DIPARTIMENTO DI INGEGNERIA
DELL'INFORMAZIONE

Dottorato in Ingegneria dell'Informazione
Curriculum: Biomedical, Electronics, and Telecommunications Engineering

Machine Learning approaches in Predictive Medicine using Electronic Health Records data

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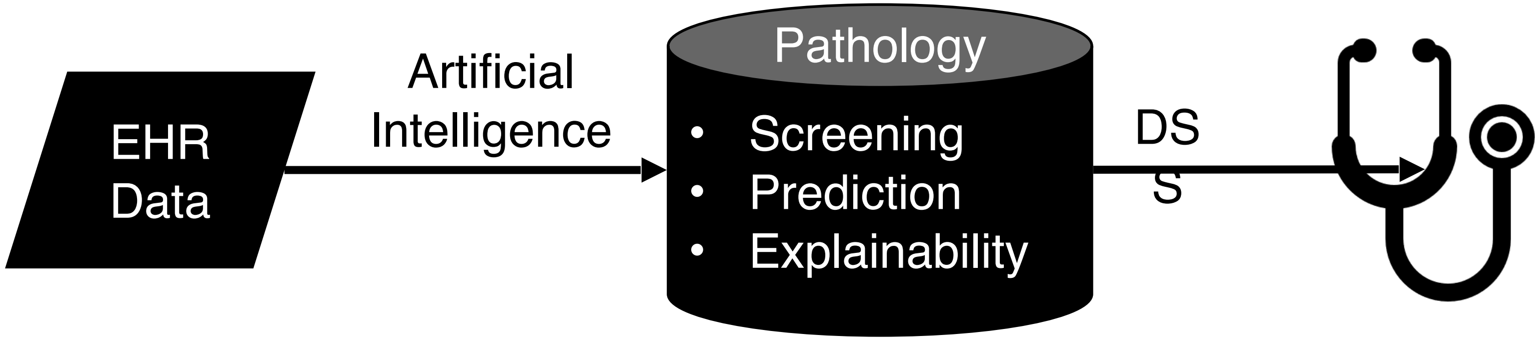
Co-Tutor: Luca Romeo

XXXIII cycle - 2019/2020

Introduction

Research topic

Machine Learning approaches in Predictive Medicine
using Electronic Health Records data



- General Practitioner
- Specialist

Introduction

Motivation

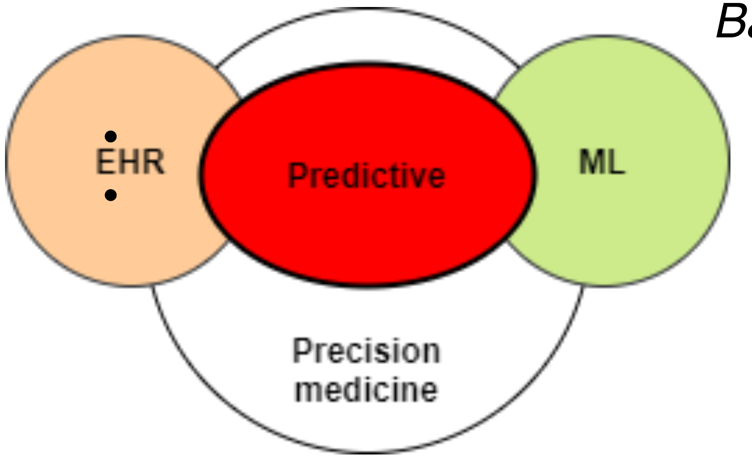
Traditional Medicine

"One-size-fits all"

- Reactive

Predictive Precision Medicine

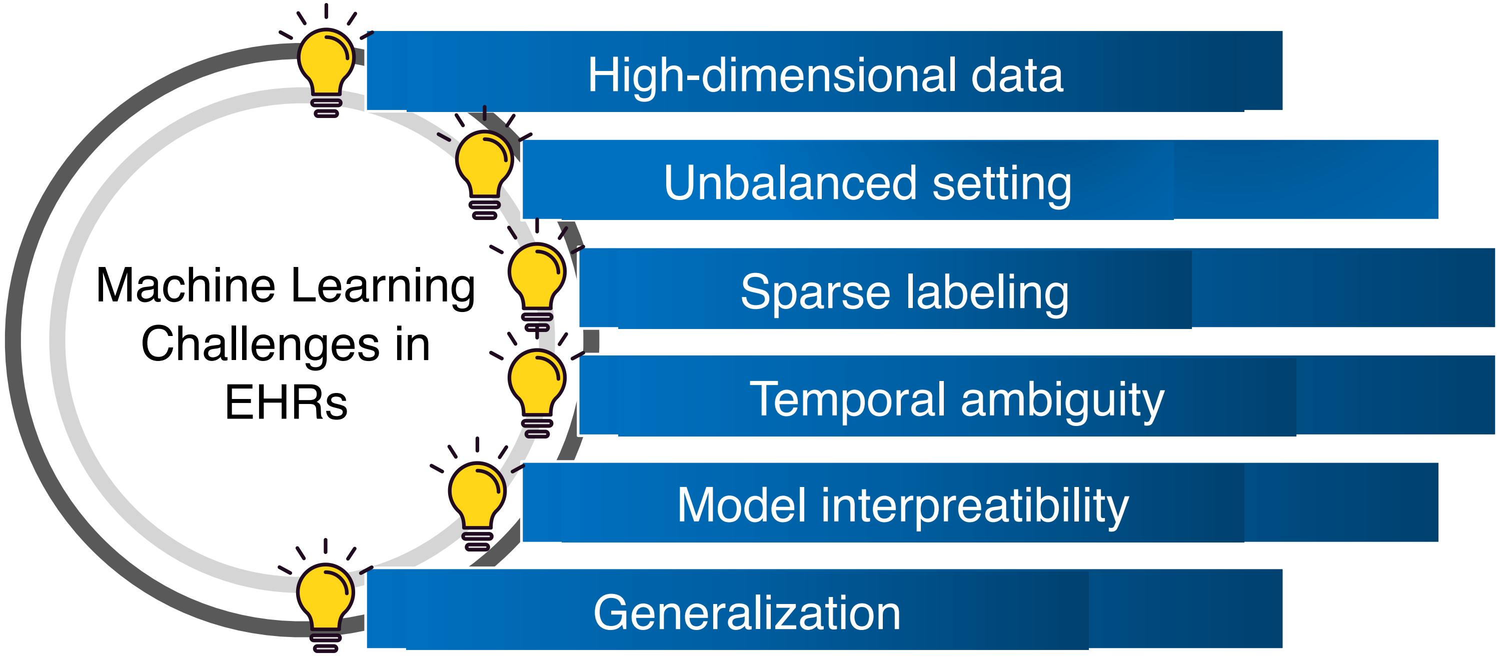
"Delivering the right treatments, at the right time, every time to the right person."
Barack Obama



