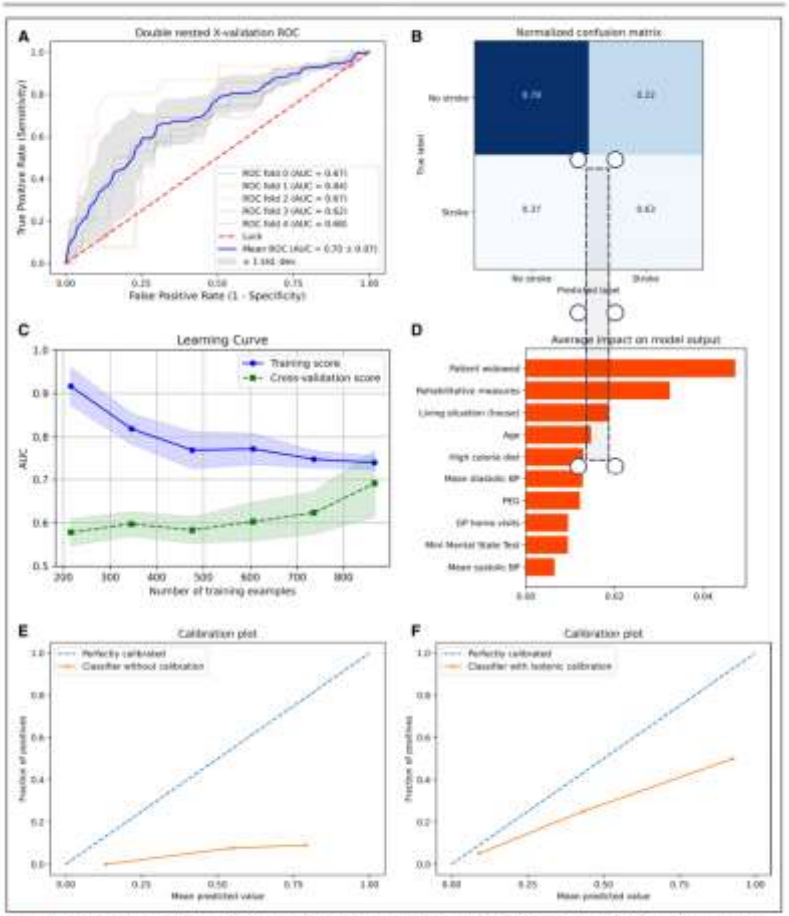
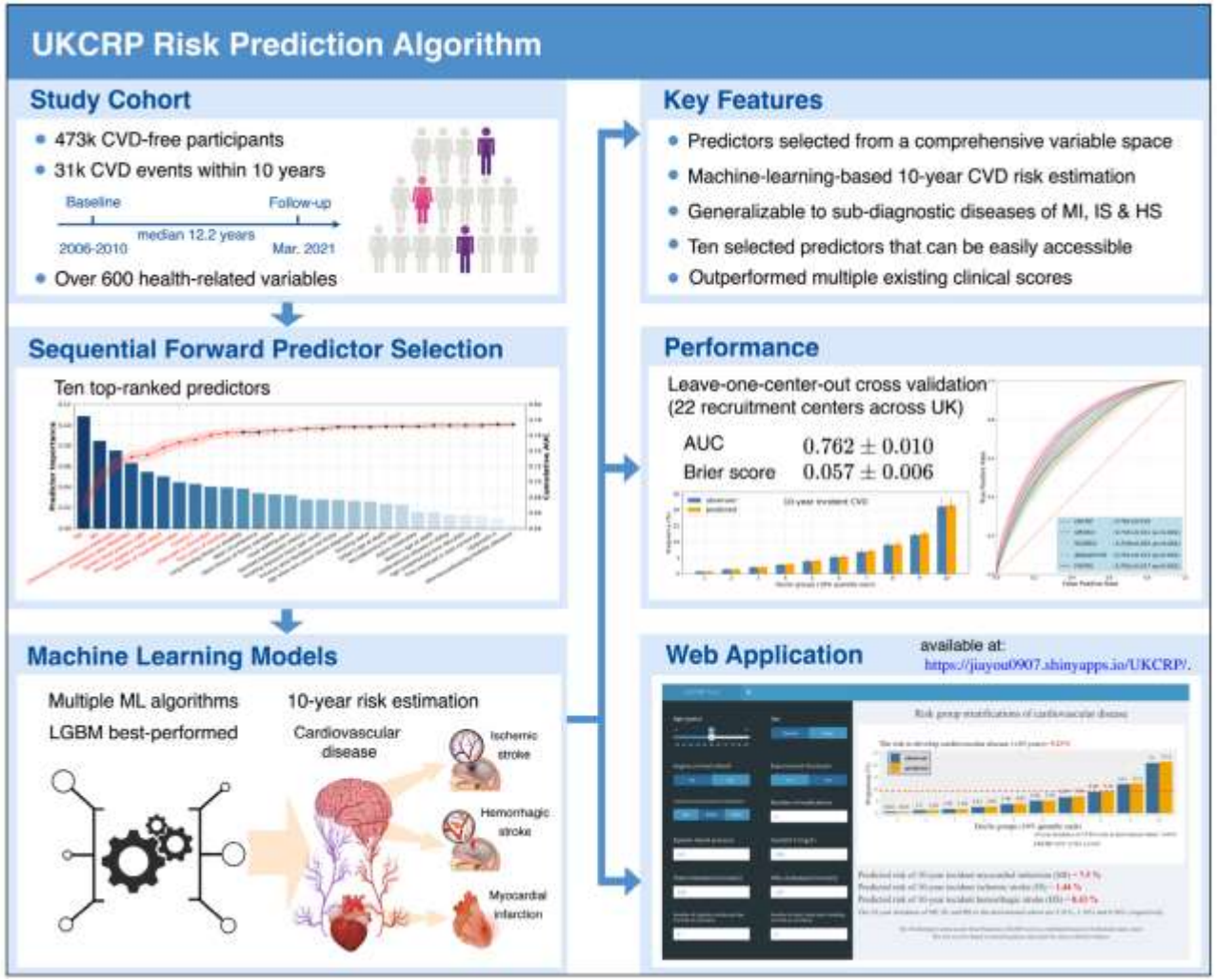


Figure 2. Model diagnostics for the linear support vector machine algorithm combined with synthetic minority oversampling technique (SMOTE) resampling technique.

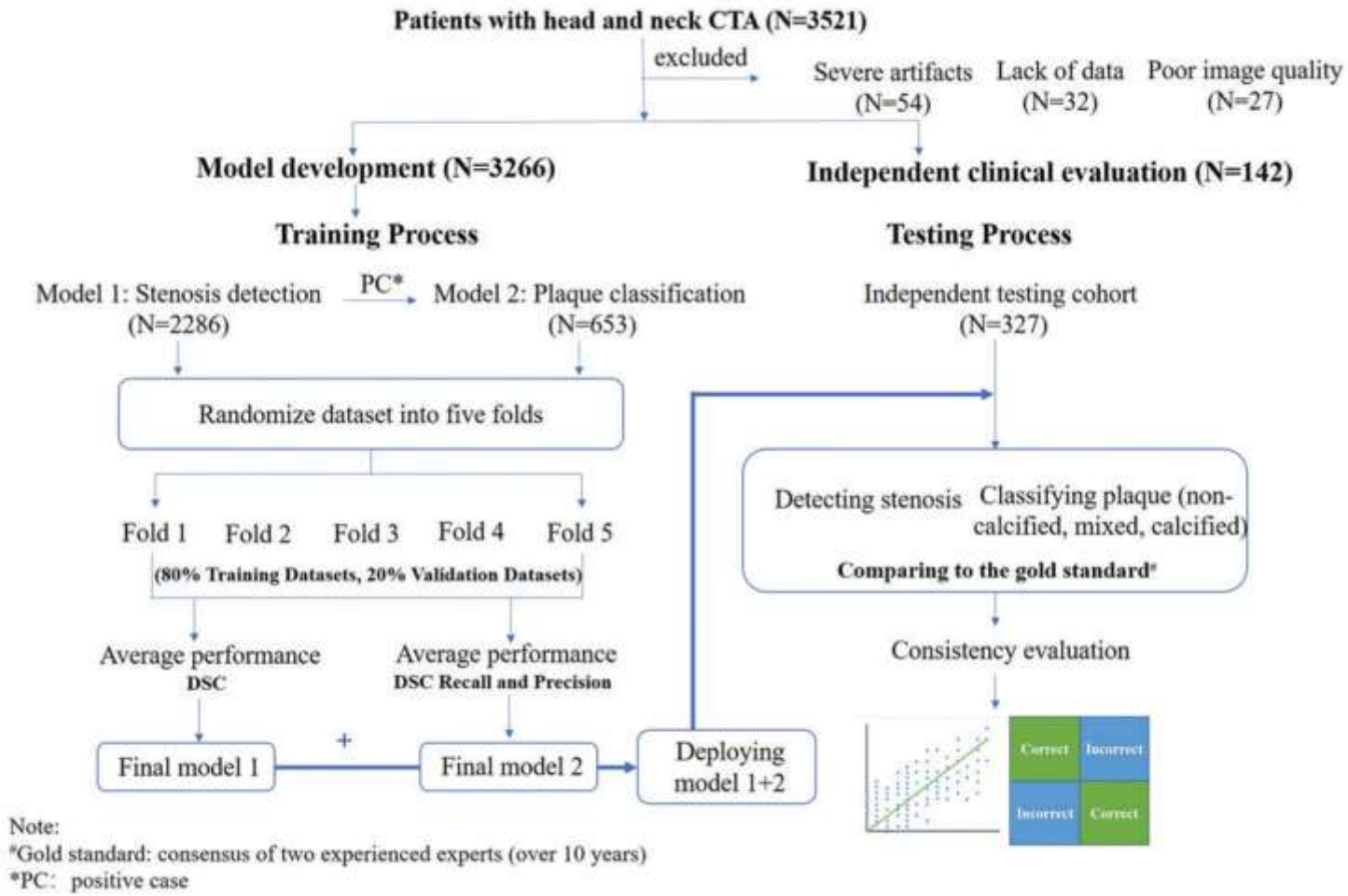
Prediction of Recurrent Ischemic Stroke Using Registry Data and Machine Learning Methods: The Erlangen Stroke Registry

Design



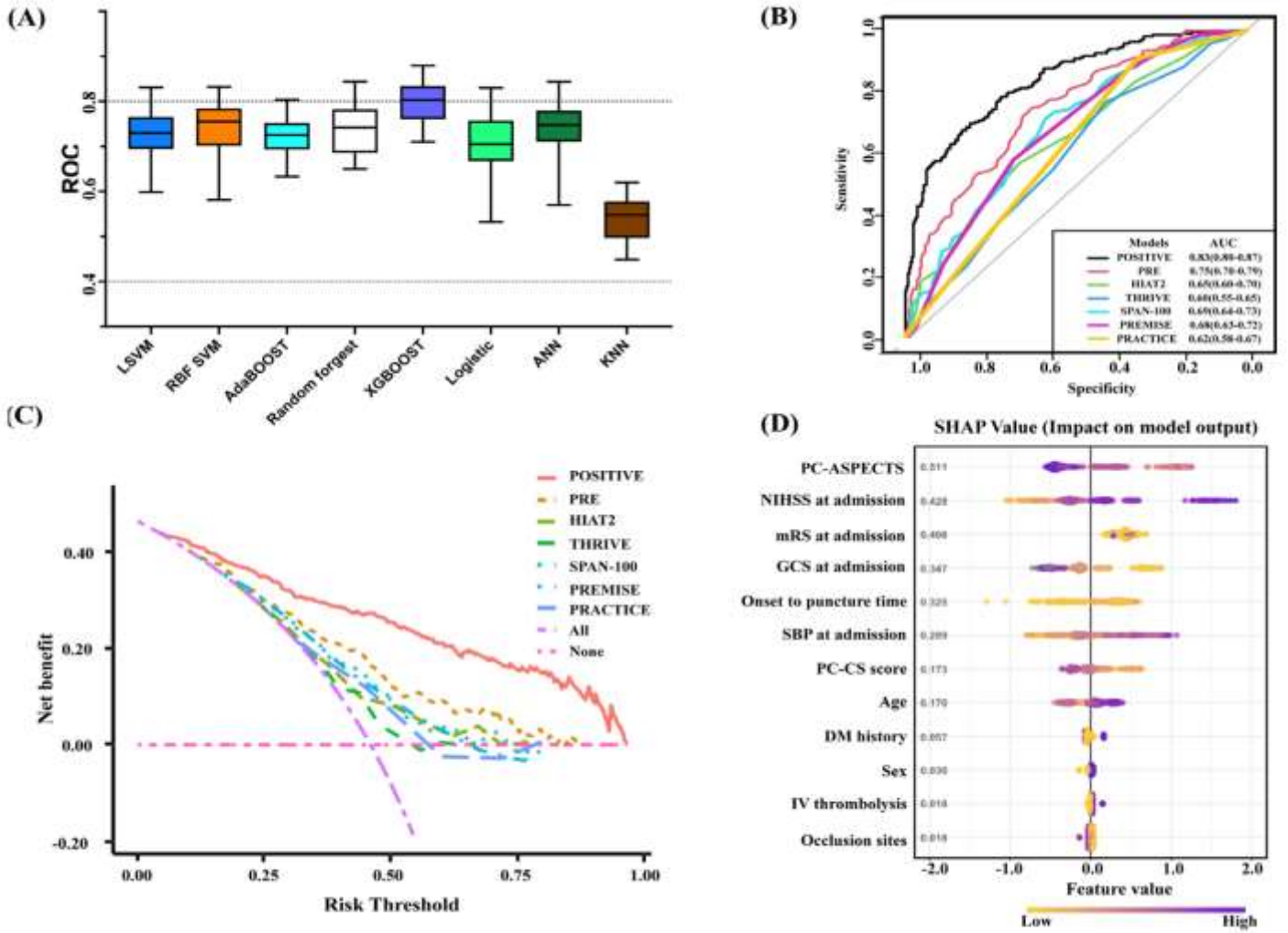
Development of machine learning based models to predict 10-year risk of cardiovascular disease: a prospective cohort study