Preventive
Proactive

Introduction

Problem statement



Introduction

Agenda

- ❑ **Type 2 diabetes (T2D) →** FIMMG dataset

Discovering the Type 2 Diabetes in Electronic Health Records using the Sparse Balanced Support Vector Machine, *JBHI, 2019*

- ❑ **Insulin resistance (IR) →** FIMMG dataset
  - TyG-er: An ensemble Regression Forest approach for identification of clinical factors related to insulin resistance condition using Electronic Health Records, *CBM, 2019*
  - Early temporal prediction of Type 2 Diabetes Risk Condition from a General Practitioner Electronic Health Record: A Multiple Instance Boosting Approach, *AIM, 2020*

- ❑ **Chronic kidney disease (CKD) →** mFIMMG dataset

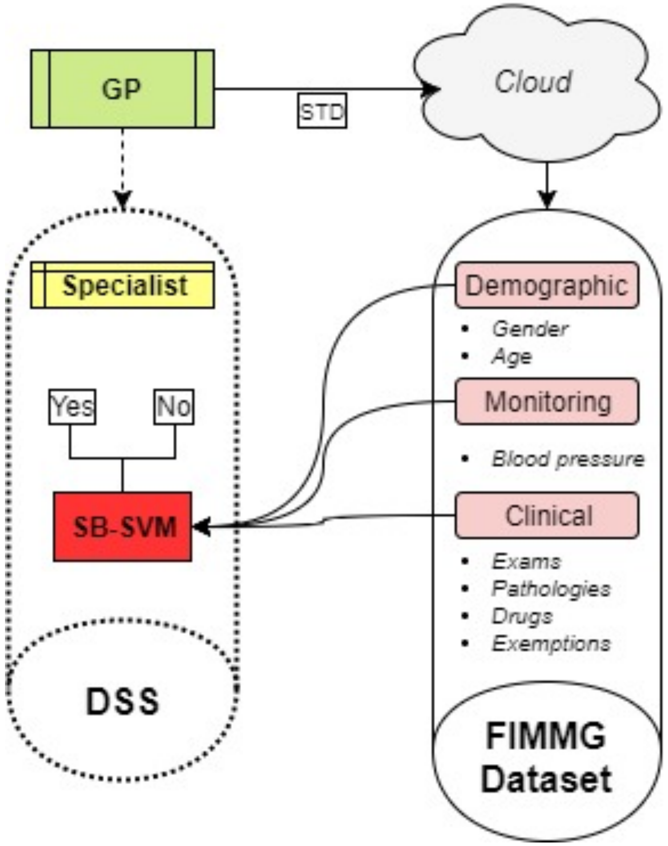
A Semi-Supervised Multi-Task Learning Approach for Predicting Short-Term Kidney Disease Evolution, *JBHI, 2020*

- ❑ **Covid-19 →** RISC-19 ICU registry

Predicting 5-day SOFA score at ICU admission in COVID-19 patients, *JAMA, 2020 [Under review]*

T2D

Objective



AIM: Type 2 Diabetes prediction from EHR

FIMMG Dataset challenges:

- High-dimensional Data *(2433x1863)*
- Sparsity *(missing values)*
- Unbalanced classes *(10:1)*

Sparse Balanced-Support Vector Machine

(SB-SVM)

- Lasso regularization

Bernardini M., Romeo L., Misericordia P., and Frontoni E., Discovering the Type 2 Diabetes in Electronic Health Records using the Sparse Balanced Support Vector Machine, IEEE *Journal of Biomedical and Health Informatics, 2019*

T2D

Experimental procedure

Case I
Is the SB-SVM approach able to predict T2D pathology using all set of EHR features?

Case II
Is the SB-SVM approach able to predict T2D pathology using only a subset of EHR features collected before T2D clinical diagnosis?

Case III
Is the SB-SVM approach able to predict T2D pathology using only a subset of EHR features collected before T2D clinical diagnosis within a uniform age group of subjects?

Dataset description	Count (%)	Mean (std)
Total patients:	2433	-
Control patients	2208 (0.91)	-
Diabetic patients	225 (0.09)	-
Total features	1841	-
Fields	**Count (%)**	**Mean (std)**
Demographic		
Gender:	-	-
Male	1186 (0.49)	-
Female	1247 (0.51)	-
Age (years)	-	58.00(±23.58)
<60	1374 (0.56)	-
60-80	535 (0.22)	-
>80	524 (0.22)	-
Monitoring		
Blood pressure (mmHg)		-
Systolic	3	135.52(±17.21)
Diastolic	3	80.83(±8.65)
Clinical		
Pathologies	877	-
Exemptions	70	-
Exams	396	-
Drugs	490	-

Bernardini M., Romeo L., Misericordia P., and Frontoni E., Discovering the Type 2 Diabetes in Electronic Health Records using the Sparse Balanced Support Vector Machine, IEEE *Journal of Biomedical and Health Informatics, 2019*

T2D

Experimental results

		CASE I		CASE II		CASE III	
Work	**Model**	**Recall%**	**AUC%**	**Recall%**	**AUC%**	**Recall%**	**AUC%**
	Baseline	mean std	mean std	mean std	mean std	mean std	mean std
[16], [18], [21]	SVM Lin	74.12 (4.02)	81.68 (5.60)	71.29 (3.65)	78.99 (4.30)	58.55 (5.80)	64.48 (5.39)
[16], [18], [21]	SVM Gauss	71.96 (4.22)	81.98 (4.84)	68.34 (4.41)	76.29 (4.40)	55.62 (8.08)	62.74 (9.22)
[18]	KNN	69.23 (4.97)	70.97 (5.06)	68.56 (5.57)	71.04 (6.09)	54.50 (7.16)	59.80 (8.10)
[17], [18], [20]	DT	80.99 (3.34)	87.79 (4.17)	72.98 (4.54)	77.56 (4.85)	58.98 (8.37)	61.87 (7.77)
[18], [20], [22]	RF	77.81 (5.66)	86.30 (4.24)	68.08 (6.36)	75.70 (4.61)	57.33 (5.74)	61.96 (9.47)
	Sparse SVM						
	SB-SVM	81.89 (4.03)	91.04 (4.16)	**74.64 (4.18)**	**81.43 (3.20)**	**65.33 (5.69)**	**68.90 (5.84)**
[24]	SCAD SVM	67.61 (4.41)	70.78 (4.20)	54.98 (4.09)	60.09 (4.13)	50.83 (9.97)	54.08 (10.41)
[25]	1-norm SVM	82.47 (3.47)	90.21 (3.65)	71.10 (4.27)	77.46 (5.76)	60.73 (7.15)	65.35 (8.38)
	Resampling						
[23]	DT + SMOTE	75.79 (4.72)	82.03 (2.73)	67.07 (3.06)	67.57 (4.26)	57.77 (8.67)	60.73 (10.35)
[22]	RF + SMOTE	71.63 (4.93)	86.34 (4.07)	58.15 (4.34)	77.10 (3.84)	57.66 (6.15)	68.57 (7.06)
	Features selection						
[16]	Ttest + LR ridge	80.91 (2.90)	89.81 (3.35)	73.14 (3.36)	78.89 (4.58)	61.35 (3.11)	67.47 (6.81)
[16]	Ttest + SVM Lin	76.81 (3.11)	88.99 (4.02)	72.42 (3.67)	79.00 (4.32)	54.07 (4.36)	60.56 (8.47)
[16]	Ttest + SVM Gauss	78.49 (3.07)	85.87 (4.34)	73.78 (2.62)	80.39 (4.02)	54.65 (7.23)	62.58 (5.15)
[16], [17]	ReliefF + LR ridge	83.02 (4.09)	91.39 (3.68)	74.03 (4.84)	80.34 (3.13)	57.54 (9.20)	66.66 (5.38)
[16], [17]	ReliefF + SVM Lin	**84.21 (3.24)**	91.24 (3.34)	74.36 (3.50)	81.01 (2.71)	58.23 (6.85)	66.16 (7.63)
[16], [17]	ReliefF + SVM Gauss	83.90 (3.15)	**91.85 (2.97)**	74.11 (2.38)	80.74 (1.84)	59.77 (5.27)	65.74 (6.53)
[16]	RFE-SVM + LR ridge	72.43 (5.27)	72.54 (5.31)	52.64 (1.51)	52.81 (1.67)	56.26 (4.12)	56.28 (4.24)
[16]	RFE-SVM + SVM Lin	71.87 (5.46)	72.26 (5.14)	52.27 (1.83)	52.31 (1.83)	55.23 (3.33)	55.50 (3.34)
	Deep Learning						
[43]	MLP	67.90 (3.55)	77.53 (4.31)	58.52 (5.43)	67.03 (6.31)	54.25 (5.37)	56.89 (7.72)
[44]	DBN	77.23 (4.23)	89.32 (3.47)	66.82 (5.91)	78.50 (6.97)	61.22 (10.26)	66.78 (14.68)

Bernardini M., Romeo L., Misericordia P., and Frontoni E., Discovering the Type 2 Diabetes in Electronic Health Records using the Sparse Balanced Support Vector Machine, IEEE *Journal of Biomedical and Health Informatics, 2019*