Design



Deep Learning for Head and Neck CT Angiography: Stenosis and Plaque Classification

Design



Development and validation of machine learning_based model for mortality prediction in patients with acute basilar artery occlusion receiving endovascular treatment: multicentric cohort analysis

1.4 单模态 到 多模态

从单模态 ⟶ 多模态

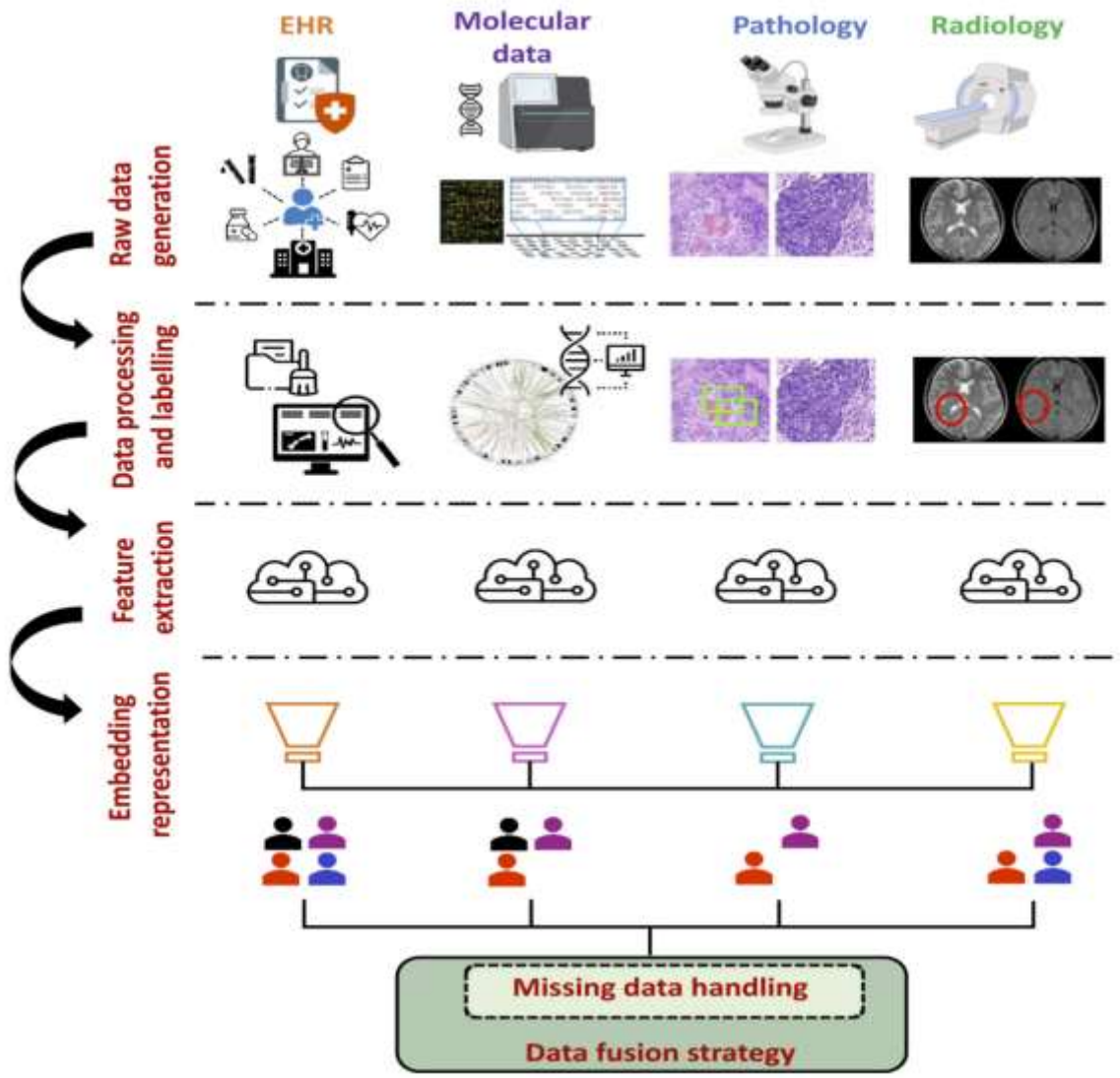


Fig. 1: Generation and processing of routinely collected biomedical modalities in oncology. Prior to data fusion, different steps are needed to go from the raw data to workable data representations for each modality, e.g. EHRs, molecular data and medical images

Fig. 2: Overview of different fusion strategies for multimodal data. a) Raw data is processed into workable formats. b) For each modality features are extracted using dedicated encoder algorithms. c) Early fusion. d) Intermediate fusion. e) Late fusion.

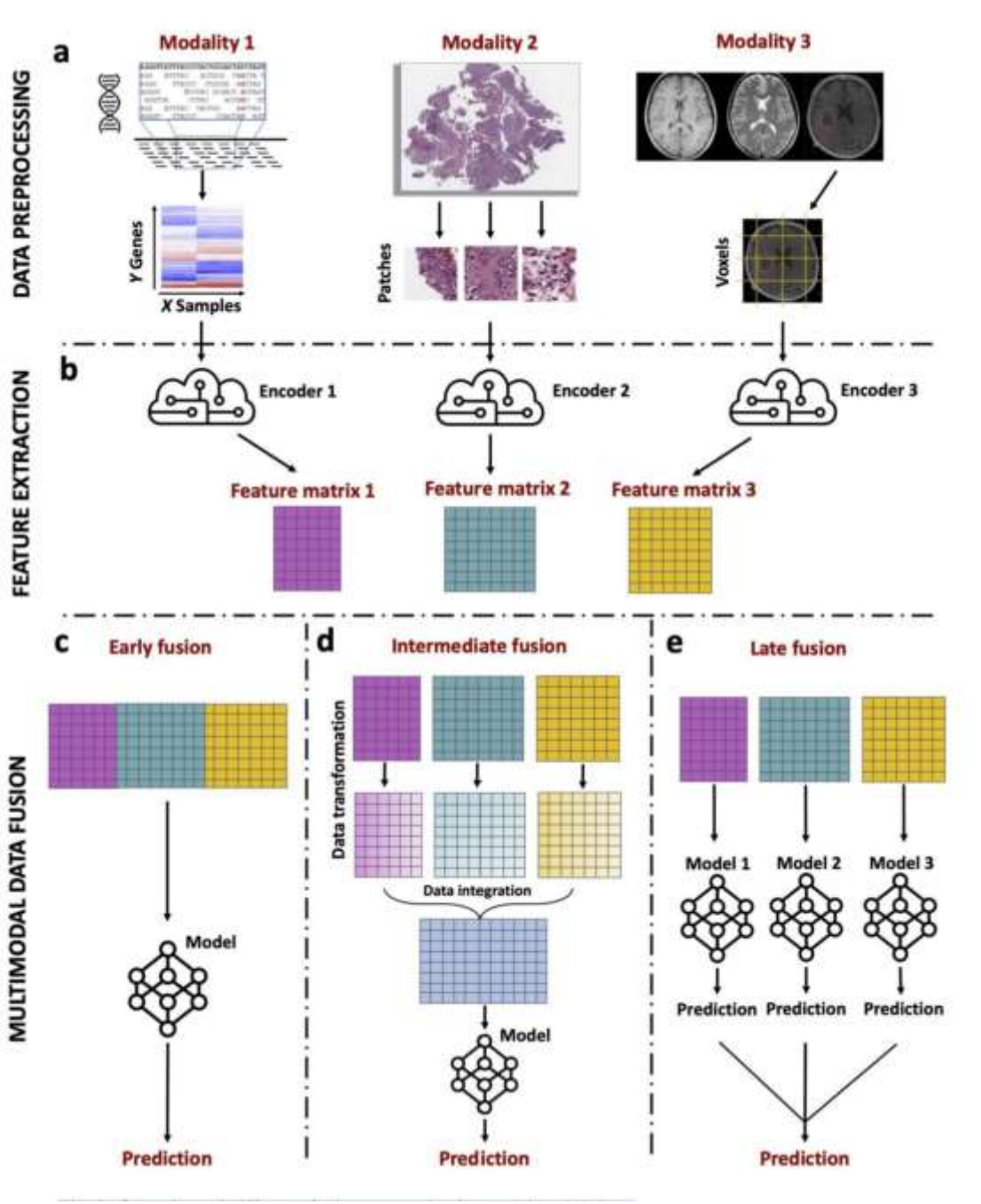
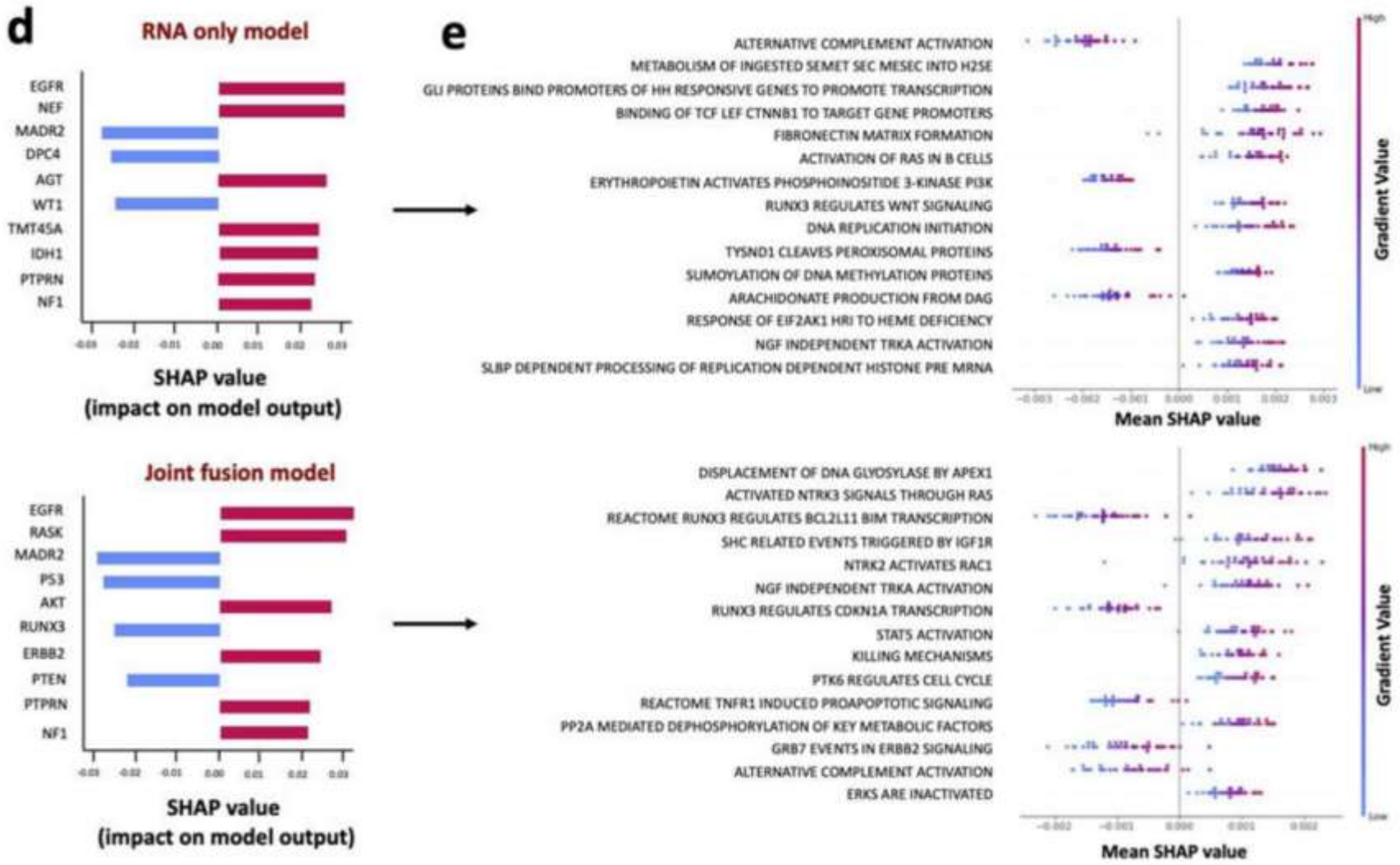
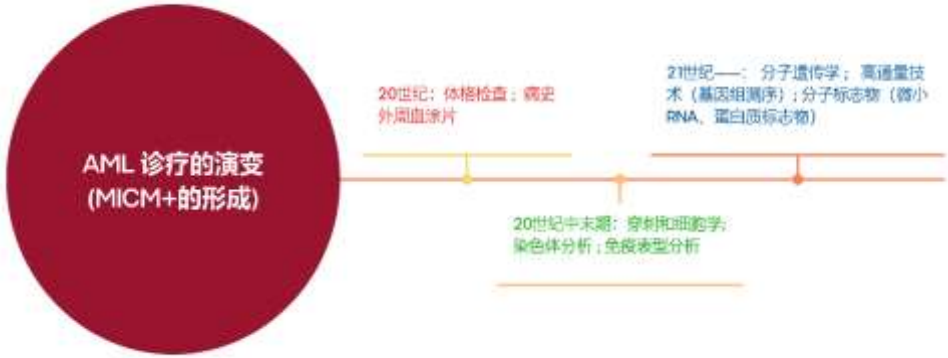
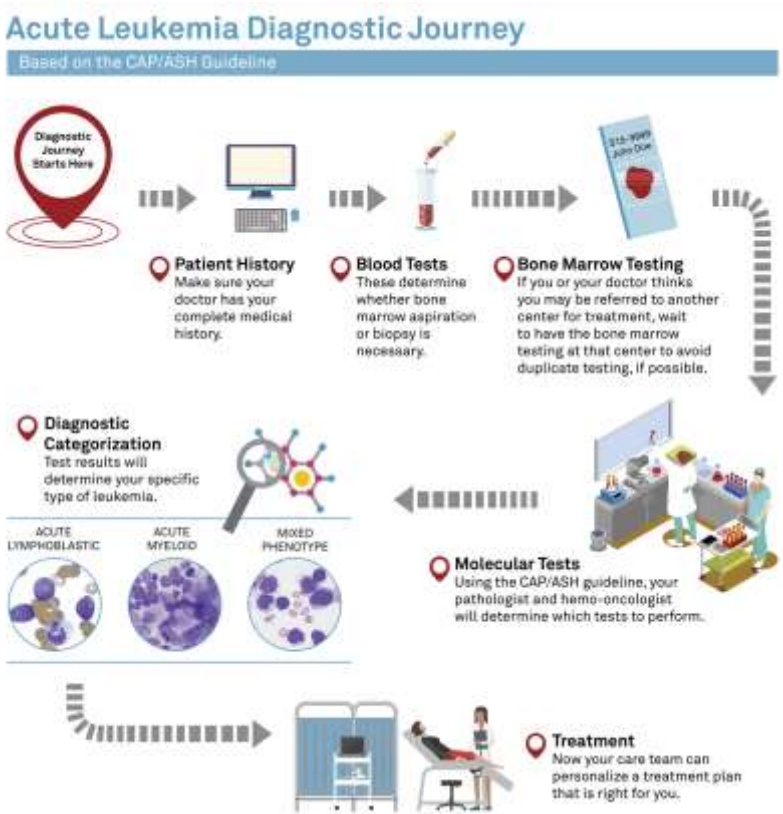


Fig. 3: Examples of model interpretability methods for histopathology and gene expression. Histopathology:
d) Examples of SHAP visualisation152 of hypothetical gene importance according to unimodal model (top) and joint multimodal model (bottom) for cancer survival prediction.
e) Example of pathway importance visualisation based on the respective gene SHAP-values in unimodal (top) versus joint multimodal (bottom) models with respect to cancer survival prediction



AML 的诊断评估标准在时间尺度上的演变





Same day*	**Morphology** • Bone marrow or peripheral blood blast count of ≥20% is required to establish diagnosis of acute myeloid leukaemia • If t(8;21), inv(16)/t(16;16), or t(15;17) present, acute myeloid leukaemia diagnosis is established even if less than 20% blasts • Presence of Auer rods is diagnostic of acute myeloid leukaemia, if ≥20% blasts • Presence of myeloperoxidase in >3% of blasts is diagnostic of acute myeloid leukaemia, if ≥20% blasts • Myeloblasts, monoblasts, promonocytes, and megakaryoblasts are included in blast count
1–3 days*	**Immunophenotype** • Precursors and progenitors: CD117, CD34, and HLA-DR (CD38, CD133, and CD123 also useful) • Myeloid lineage: CD33, CD13, and cytoplasmic myeloperoxidase • Myeloid maturation markers: CD11b, CD15, CD64, CD14, and CD65 • Monocytic markers: CD4, CD14, CD36, and CD64 • Erythroid markers: CD71, CD235a (glycophorin A), and CD36 • Megakaryocytic markers: CD36, CD41 (glycoprotein IIb or IIIa), and CD61 (glycoprotein IIIa)
5–7 days*	**Cytogenetic analysis** • Fluorescence in-situ hybridisation might be helpful if metaphases are not obtained and for rapid identification of therapeutic targets such as PML::*RARA* • Cytogenetic information needed to define acute myeloid leukaemia subtypes by WHO classification and for prognosis: • Acute myeloid leukaemia with recurrent genetic abnormalities including t(8;21), inv(16)/t(16;16), t(15;17), t(9;11), inv(3)/t(3;3), t(6;9), t(1;22), t(9;22) • Acute myeloid leukaemia with myelodysplasia-related change (eg, -5/5q-, -7/7q-, complex structural and numeric changes)
3–5 days*	**Molecular genetics** • PCR or next generation sequencing analysis required to define prognosis and guide therapeutic interventions • *NPM1* and *bzip CEBPA* mutations might define favourable risk • FLT3–ITD and FLT3–TKD mutations may guide therapeutic choices (and prognostic data in case of ITD) • *TP53*, *RUNX1*, and *ASXL1* mutations define poor risk • *IDH1* and *IDH2* mutations might guide therapeutic choices • RNA next generation sequencing can screen for fusion transcripts (eg, *RUNX1*::*RUNX1T1*, *CBFB*::*MYH11*, and *PML*::*RARA*) • Familial acute myeloid leukaemia (eg, *RUNX1*, *CEBPA*, *TP53*, *BRCA1*, *BRCA2*, *GATA2*, *DDX41*, *TERC*, and *TERT*)

Figure 1: **Recommended acute myeloid leukaemia diagnostic evaluation**
*Recommended timelines.

https://www.lls.org/leukemia/acute-myeloid-leukemia/diagnosis

Not only Aggressive T-cell lymphomas: 2024: Updates on diagnosis, riskstratification, and management

Panel 2: 2022 European LeukemiaNet risk categorisation

Favourable
- t(8;21)(q22;q22.1)/*RUNX1::RUNX1T1*
- inv(16)(p13.1q22)or t(16;16)(p13.1;q22)/*CBFB::MYH11*
- Mutated *NPM1* without *FLT3-ITD**
- Bzip region in-frame mutated *CEBPA*

Intermediate
- Mutated *NPM1* with *FLT3-ITD**
- Wild-type *NPM1* with *FLT3-ITD*
- t(9;11)(p21.3;q23.3)/*MLLT3::KMT2A*
- All other cytogenetic and molecular abnormalities not classified as favourable or adverse

Adverse
- t(6;9)(p23;q34.1)/*DEK::NUP214*
- t(v;11q23.3)/*KMT2A*-rearranged
- t(9;22)(q34.1;q11.2)/*BCR::ABL1*
- t(8;16)(p11;p13)/*KAT6A::CREBBP*
- inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2)/*GATA2,MECOM(EVI1)*
- t(3q26.2;v)/*MECOM(EVI1)*-rearranged
- -5 or del(5q); -7; -17/abn(17p)
- Complex karyotype, monosomal karyotype
- Mutated *ASXL1*, *BCOR*, *EZH2*, *RUNX1*, *SF3B1*, *SRSF2*, *STAG2*, *U2AF1*, or *ZRSR2* (these mutations should not be used as adverse prognostic markers if they occur with favourable-risk acute myeloid leukaemia subtypes)
- Mutated *TP53*

* Acute myeloid leukaemia with NPM1 mutation and adverse risk cytogenetic abnormalities are categorised as adverse-risk

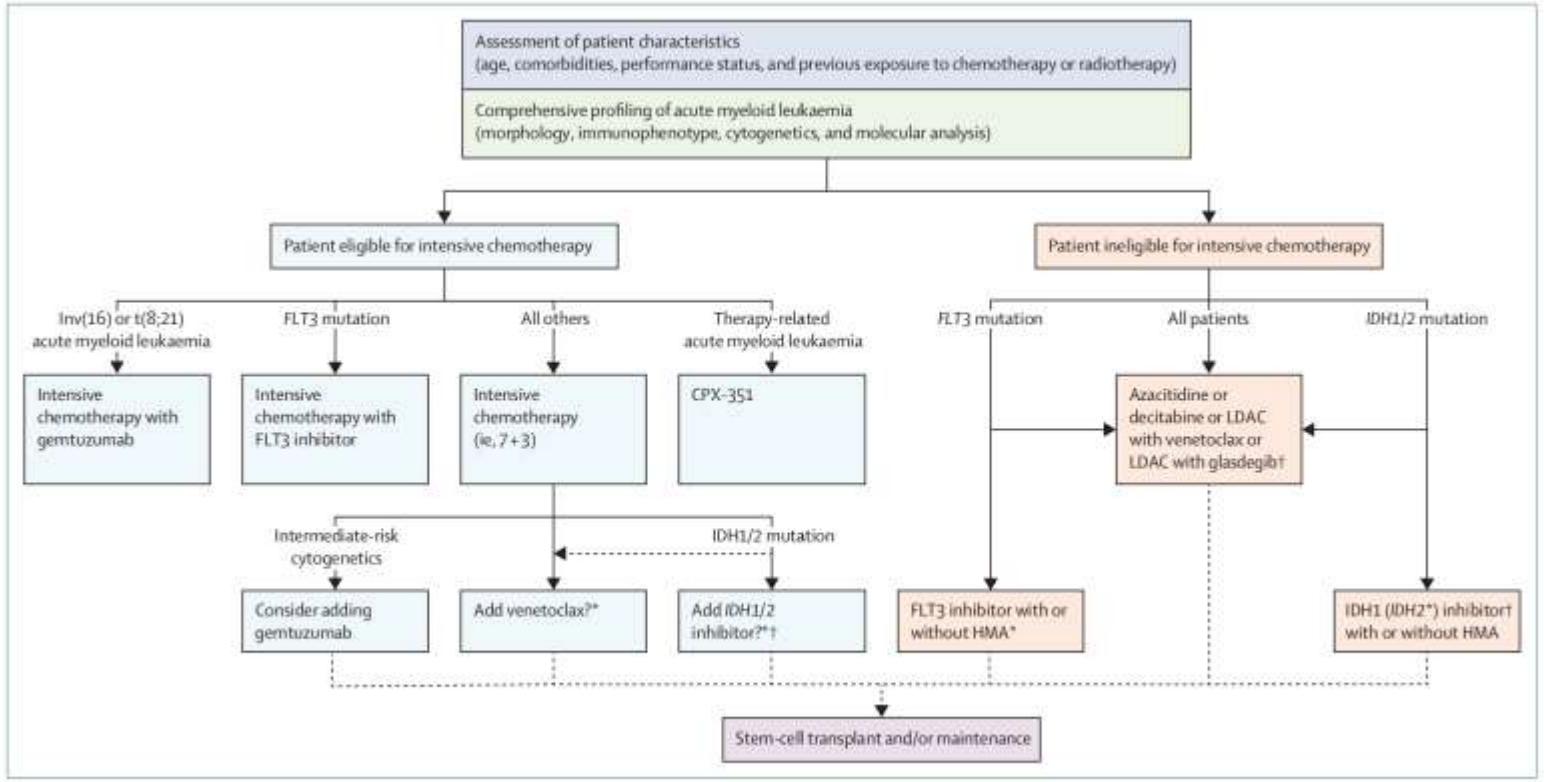


Figure 2: **Evolving treatment paradigm for newly diagnosed acute myeloid leukaemia**
HMA=hypomethylating agent. LDAC=low-dose cytarabine. *Not standard treatment; currently under investigation. †Inhibitors not globally available.

(2023 Lancet) **Acute myeloid leukaemia** *Courtney D DiNardo, Harry P Erba, Sylvie D Freeman, Andrew H Wei* https://onlinelibrary.wiley.com/doi/epdf/10.1002/ajh.27165

Table 2:

Genomic risk stratification of acute myeloid leukaemia

	Favourable	Intermediate	Adverse
Cytogenetic	t(8;21)(q22;q22.1) for *RUNX1-RUNX1T1*, and inv(16)(p14.1q22) or t(16;16)(p13.1;q22) for *CBFB-MYH11*	t(9;11)(p21.3;q23.3) for *MLL3-KMT2A*[‡], and cytogenetic abnormalities not classified as favourable or adverse	t(6;9)(p23;q34.1) for *DEK-NUP214*; t(v;11q23.3) for *KMT2A* rearranged; t(9;22)(p34.1;q11.2) for *BCR-ABL1*; inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2) for *GATA2* and *MECOM(EVI1)*; −5 or del(5q); −7; and -17/abn(17p); complex karyotype[‡]; and monosomal karyotype[‡]
Molecular	Mutated *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}[§], and biallelic mutated *CEBPA*	Mutated *NPM1* and *FLT3*-ITD^{high}[§], and wild-type *NPM1* without *FLT3*-ITD or with *FLT3*-ITD^{low}[§] (without adverse-risk genetic lesions)	Wild-type *NPM1* and *FLT3*-ITD^{high}[§], mutated *RUNX1*[¶], mutated *ASXL1*[¶], and mutated *TP53*[¶]