T2D

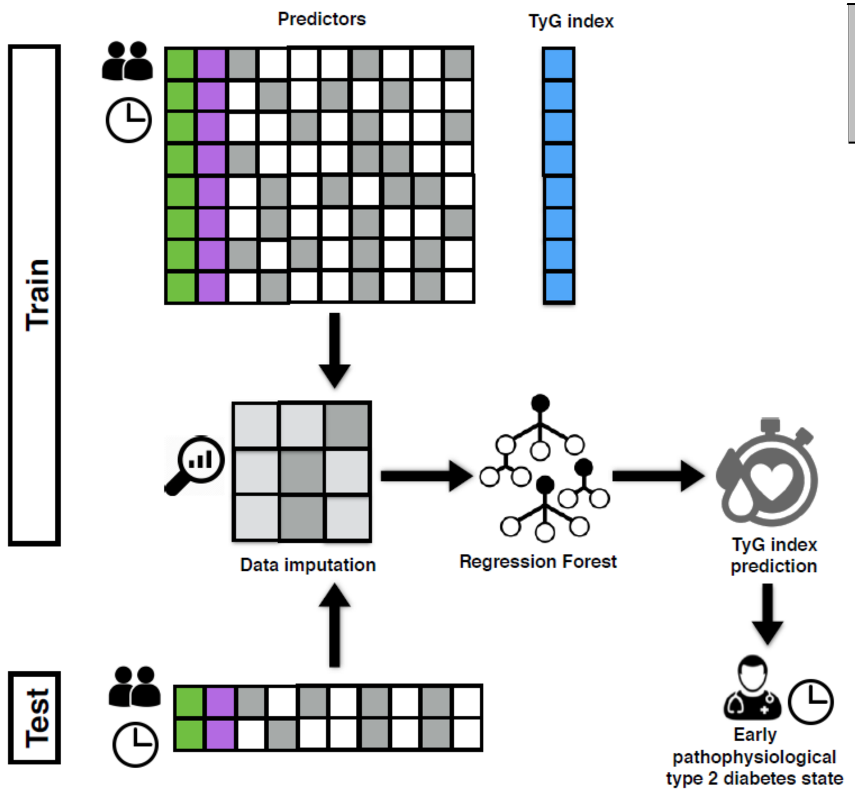
Experimental results

Rank	Case I	Case II	Case III
1	HbA1c (*EP*)	Age	Arterial hypertension(stage II, III) (*E*)
2	Age	Mean diastolic (*BP*)	Weight (*EP*)
3	Gfr using MDRD formula (*EP*)	Max diastolic (*BP*)	Arterial hypertension(none organ damage) (*E*)
4	Metformin (*D*)	Mean systolic (*BP*)	Creatinine clearance (*EP*)
5	Heart failure (*P*)	Arterial hypertension (*P*)	Fundus oculi (*EP*)
6	Microalbuminuria (*EP*)	Max systolic (*BP*)	Aorta aneurysm (*P*)
7	Insulin glargine (*D*)	Min diastolic (*BP*)	Moxifloxacin (*D*)
8	Arterial hypertension (*P*)	Min systolic (*BP*)	Myasthenia gravis (*P*)
9	Hyperlipidaemia/Dyslipidaemia (*P*)	Creatinine clearance (*EP*)	Netilmicin (*D*)
10	Cancer pancreas (*P*)	Heart failure (*P*)	Myasthenia gravis (*E*)

Bernardini M., Romeo L., Misericordia P., and Frontoni E., Discovering the Type 2 Diabetes in Electronic Health Records using the Sparse Balanced Support Vector Machine, IEEE *Journal of Biomedical and Health Informatics, 2019*

IR-1

Objective



AIM: Identification of T2D early-risk clinical factors based on TyG index

$$\mathrm{TyG}_i = \frac{\ln(TG_i \cdot Gb_i)}{2}$$

FIMMG_obs Dataset challenges:

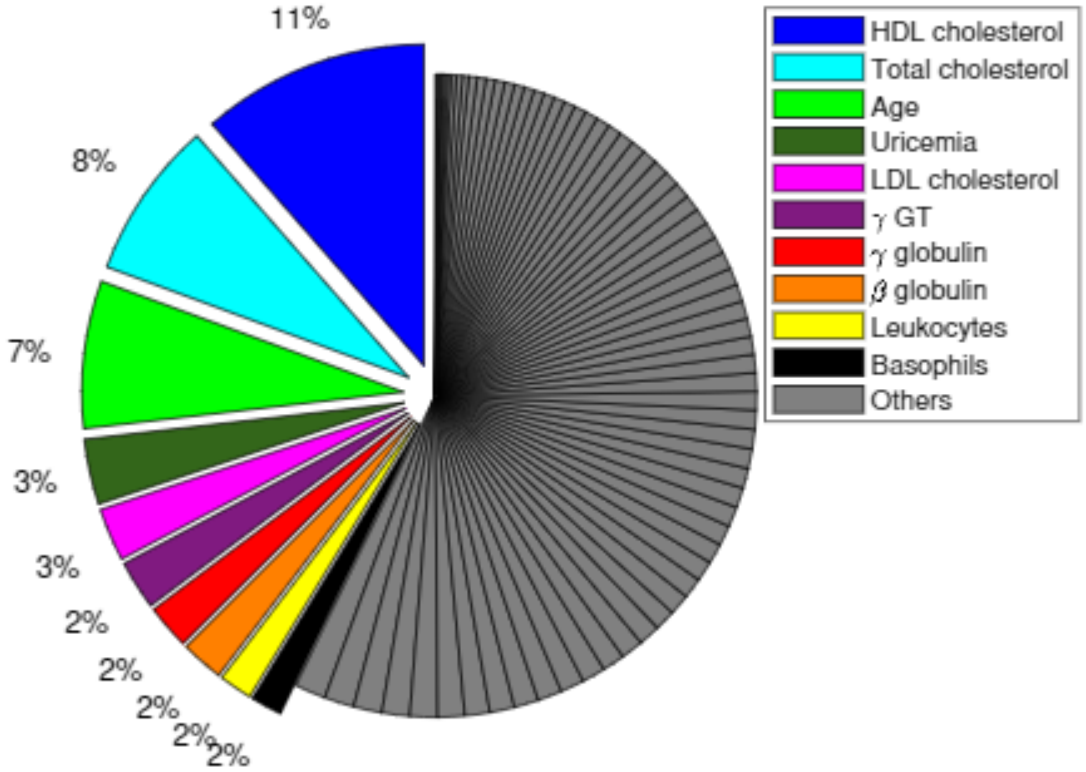
- Temporal sequence data (lab test values)
  - 968 patients not affected by T2D
  - 2276 TyG observations
- Longitudinal time window (9 years)
- Sparsity (missing values)