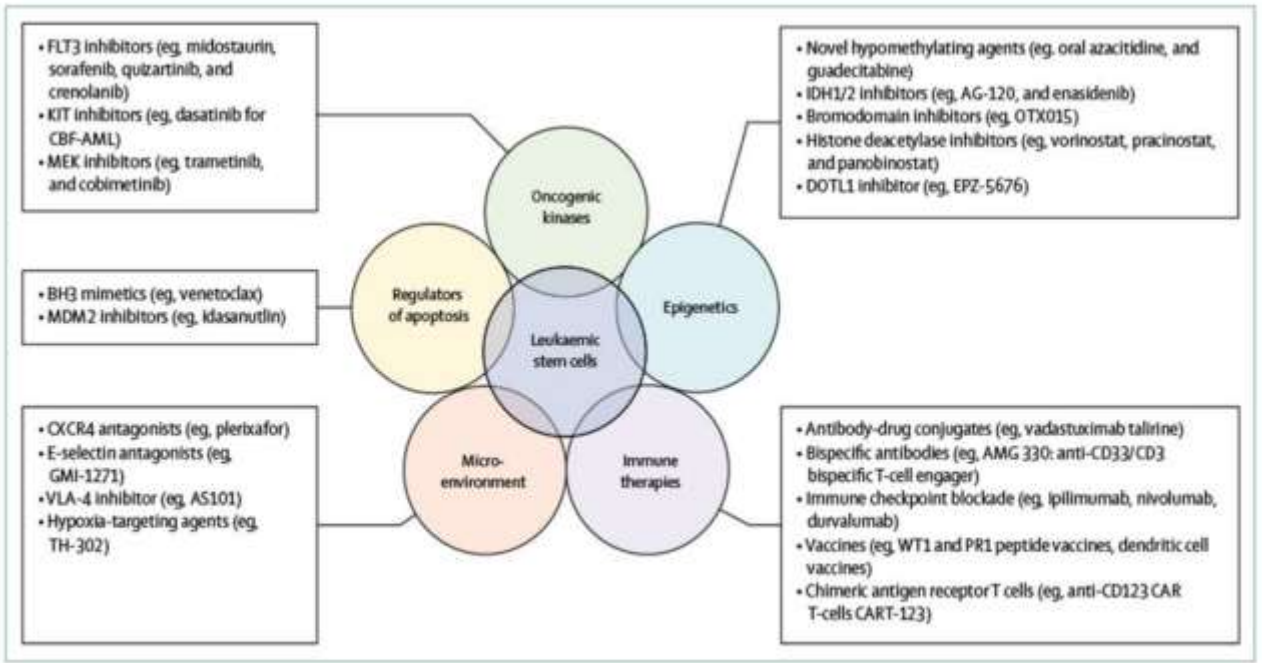


Figure 2: Examples of selected novel therapeutic strategies in acute myeloid leukaemia

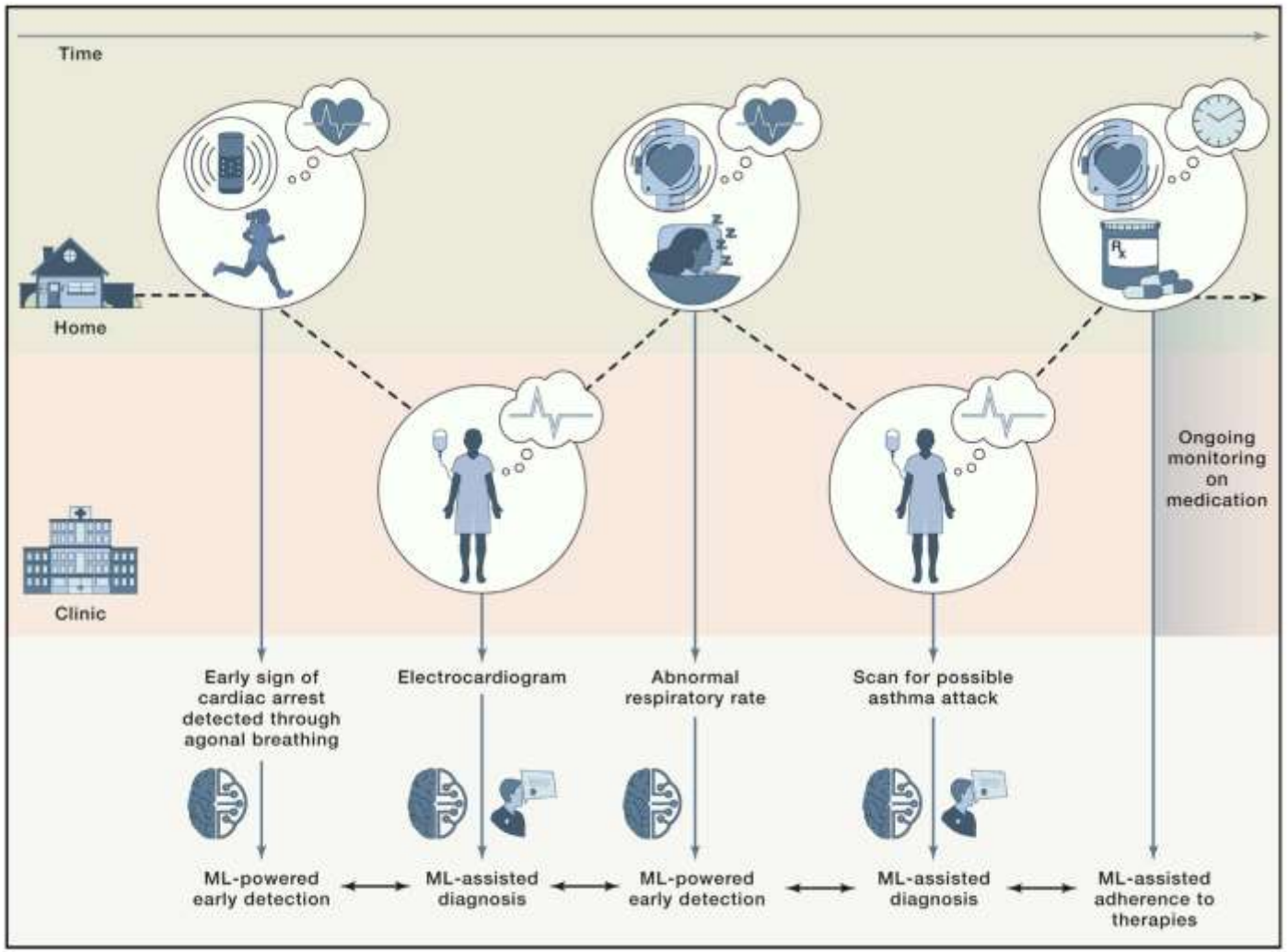
(2018 Lancet) Acute myeloid leukaemia Nicholas J Short,

“Biomarker 的寻找”

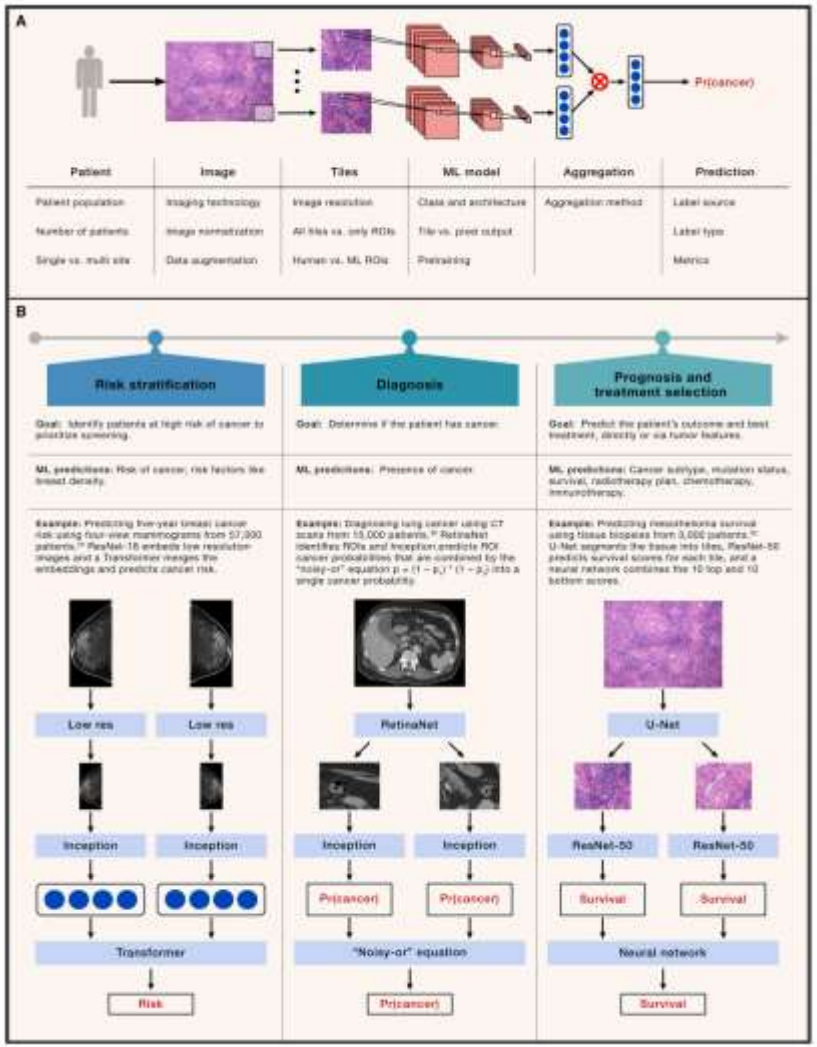
- 诊断的 Biomarker
- 疗效的 Biomarker
- 预后的 Biomarker

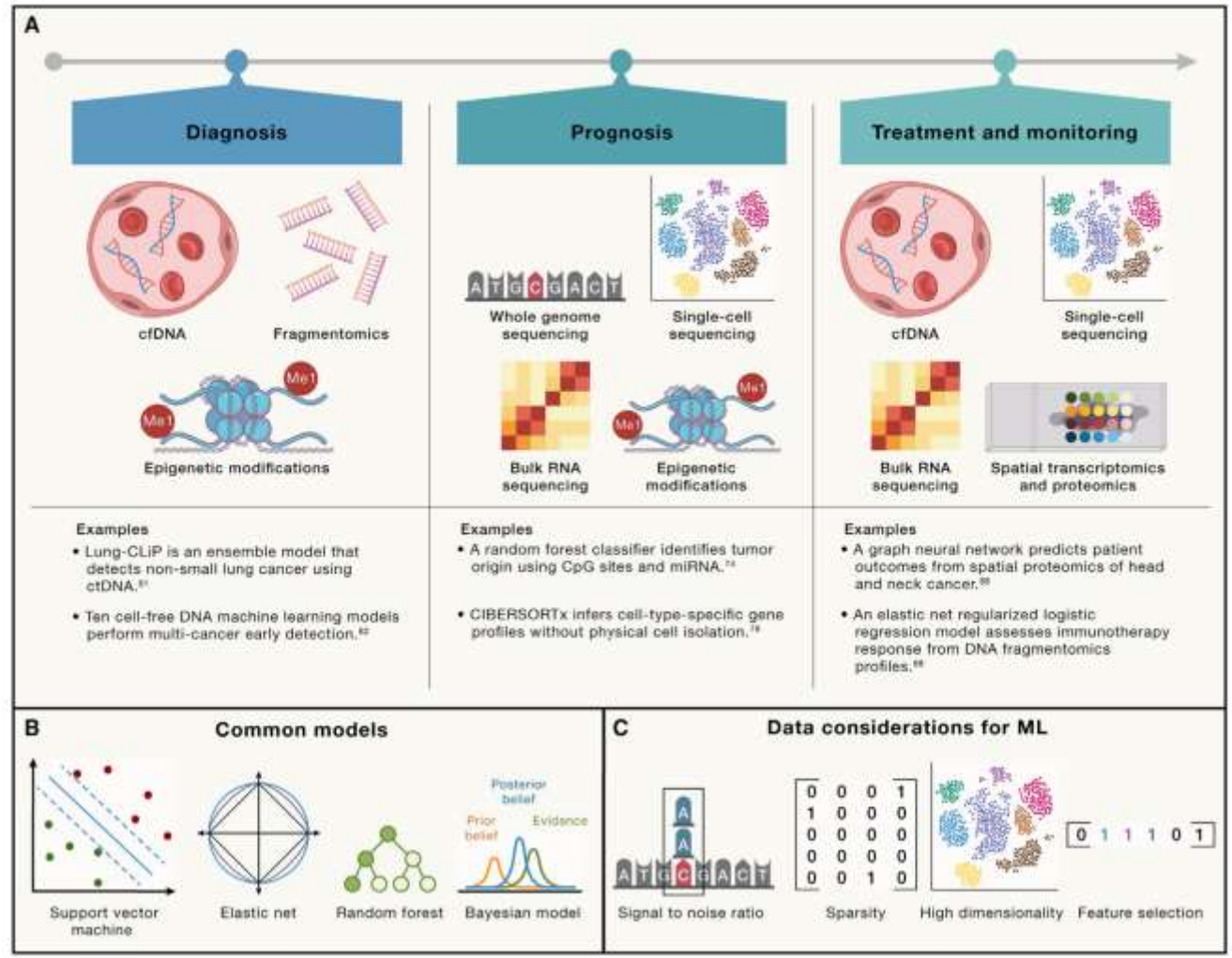
1. 单模态： y = f (x1) 注：y是疾病，x1 可以是症状 、体征、生化检查等
2. 多模态：y = f (x1,x2,x3...) x 是不同载体的检查： 从文字（电子病历）到图像（CT PET-CT etc.）

NOT only ML： How Machine Learning Applications Could Help Individuals Maintain Health