TyG based-Ensemble Regression Forest (TyG-er)

Bernardini M., Morettini M., Romeo L., Frontoni E., and Burattini L., TyG-er: an Ensemble Regression Forest Approach for Identification of Clinical Factors related to Insulin Resistance Condition using Electronic Health Records, *Computers in Biology and Medicine, 2019*

IR-1

Experimental results



Bernardini M., Morettini M., Romeo L., Frontoni E., and Burattini L., TyG-er: an Ensemble Regression Forest Approach for Identification of Clinical Factors related to Insulin Resistance Condition using Electronic Health Records, *Computers in Biology and Medicine, 2019*

IR-2

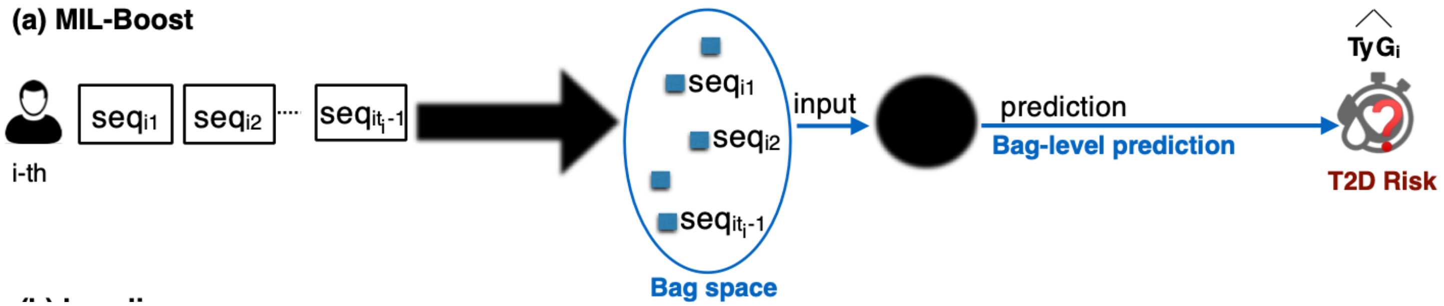
Objective

AIM: Prediction of the pre-diabetes risk condition based on TyG index

$$\mathrm{TyG}_i = \frac{\ln(TG_i \cdot Gb_i)}{2}$$

FIMMG_pred Dataset challenges:

- 179 control patients (70%)
- 77 high-risk patients (30%)
- 681 '*seq*' past instances



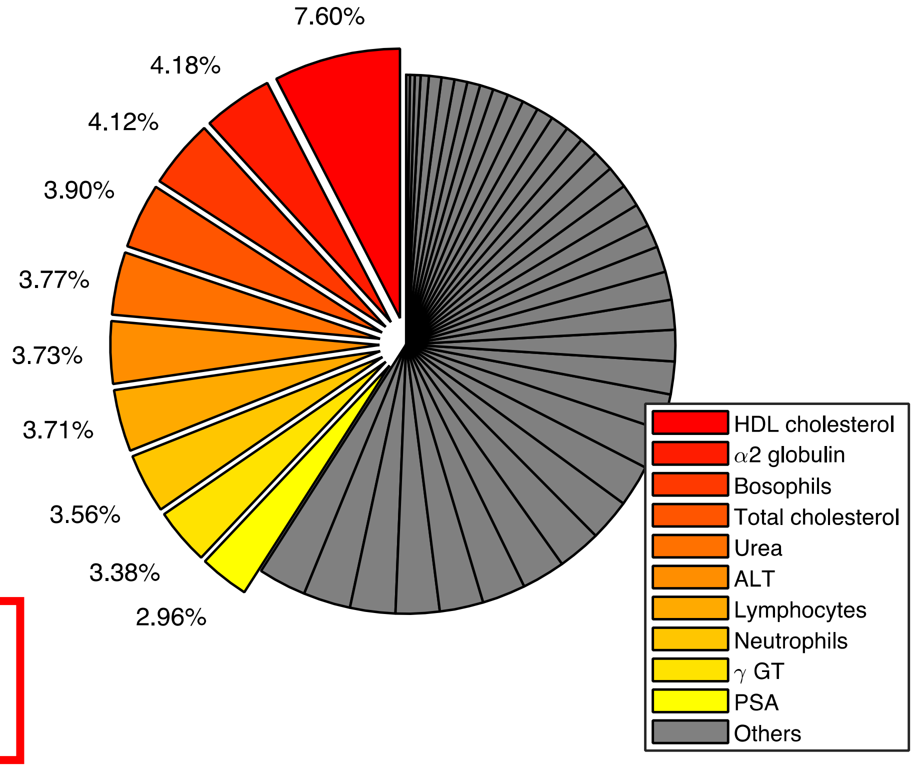
TyG based-Multiple Instance Learning Boosting (MIL-Boost)

Bernardini M., Morettini M., Romeo L., Frontoni E., and Burattini L., Early temporal prediction of Type 2 Diabetes Risk Condition from a General Practitioner Electronic Health Record: A Multiple Instance Boosting Approach, *Artificial Intelligence in Medicine, 2019*