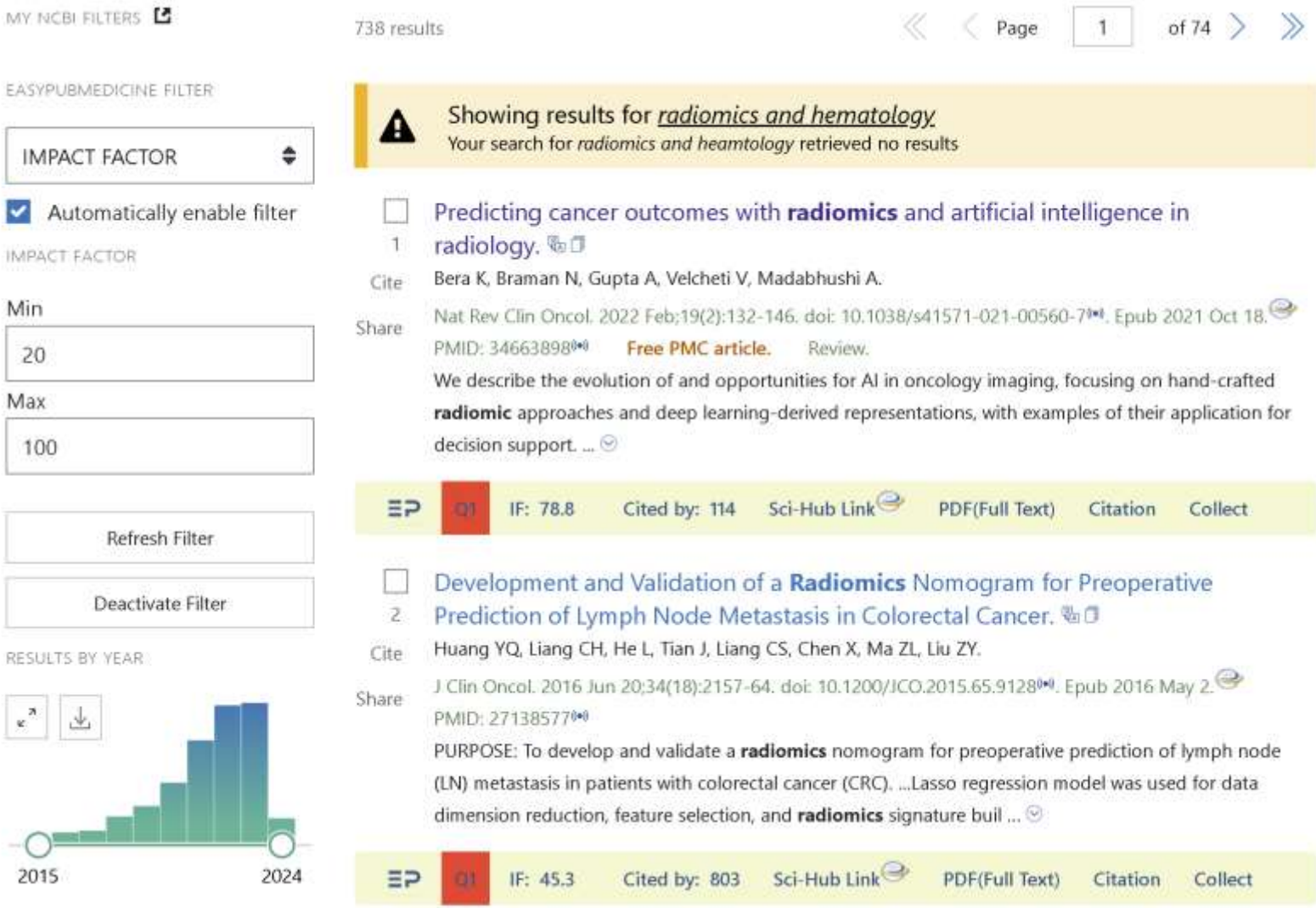


(2020 CELL) How Machine Learning Will Transform Biomedicine





(2023 CELL) From patterns to patients: Advances in clinical machine learning for cancer diagnosis, prognosis, and treatment



https://pubmed.ncbi.nlm.nih.gov/?term=radiomics++++and++heamtology

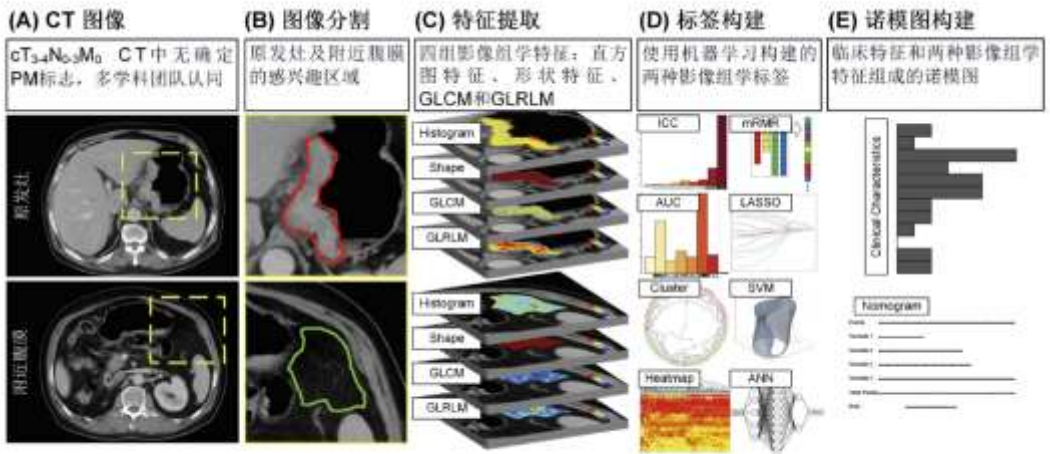


图 1 影像组学预测胃癌腹膜转移模型构建流程[4]

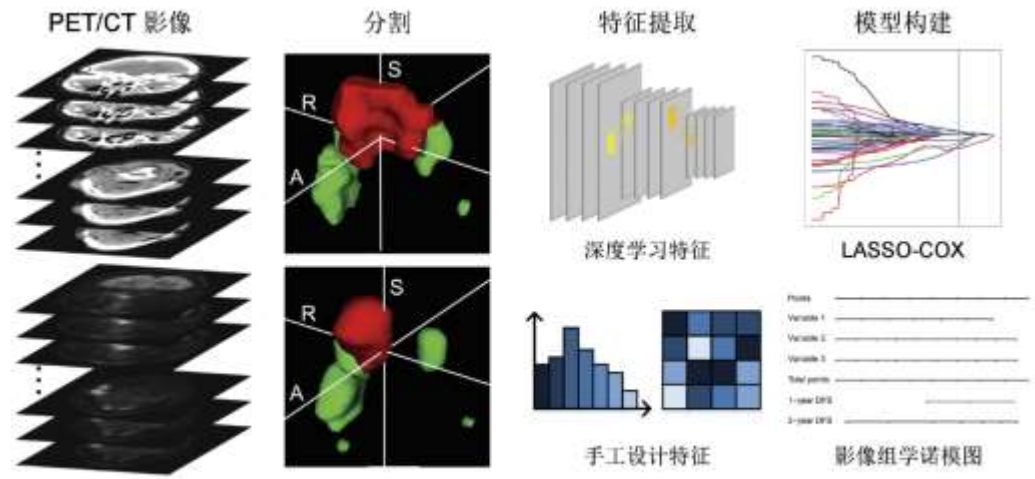
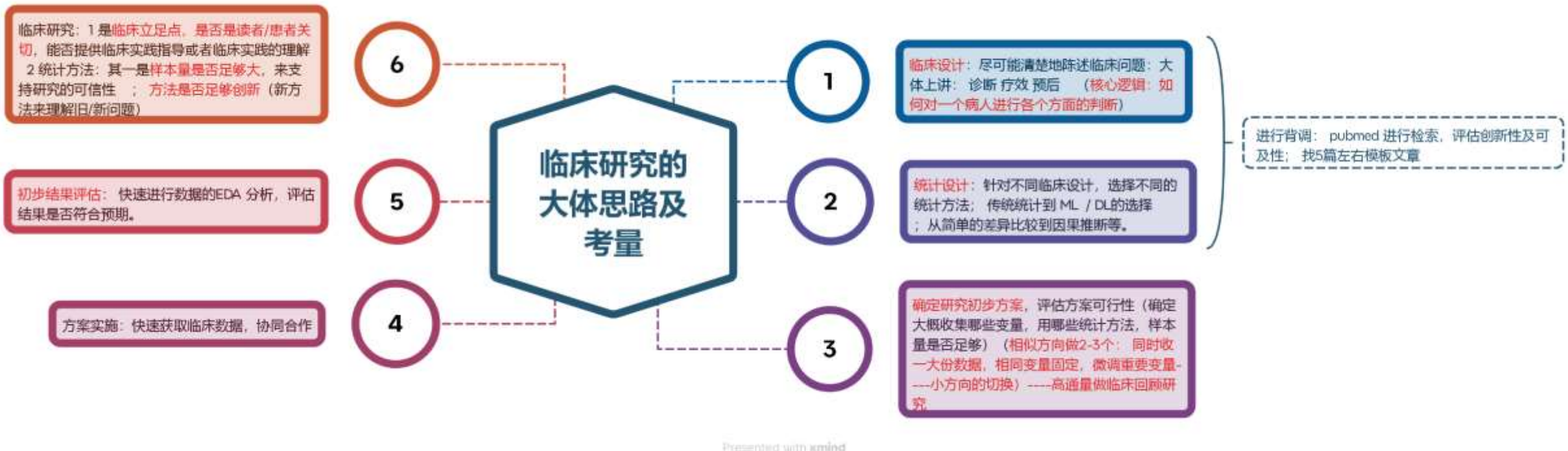


图 2 构建影像组学模型预测鼻咽癌患者治疗后的无进展生存期[12]

https://www.nsfc.gov.cn/csc/20345/20348/pdf/2021/202101-85-91.pdf

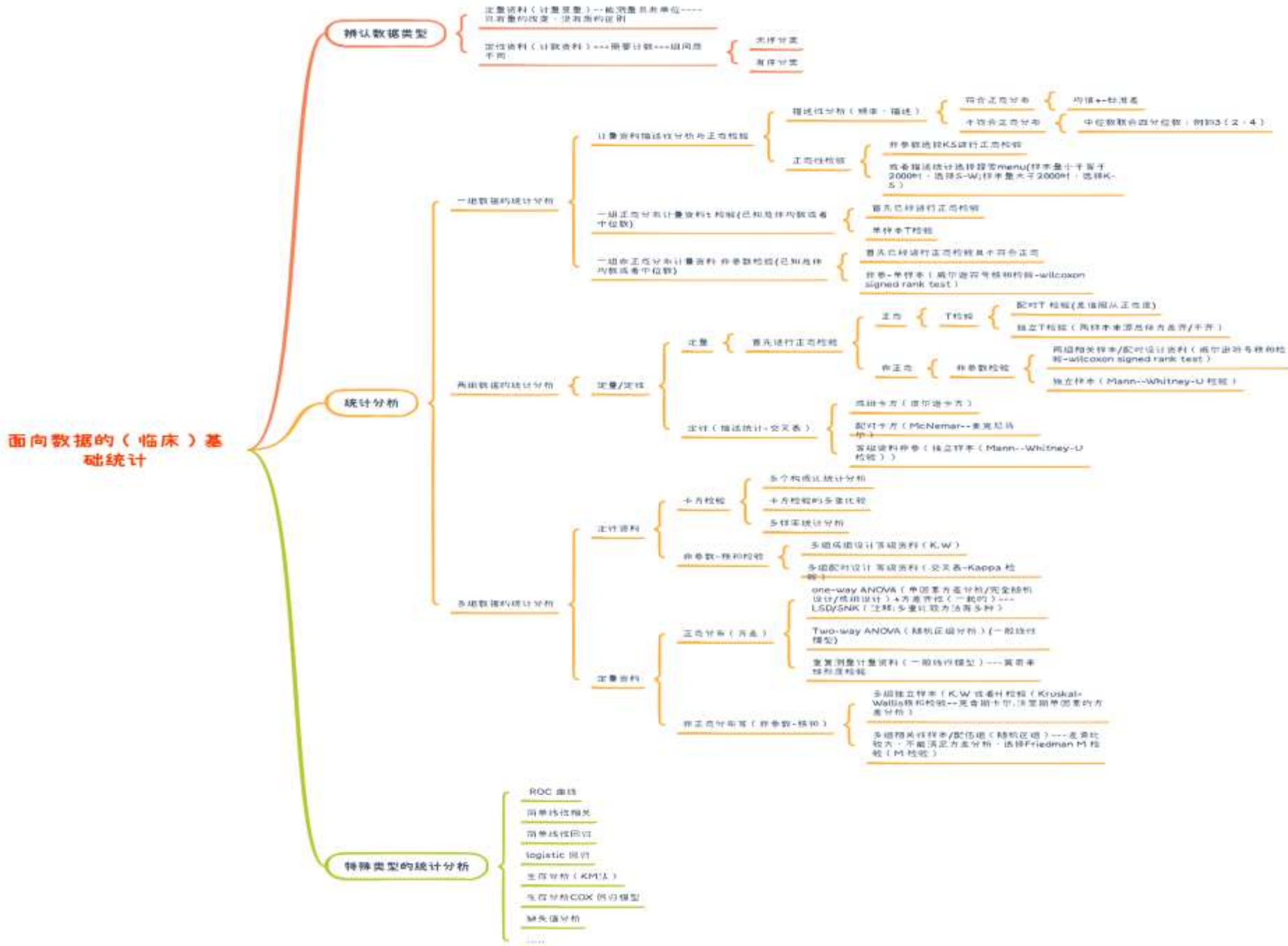
Summary


临床研究的大体思路及考量
1
临床设计：尽可能清楚地陈述临床问题：大体上讲： 诊断 疗效 预后 （核心逻辑：如何对一个病人进行各个方面的判断）
进行背调： pubmed 进行检索，评估创新性及可及性； 找5篇左右模板文章
2
统计设计：针对不同临床设计，选择不同的统计方法； 传统统计到 ML / DL的选择；从简单的差异比较到因果推断等。
3
确定研究初步方案，评估方案可行性（确定大概收集哪些变量，用哪些统计方法，样本量是否足够）（相似方向做2-3个： 同时收一大份数据，相同变量固定，微调重要变量----小方向的切换）----高通量做临床回顾研究
4
方案实施：快速获取临床数据，协同合作
5
初步结果评估： 快速进行数据的EDA 分析，评估结果是否符合预期。
6
临床研究：1是临床立足点，是否是读者/患者关切，能否提供临床实践指导或者临床实践的理解
2 统计方法：其一是样本量是否足够大，来支持研究的可信性 ； 方法是否足够创新（新方法来理解旧/新问题）
Presented with xmind