IR-2

Experimental results

Baseline	*Accuracy*		*F1*		*Precision*		*Recall*		*AUC*	
	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG
DT	0.77	0.67	0.72	0.60	0.75	0.61	0.71	0.61	0.79	0.64
RF	0.77	0.68	0.72	0.57	0.74	0.61	0.72	0.58	0.84	0.66
Boost	0.76	**0.70**	0.71	0.59	0.73	0.62	0.72	0.59	0.82	0.58
KNN	0.69	0.63	0.57	0.49	0.62	0.50	0.58	0.51	0.64	0.56
SVM lin	0.73	0.67	0.68	0.62	0.70	0.63	0.68	0.62	0.75	0.66
SVM lasso	0.77	0.65	0.70	0.57	0.76	0.60	0.70	0.57	0.80	0.63
SVM Gauss	0.70	**0.70**	0.41	0.41	0.35	0.35	0.50	0.50	0.50	0.50
Majority vote	*Accuracy*		*F1*		*Precision*		*Recall*		*AUC*	
	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG
DT	0.78	0.68	0.74	0.62	0.74	0.65	0.76	0.66	0.84	**0.74**
RF	0.77	0.65	0.73	0.57	0.73	0.60	0.75	0.59	0.83	0.69
Boosting	0.79	**0.70**	0.74	0.61	0.75	0.63	0.75	0.62	0.87	0.68
KNN	0.63	0.60	0.50	0.42	0.51	0.41	0.52	0.46	0.64	0.54
SVM lin	0.75	0.64	0.69	0.57	0.70	0.59	0.71	0.60	0.81	0.65
SVM lasso	0.77	0.66	0.69	0.57	0.71	0.59	0.70	0.59	0.81	0.66
SVM Gauss	0.63	0.66	0.38	0.39	0.31	0.33	0.50	0.50	0.46	0.50
MIL-Boost	*Accuracy*		*F1*		*Precision*		*Recall*		*AUC*	
	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG	yesTyG	noTyG
	0.83	**0.70**	**0.81**	**0.68**	**0.82**	**0.69**	**0.83**	**0.70**	**0.89**	0.71



Bernardini M., Morettini M., Romeo L., Frontoni E., and Burattini L., Early temporal prediction of Type 2 Diabetes Risk Condition from a General Practitioner Electronic Health Record: A Multiple Instance Boosting Approach, *Artificial Intelligence in Medicine, 2019*

SS-MTL x CKD

Objective

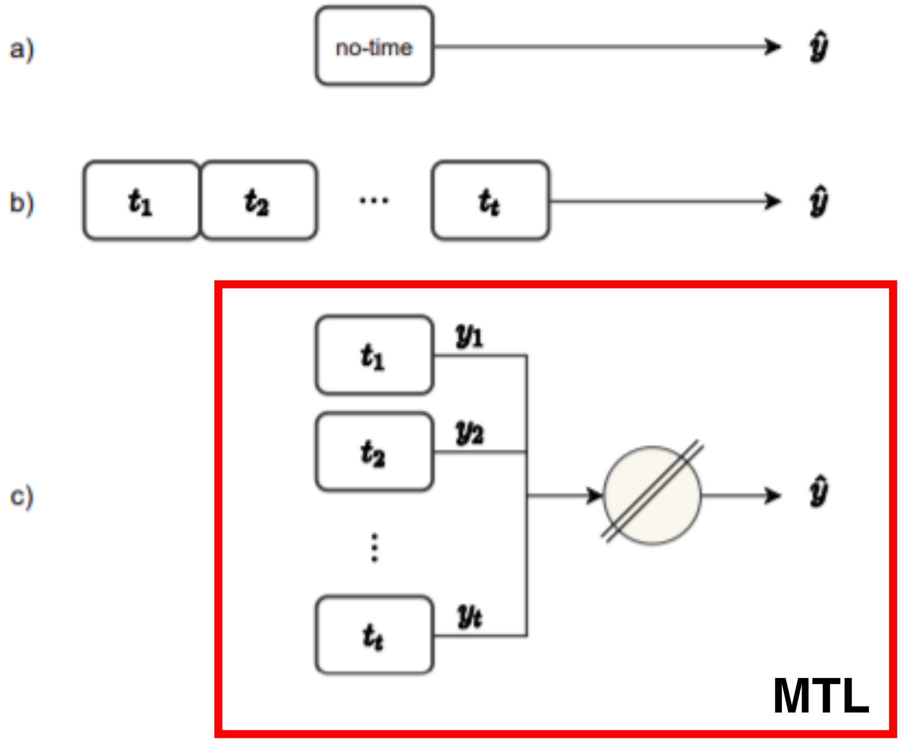
AIM: Prediction of eGFR index (kidney disease marker) based on a fused semi-supervised (SSL) and multi-task learning

eGFR=f(creatinin, sex, age)

SS-MTL

CKD stage	eGFR [ml/min/1.73m^2]	%
I	$\geq$ 90: normal	19.35
II	60–89: mild reduction	53.31
IIIa	45–59: mild-moderate reduction	16.59
IIIb	30–44: moderate-severe	7.49
IV	15–29: sever reduction	2.85
V	< 15: kidney failure	0.41

	Pathologies	Drugs	Exams	Lab tests	Overall	Overall*
Predictors	38	309	135	50	494	496
Total samples	5660	9533	9530	7479	6829	6829
Labeled samples	707	1853	1887	1877	1833	1833
Unlabeled samples	4953	7680	7643	5602	4996	4996



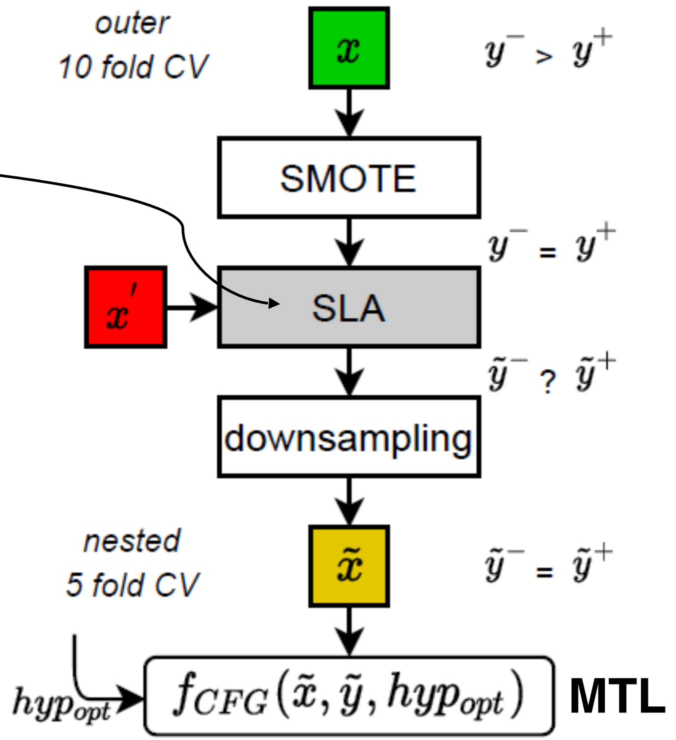
Bernardini M., Romeo L., Frontoni E., and Amini M. R., A Semi-Supervised Multi-Task Learning Approach for Predicting Short-Term Kidney Disease Evolution, *IEEE Journal of Biomedical and Health Informatics, 2021*

CKD

Experimental procedure

Self-Learning Algorithm (SLA)

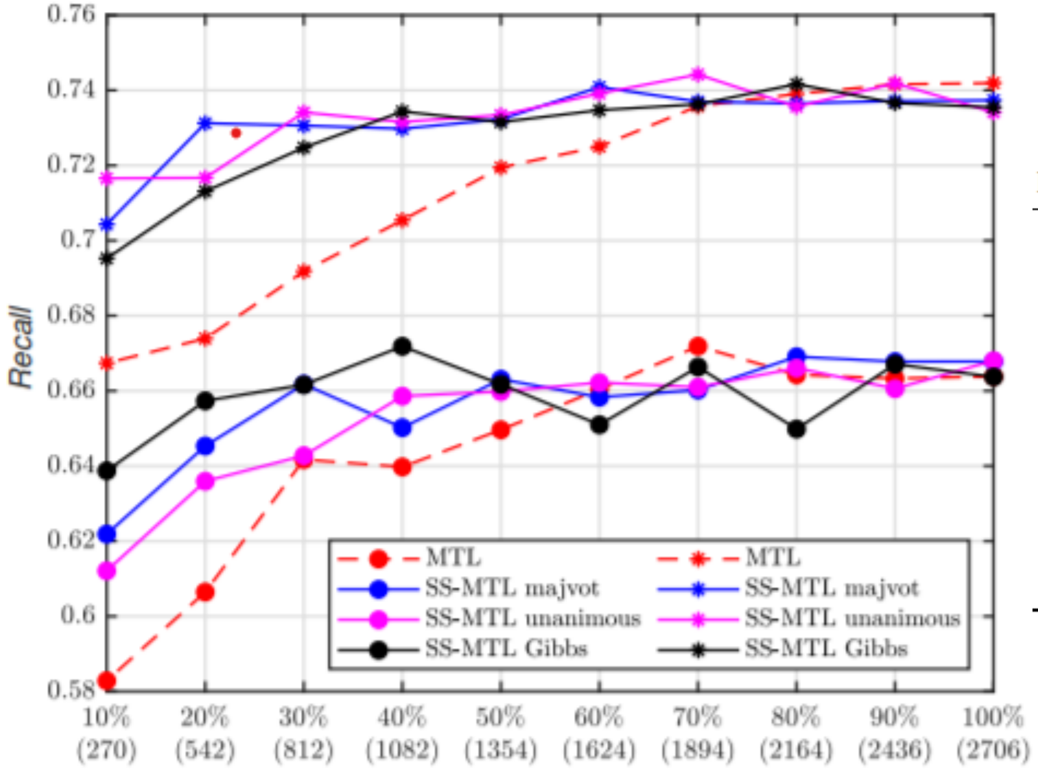
Input: Labeled and Unlabeled training sets: Z_l, V_u
Initialize
Train a classifier H on Z_l
Set $\widetilde{Z}_u \leftarrow \varnothing$
repeat
  Compute the margin threshold θ from (8)
  $S \leftarrow \{ (x', y') \mid x' \in V_u; m_Q(x') \geq \theta \wedge y' = sign(H(x')) \}$
  $\widetilde{Z}_u \leftarrow \widetilde{Z}_u \cup S$, $V_u = V_u \backslash S$
  Learn a classifier H by optimizing a global loss function on Z_l and $\widetilde{Z}_u$
until V_u is empty or no adds to $\widetilde{Z}_u$;
Output: The final $\widetilde{Z} = Z_l \cup \widetilde{Z}_u$



Bernardini M., Romeo L., Frontoni E., and Amini M. R., A Semi-Supervised Multi-Task Learning Approach for Predicting Short-Term Kidney Disease Evolution, *IEEE Journal of Biomedical and Health Informatics, 2021*

CKD

Experimental results



	Overall			Overall*		
Rank	Field	Predictors	W [%]	Field	Predictors	W [%]
1)	D	Valsartan and diuretics	3.78	M	Age	44.85
2)	D	Colecalciferol (vitamin D3)	3.59	D	Furosemide	3.26
3)	D	Levothyroxine	3.17	D	Metformin	2.42
4)	D	Alfuzosin	3.16	D	Amlodipine	1.40
5)	D	Lansoprazole	3.08	D	Ramipril and amlodipine	1.38
6)	D	Furosemide	2.89	D	Valsartan and diuretics	1.32
7)	D	Acetylsalicylic acid	2.78	D	Pravastatin	1.28
8)	D	Pantoprazole	2.67	D	Atorvastatin	1.27
9)	E	Interview and evaluation	2.51	D	Bisoprolol	1.19
10)	D	Nebivolol	2.28	D	Omeprazole	1.16
		Others	70.09		*Others*	40.47