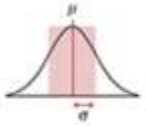
PART 2 统计

统计分析－－－－－－差异分析

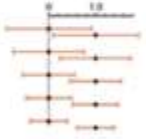

GraphPad Prism
差异分析
单因素
（一维分组）
双因素
（二维分组）
两组
多组
独立样本（unpaired）
配对样本（paired）
服从正态分布（①）
不服从正态分布
参数t检验
非参数t检验
方差齐性
方差不齐
非配对t检验
Welch's校正非配对t检验
Mann-Whitney秩和检验或Kolmogorov-Smirnov（②）
差值服从正态分布
差值不服从正态分布
参数t检验
非参t检验
差值一致
差值不同（③）
配对t检验
比值配对t检验
Wilcoxon 配对检验
One-way ANOVA（and Nonparametric）
服从正态分布
不服从正态分布
ANOVA
非参检验
Fired man检验或Kruskal-Wallis检验
two-way ANOVA


面向数据的（临床）基础统计
辨认数据类型
定量资料（计量变量）--能测量具有单位----具有量的改变，没有质的区别
定性资料（计数资料）---需要计数---组间质不同
无序分类
有序分类
统计分析
一组数据的统计分析
计量资料描述性分析与正态检验
描述性分析（频率，描述）
符合正态分布
均值+-标准差
不符合正态分布
中位数取四分位数，例如3（2，4）
正态性检验
非参数选择KS进行正态检验
或者描述统计选择探索menu(样本量小于等于2000时，选择S-W;样本量大于2000时，选择K-S)
一组正态分布计量资料t 检验(已知总体均数或者中位数)
首先已经进行正态检验
单样本T检验
一组非正态分布计量资料 非参数检验(已知总体均数或者中位数)
首先已经进行正态检验且不符合正态
非参-单样本（或作符号秩和检验-wilcoxon signed rank test）
两组数据的统计分析
定量/定性
定量
首先进行正态检验
正态
T检验
配对T 检验(差值服从正态性)
独立T检验（两样本来源总体方差齐/不齐）
非正态
非参数检验
两组相关样本/配对设计资料（或作进行符号秩和检验-wilcoxon signed rank test）
独立样本（Mann--Whitney-U 检验）
定性（描述统计-交叉表）
四格卡方（或作连卡方）
配对卡方（McNemar--麦克尼马卡方）
等级资料非参（独立样本（Mann--Whitney-U 检验））
多组数据的统计分析
定性资料
卡方检验
多个构成比统计分析
卡方检验的多重比较
多样本统计分析
非参数-秩和检验
多组成组设计等级资料（K.W）
多组配对设计 等级资料（交叉表-Kappa 检验）
定量资料
正态分布（方差）
one-way ANOVA（单因素方差分析/完全随机设计/成组设计）+方差齐性（一般的）---LSD/SNK（注释：多重比较方法有5种）
Two-way ANOVA（随机区组分析）(一般线性模型)
重复测量计量资料（一般线性模型）---莫奇来球形度检验
非正态分布等（非参数-秩和）
多组独立样本（K.W 或者H 检验（Kruskal-Wallis秩和检验--更专用卡方，注意用单因素的方差分析）
多组相关性样本/配伍组（随机区组）---差异比较大，不能满足方差分析，选择Friedman M 检验（M 检验）
特殊类型的统计分析
ROC 曲线
简单线性相关
简单线性回归
logistic 回归
生存分析（KM法）
生存分析COX 回归模型
缺失值分析
.....

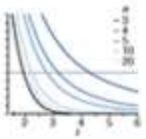
《Nature Methods》统计、作图专栏



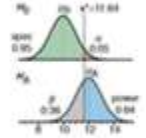
Importance of being uncertain - How samples are used to estimate population statistics and what this means in terms of uncertainty.



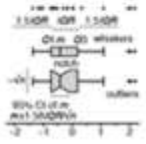
Error Bars - The use of error bars to represent uncertainty and advice on how to interpret them.



Significance, *P* values and *t*-tests - Introduction to the concept of statistical significance and the one-sample t-test.



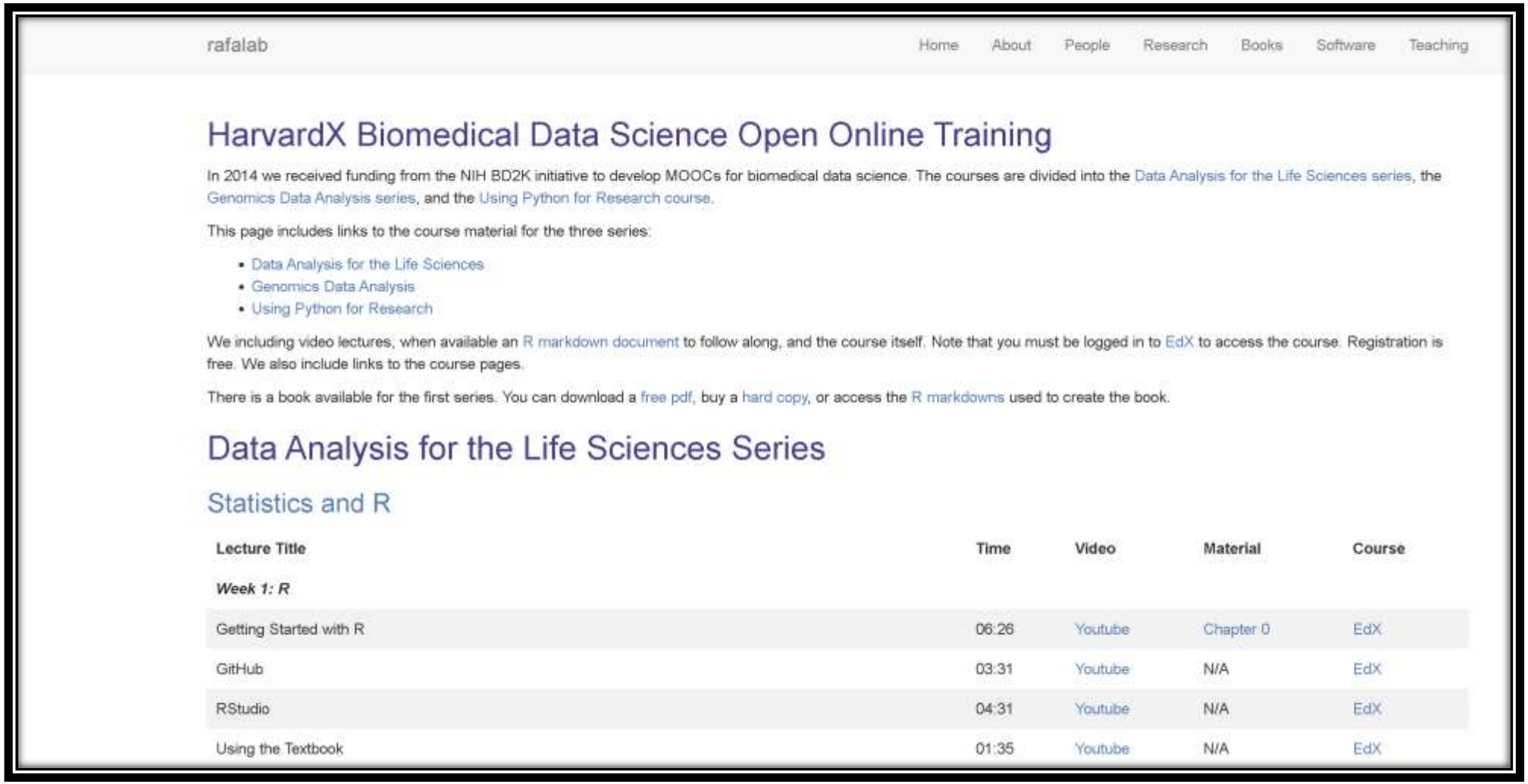
Power and sample size - Use of statistical power to optimize study design and sample numbers.



Visualizing samples with box plots - Introduction to box plots and their use to illustrate the spread and differences of samples. See also: Kick the bar chart habit and BoxPlotR: a web tool for generation of box plots

https://www.nature.com/collections/qghhqm/pointsofsignificance
https://www.nature.com/collections/qghhqm/resources

基础：Statistics and R



rafalab

Home About People Research Books Software Teaching

HarvardX Biomedical Data Science Open Online Training

In 2014 we received funding from the NIH BD2K initiative to develop MOOCs for biomedical data science. The courses are divided into the Data Analysis for the Life Sciences series, the Genomics Data Analysis series, and the Using Python for Research course.

This page includes links to the course material for the three series:

- Data Analysis for the Life Sciences
- Genomics Data Analysis
- Using Python for Research

We including video lectures, when available an R markdown document to follow along, and the course itself. Note that you must be logged in to EdX to access the course. Registration is free. We also include links to the course pages.

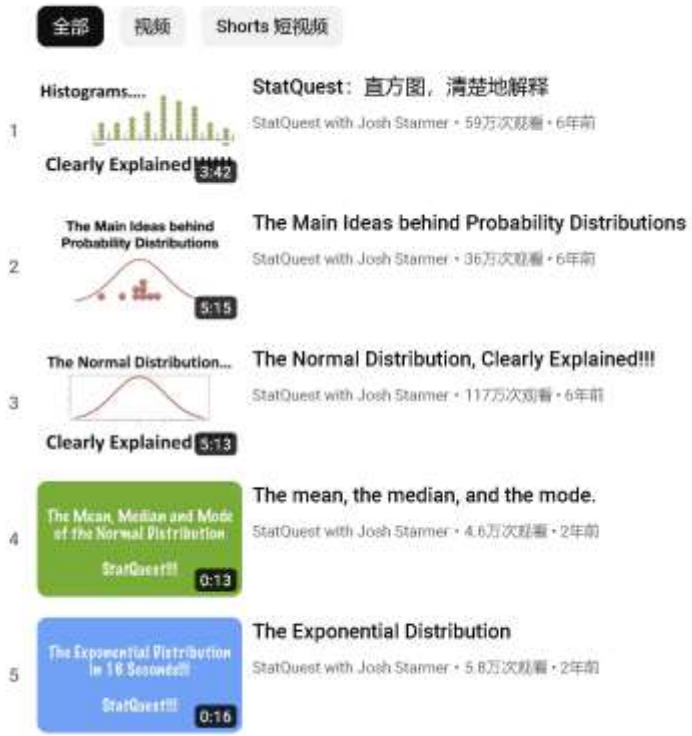
There is a book available for the first series. You can download a free pdf, buy a hard copy, or access the R markdowns used to create the book.

Data Analysis for the Life Sciences Series

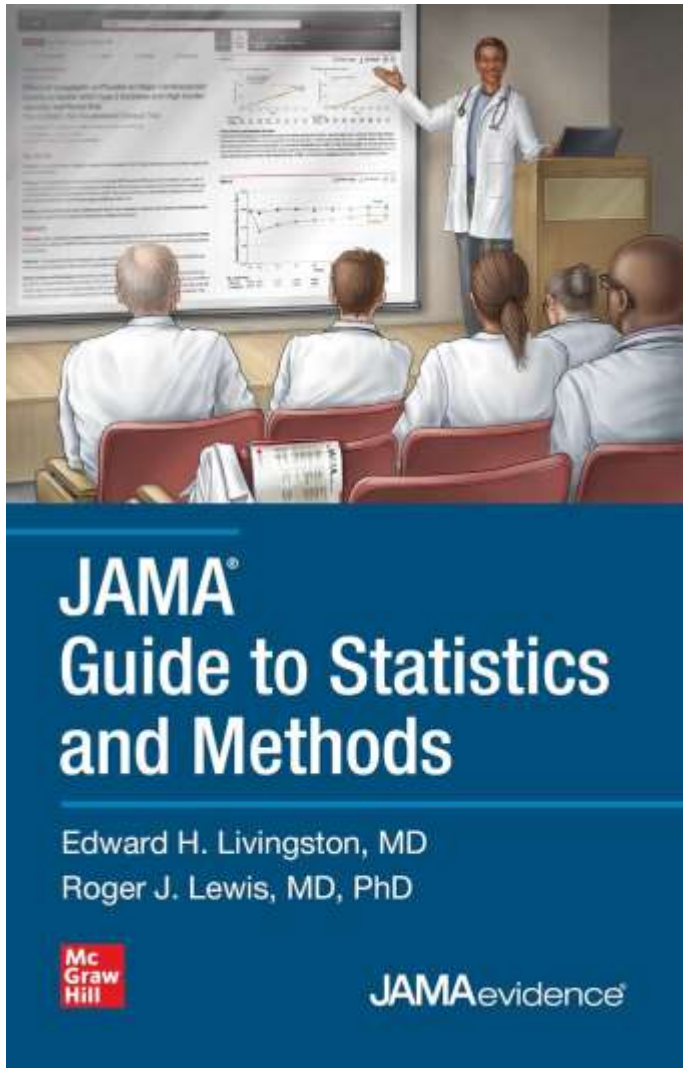
Statistics and R

Lecture Title	Time	Video	Material	Course
Week 1: R				
Getting Started with R	06:26	Youtube	Chapter 0	EdX
GitHub	03:31	Youtube	N/A	EdX
RStudio	04:31	Youtube	N/A	EdX
Using the Textbook	01:35	Youtube	N/A	EdX

https://rafalab.dfci.harvard.edu/pages/harvardx.html



https://statquest.org/
https://statquest.org/video-index/



JAMA Guide to Statistics and Methods

1st Edition
1260455327 · 9781260455328

By Edward H. Livingston, Roger J. Lewis
© 2020 | Published: November 8, 2019

Publisher's Note: Products purchased from Third Party sellers are not guaranteed by the publisher for quality, authenticity, or access to any online entitlements included with the product.The world-renowned experts at JAMA® explain statistical analy...

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https://www.mhprofessional.com/jama-guide-to-statistics-and-methods-9781260455328-usa

PART 3 课题设计

课题选择与设计

通过新文献、学术微信号关注新 技术方向，思考新实验技术（或 公司服务）和相应公共数据能否 应用到自己的研究课题中?

期刊编辑看重：**概念突破 + 广泛兴趣**

面向审稿人（Cell）：

As usual, we would appreciate advice not only on the technical competence, but also on the issue of whether the paper is of **general interest** and presents a sufficiently **significant conceptual advance** to be a strong candidate for publication in Cell versus another, potentially more specialized journal. As you know, the principal criterion for publication in Cell is that the work should be of unusual significance in the field, but it should also interest a range of researchers outside the immediate area.

面向作者（Nature Aging）：

It is our policy to decline a substantial proportion of manuscripts without sending them to referees so that they may be sent elsewhere without further delay. Such decisions are made by the editorial staff when it appears that papers do not meet the criteria for publication in Nature Aging. These editorial judgments are based on such considerations as the **degree of conceptual advance** provided, the **potential interest to our broad and multidisciplinary audience** and timeliness

如何选择课题或合作?

与研究组主要研究方向关联

从老师和同学处获得更多交流

不囿于自己熟悉的技术或方向，可学习或合作

个人兴趣：大脑、血液、统计方法。

想增强的技能：新技术、实验、管理。

发展潜力：课题前沿性、近期发表文章

合作环境：组内或组间的合作者

事半功倍

- 读一篇文献：和多个课题、课程内容相关
- 在线文献组会：和多位合作者一起学习

学术交流

- 通过微信、组会，交流文献和进展
- 不仅报告成功进展，也讲失败经验（组会、学术报告、考核中），供大家借鉴、提建议
- 兼顾深度和广度
  - 交叉研究和创新

课题选择、设计与平衡

• 技术 vs. 应用

– 技术开发：实验、算法、理论。。
– 应用：重要科学问题

• 主导 vs. 合作
• 常规 vs. 冒险
– 常规：满足毕业要求、缓解考核压力
– 冒险：领域中的硬核问题

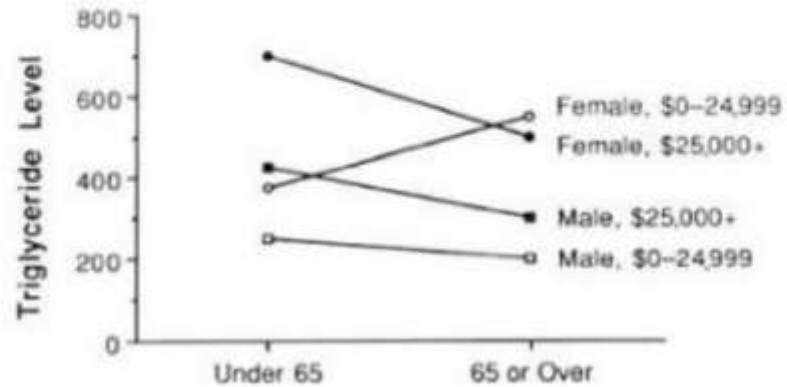
通过在2-3个课题之间切换、调整优先级、相互启发，缓解课题的**中性结果**（大多数情况）带来的紧张和压力

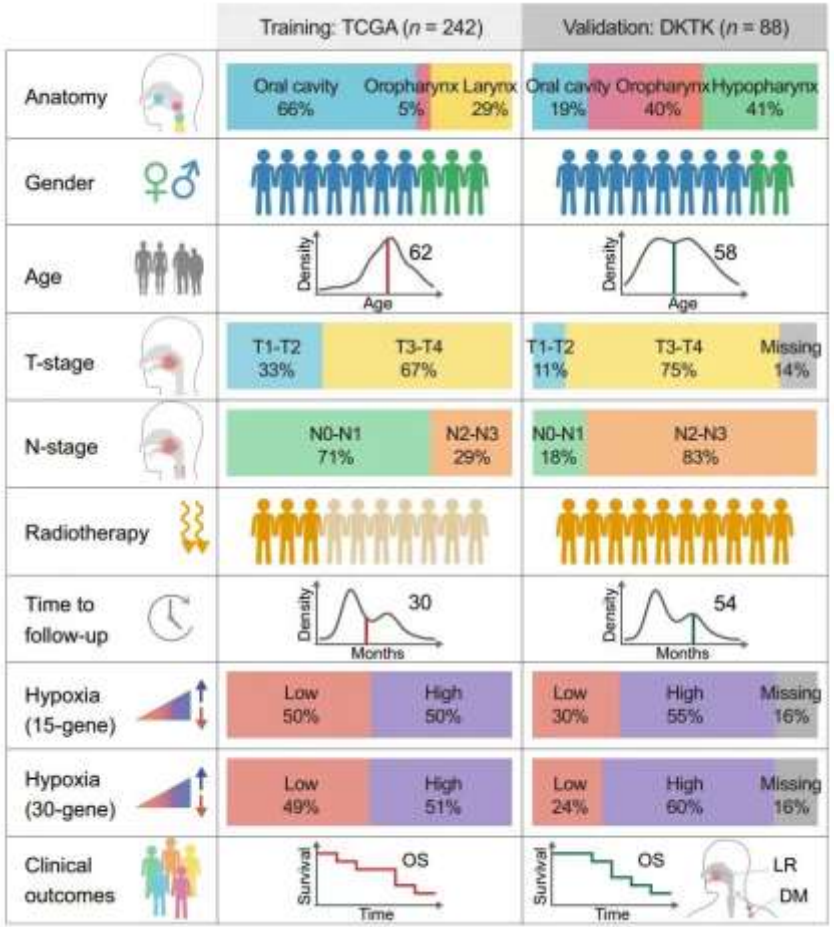
Table vs. graph

Triglyceride Level by Income Group, Sex, and Age Group

	MALES		FEMALES	
INCOME GROUP	Under 65	65 or Over	Under 65	65 or Over
$0–24,999	250	200	375	550
$25,000+	430	300	700	500

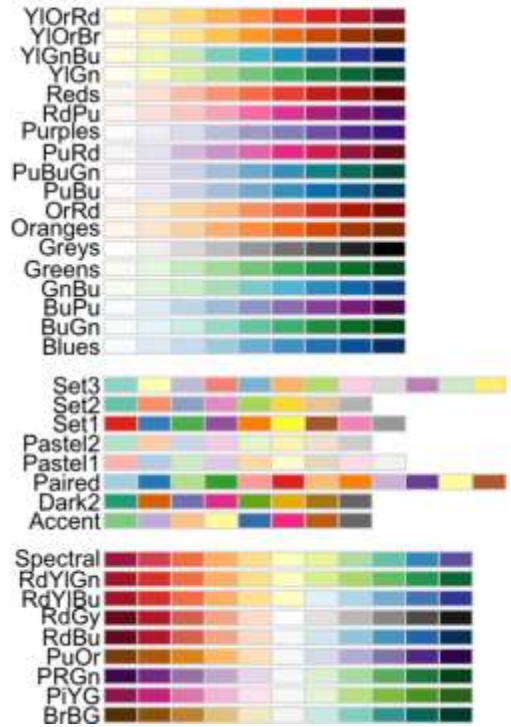
Triglyceride Level for Age Group, by Sex and Income Group



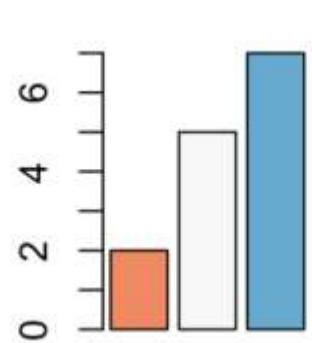


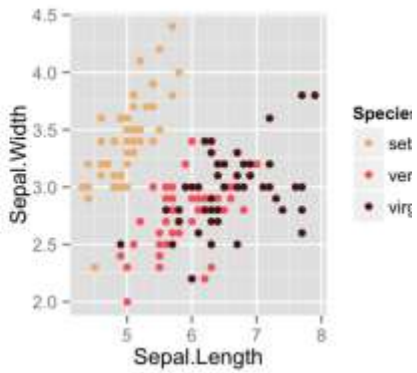
Color palettes in the **RColorBrewer** package

```
library("RColorBrewer")
display.brewer.all()
```




```
barplot(c(2,5,7),
col=brewer.pal(n = 3, name =
"RdBu"))
```






```
ggplot(iris, aes(Sepal.Length,
Sepal.Width, color = Species)) +
geom_point(size = 2) +
scale_color_manual(values =
wes.palette(n=3, name="GrandBudapest"))
```

https://colorbrewer2.org/#type=sequential&scheme=YlOrBr&n=9

文稿组织建议

- **文稿**

立意不高，行而不远
写作顺序：结果、介绍、讨论、方法

- **故事**

做实验（分析）和讲故事的顺序不一样
做的不一定都要讲，分主次（主图、补充图）

结果部分

- 关注每一标题节或自然段的开始和结尾

开始：关注提出了什么问题，为什么做这个实验或分析，假说（对问题答案的猜测）和预期是什么？

结尾：作者如何解读一个图或结果，推理出什么结论，你是否同意这个解读或推理？

- 锻炼读图能力

熟悉各种临床研究图（快速理解文献的分析、自己的课题设计和分析）

主图：关键数据、推动故事

补充图：额外的例子、证明数据可靠性、阴性结果

许多图和数据：与文献结果吻合，证明方法和数据可靠

讨论部分：关注对结果的升华

- 自己主动说出工作的创新点和科学贡献

与领域经典模型的异同，补充或修改（Waddingtong的epigenetic landscape模型）

与领域新概念的关联、对比异同（pioneer factor）

工作局限性、未来研究问题和方向

文献/课题报告：故事性与逻辑性

• 医学、生物学论文大多强调故事性（参考优秀的电影）。
从课题背景开始，依次讲解科学问题、假说、方法、结果、讨论和未来计划。

• 要讲出论文的前因后果，每一篇文献都是基于已有的科学进展。
要精读论文的介绍部分，需要时翻阅它引用的文献。
讲解领域前沿发展到哪里，未知和困难是什么，作者如何想到了这个科学问题和技术开发，想用什么思路和手段解决？

• 讲解论文中重要图对应的实验或分析是想回答什么问题？
做了分析图后，问题是否得到回答？又产生了什么样的思路去做下一个分析？这样就建立了从背景到图1，到图2……之间的联系，更有逻辑性和故事性。如需要可用文字页承上启下。

• 不一定要讲论文中所有的图，选最重要的三个结果讲清楚，让大家能 听懂和有收获，就是成功

学习任务（时间分配比例）如下：

• **统计分析**（25%）：R语言和统计分析是大数据分析的基础。系统学习这本书并完成其中的练习：An Introduction to Statistical Learning with Applications in R（中文版）

• **文献重复**（50%）：从感兴趣的领域或课题方向中选择文献仔细阅读。选择一篇分析方法有代表性、原始数据可下载的论文仔细阅读这篇论文的方法和补充材料中的分析方法，从尽 可能原始的数据开始做数据处理、分析和做图，目标是自己做出论文中 的大部分图表并与它们比较，证明自己掌握了分析方法和流程--- 建议项目驱动

• **科研探索**（15%）：参考导师的建议，关注一个科研问题，搜索文献，了解文献里关于这个问题有什么样的答案和前沿进展？有哪些没有回答的问题，你可以产生什么新的生物假说和预测？写出研究计划并做初步分析。

• **计划总结**（10%）：计划和实施研究项目。定期在组会上做进展或文献报告、写书面总结。展示课题进展、难点、解决办法、计划未来任务，征求课题成员的建议。

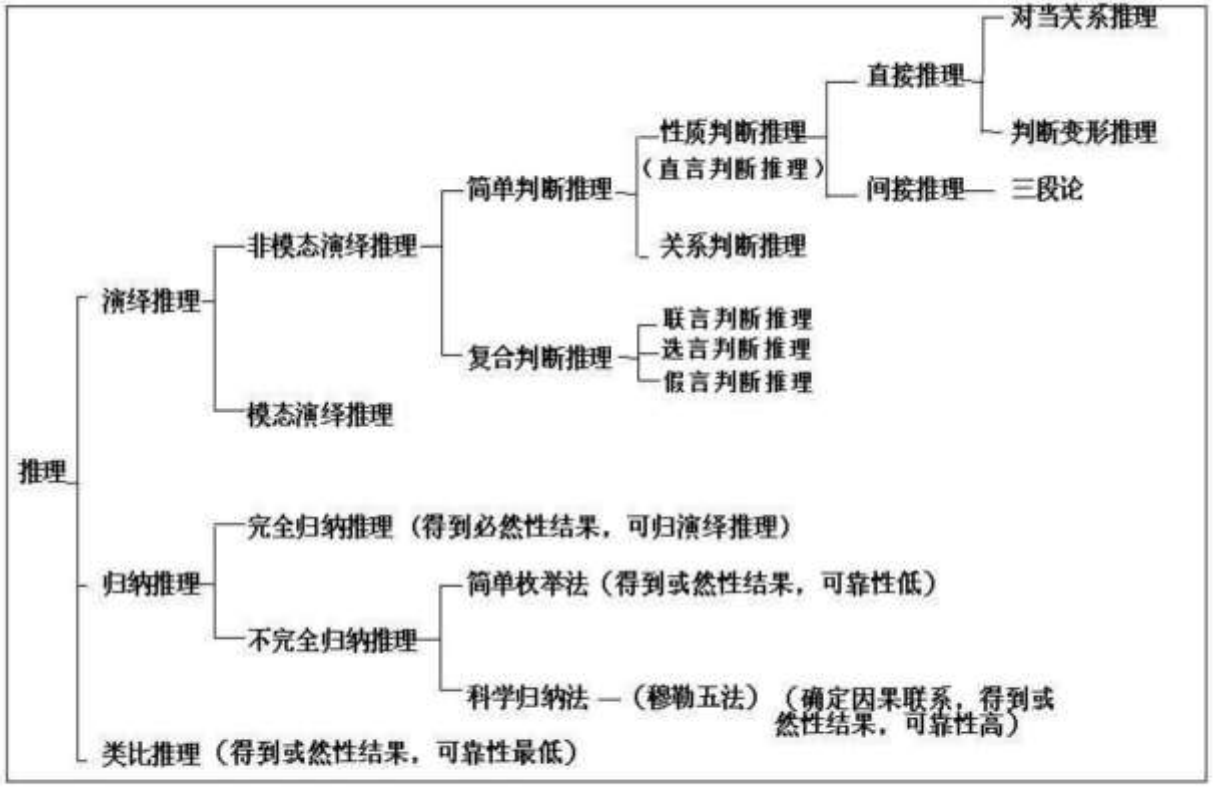
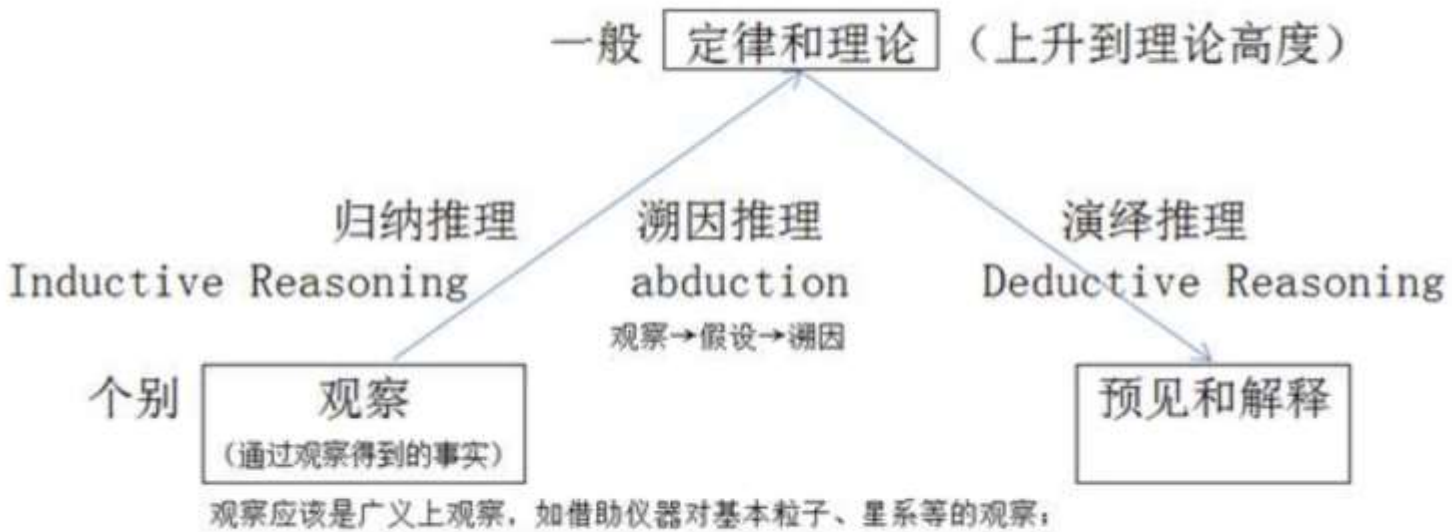


图0-3 不同形式的逻辑推理

穆勒五法
• 包括“求同法”、“求异法”、“求同求异并用法”、“共变法”、“剩余法”等5种逻辑方法。
• 现代医学验证化学药品和生物学制剂疗效的“大样本双盲对照实验”是一个具体应用：个体有差异，需要大样本统计；疾病有自愈现象，需要对照（求异法）；人有心理作用，需要双盲。通过严格设计、严格操作的现代医药学试验，一般能够确定某种疗法的临床效应。
• 1890年，德国细菌学家Robert Koch提出的“科赫法则”也是一个应用。
(1）致病微生物必须存在于患病的所有宿主生物体内，而不存在于健康生物体内；（2）从患病生物中可分离到该微生物的纯培养物；（3）将培养物接种至敏感宿主时，同样的疾病必定再次发生；（4）从人工接种的宿主中，可再次分离得到这种微生物的纯培养物。依据这4个条件，科赫证明了炭疽病和结核病分别由炭疽杆菌和结核杆菌引起。

https://blog.sciencenet.cn/blog-279293-1247462.html

科学方法就是科学要有逻辑化（用逻辑推理）、定量化（用数据说话）、实证化（用实践检验）的方法。



http://www.5itupu.com/KnowledgeShow-115,1338,0,8079,2.html

PART 4 投稿


iScience
2023.8.8
under review
2023.9.7
Major revision
2023.12.11
Minor revision
2024.1.11
Pre-accept
2024.1.25
Finalize
2023.8.4
投稿
2023.9.1
All reviews
completed
2023.11.16
提交修改稿
2023.12.14
提交修改稿
2024.1.19
提交修改稿
2024.1.31
Accept!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3. Independent Review
4. Interactive Review
5. Review Finalized
6. Final Validation
7. Final Decision

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✓ 1. Initial Validation ✓ 2. Editorial Assignment ✓ 3. Independent Review 4. Interactive Review 5. Review Finalized 6. Final Validation ✓ 7. Final Decision

Screening of novel diagnostic biomarkers in multiple myeloma comorbid with depression based on weighted gene co-expression network analysis

[redacted]

Original Research, Front. Psychiatry - [redacted]
Received on: 20 Dec 2022, Edited by: Dawei Zhang
Manuscript ID: 1127899
Research Topic: Objective Diagnostic and/or Prognostic Biomarkers in Major Depressive Disorder
Keywords: Depression, Multiple Myeloma, bioinformatics, weighted gene co-expression network analysis, hub gene, Diagnostic biomarkers for comorbidity

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NO ACTION IS REQUIRED FROM YOU

This manuscript has been rejected.

History | Editor Active | Reviewer 1 Active | Reviewer 2 Rejected | Me Active | Reviewer 4 Finalized | •A•I•R•A•

Date	Updates
23 Feb 2023	Article rejected by Specialty Chief Editor Ming D Li.
21 Feb 2023	Review Editor 4 submitted the review report and finalized review.
05 Feb 2023	Interactive review forum activated automatically.
31 Jan 2023	You submitted your independent review report.
26 Jan 2023	You accepted to review this article.
25 Jan 2023	The Editorial Office invited you to review this article.
20 Dec 2022	Corresponding Author [redacted] submitted manuscript.

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To standardize the referencing style across Cell Press journals, starting from October 2022, we ask that all in-text citations be formatted as superscripted numbers (e.g. "Multiple reports support this observation.1,2"). Moving away from the Harvard referencing style (e.g. Smith et al., 2020) will improve author and reader experiences. All manuscripts accepted from now on must use **superscript numbered Cell Press referencing style**. Switching is easy. Just use the updated CSL and EndNote referencing styles for Cell Press articles.

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- Submit New Manuscript
- Submissions Sent Back to Author (0)
- Incomplete Submissions (0)
- Submissions Waiting for Author's Approval (0)
- Submissions Being Processed (0)

Revisions

- Submissions Needing Revision (0)
- Revisions Sent Back to Author (0)
- Incomplete Submissions Being Revised (0)
- Revisions Waiting for Author's Approval (0)
- Revisions Being Processed (0)
- Declined Revisions (0)

Completed

- Submissions with a Decision (0)
- Submissions with Production Completed (0)

Author webinars

We've finished our Author webinar series for 2023 and we're preparing new content for 2024 when we will relaunch the series. Until then, you'll find our latest Author webinar recordings here.

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- Submitting a LaTeX file in Editorial Manager
- Article Transfer Service (ATS) author overview

Resources

- User guide for authors to Editorial Manager
- Information on Open Access
- Be aware of potential scams. Read these 7 top tips to

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by Topic


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Aging


Cancer Metabolism


Cardiovascular Biology


COVID-19


Diabetes & Obesity


Diet & Exercise


Microbiota & Metabolism


Mitochondria

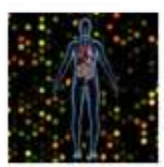

Neuroscience & Metabolism


Stem Cells


Immunometabolism


Diversity in Metabolism

by Type


Resource Articles


Review Articles


Clinical and Translational Reports


Special Issues


Voices


SnapShots

知乎 首发于 书籍电影生活世界

切换模式 写文章

论文投稿流程（已完结）

汽车小科普
北京理工大学 工学硕士

278 人赞同了该文章

赞同 278

分享

目录 收起

个人在论文投稿过程中曾参考过的一个[非常有用的帖子链接]

1. 注册账号

在目标期刊网站注册一个个人账号。

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https://zhuanlan.zhihu.com/p/54766177

让ChatGPT快速提高你的生产力/学习力 ……

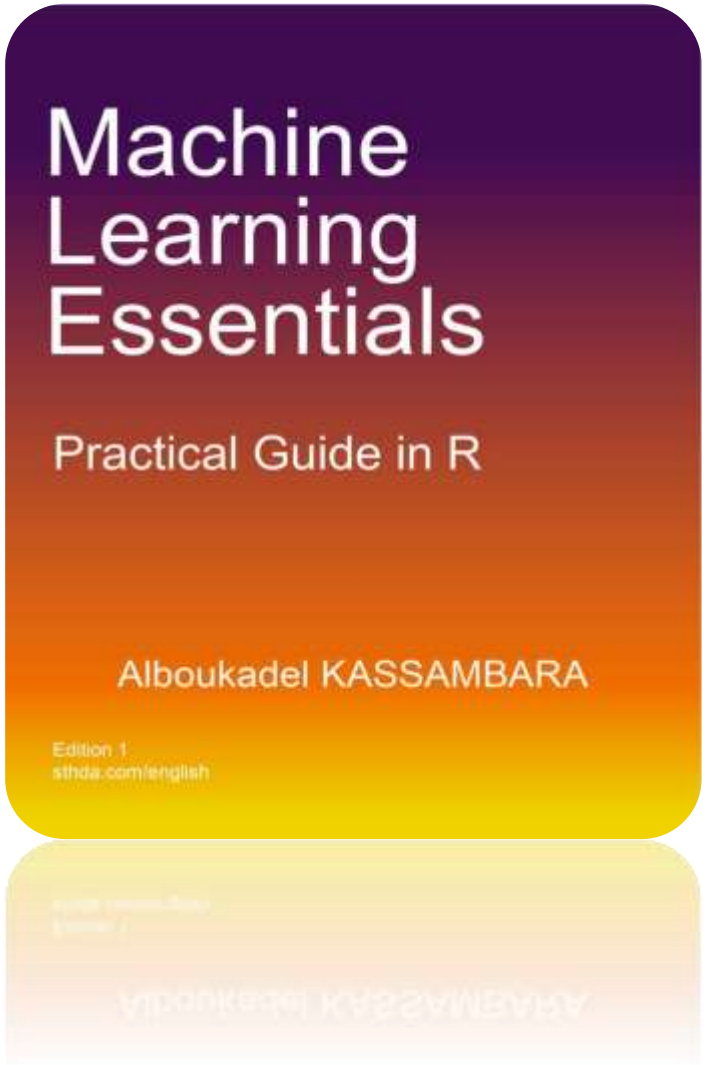
PART 5 Recommended reading list

推荐的2本中文R 入门书籍

https://bookdown.org/wangminjie/R4DS/

https://www.zhihu.com/people/huc_zhangjingxin

用R 进行临床统计实践



第四十六讲 R-逻辑回归结果解读

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有了第四十五讲对逻辑回归原理的学习投必得论文编译：第四十五讲 R-逻辑回归概论，今天就带大家来一一解读R运行结果的内容，以及如何在论文写作中，解释这些变量。

1 数据前期准备

详情请参见第四十五讲投必得论文编译：第四十五讲 R-逻辑回归概论

```
library(tidyverse)
library(caret)
#导入数据：(如需获取数据Outcome.csv，请关注投必得医学公众号，后台回复"Outcome.csv"获取数据。
my_data<-read.csv('Outcome.csv')
#检查数据
dim(my_data)
head(my_data)
summary(my_data)
```

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