Bernardini M., Romeo L., Frontoni E., and Amini M. R., A Semi-Supervised Multi-Task Learning Approach for Predicting Short-Term Kidney Disease Evolution, *IEEE Journal of Biomedical and Health Informatics, 2021*

Covid-19

Motivation

University of Zurich[UZH]

SOFA: Sequential **O**rgan **F**ailure **A**ssessment **score**

SOFA score

Continuous monitoring of COVID-19 ICU care quality

Predicting complications based on 6 organs dysfunction factors

Respiratory

Cardiovascula
r

Hepatic

Coagulation

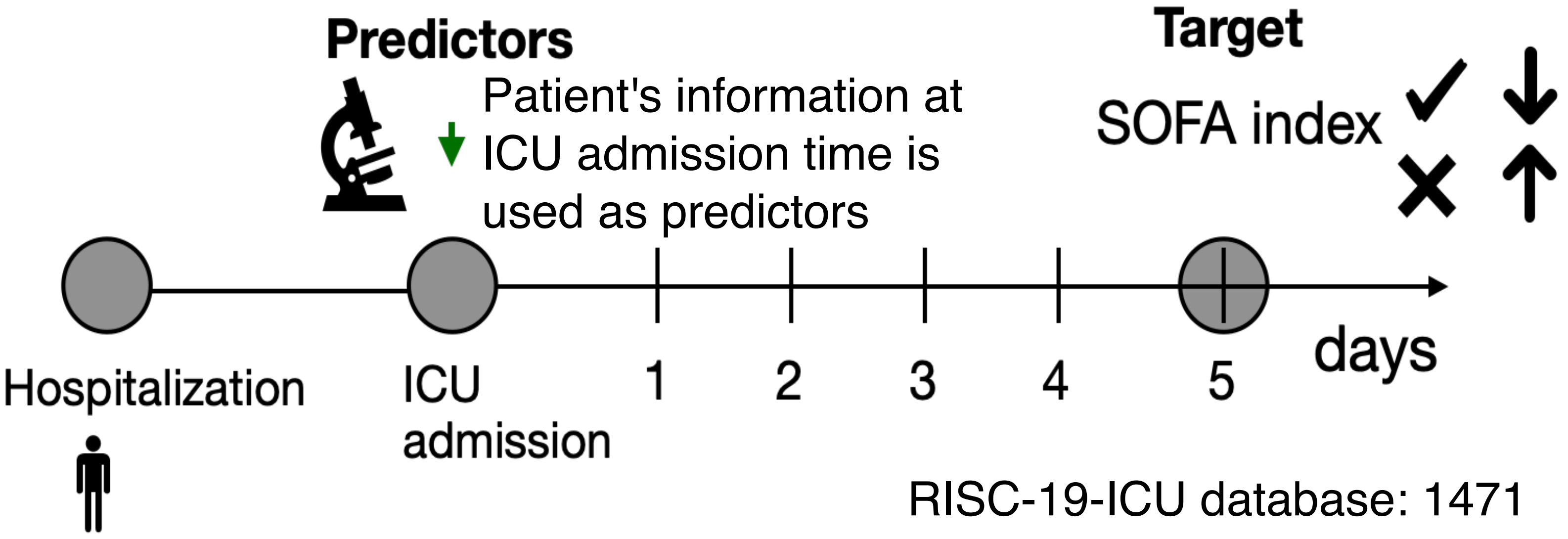
Renal

Neurological

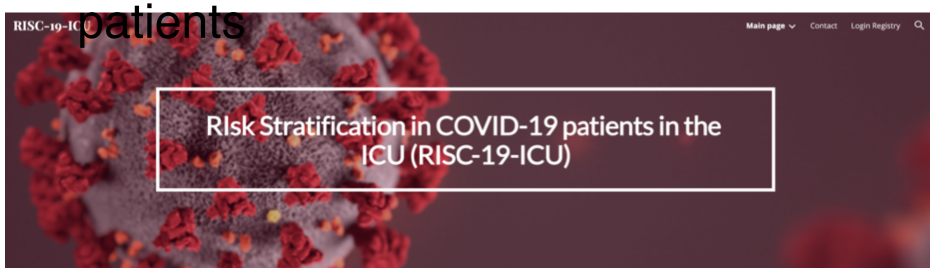
Montomoli J., Romeo L., Moccia S., **Bernardini M.**, Migliorelli L., Donati A., Carsetti A., Garcia P., Fumeaux T., Guerci P., Schuepbach R., Frontoni E., RISC-19-ICU Investigators, Hilty M., Predicting 5-day SOFA score at ICU admission in COVID-19 patients: a proof-of-concept study using prospectively collected data from 1613 patients in the RISC-19-ICU registry, *Journal of the American Medical Association*, *2020 [Under Review]*

Covid-19

Objective



RISC-19-ICU database: 1471 patients



<u>AIM:</u> Prediction of complications and risk stratification of COVID-19 ICU patients based on SOFA score using longitudinal EHR data

Montomoli J., Romeo L., Moccia S., **Bernardini M.**, Migliorelli L., Donati A., Carsetti A., Garcia P., Fumeaux T., Guerci P., Schuepbach R., Frontoni E., RISC-19-ICU Investigators, Hilty M., Predicting 5-day SOFA score at ICU admission in COVID-19 patients: a proof-of-concept study using prospectively collected data from 1613 patients in the RISC-19-ICU registry, *Journal of the American Medical Association*, *2020* *[Under Review]*

Covid-19

Experimental procedure

Clinical → Preprocessing → ML model → Clinical Decision Support System

- Clinical: ICU
- Preprocessing: Filtering; Data standardization
- ML model: XGBoost; Regression; Classification
- Clinical Decision Support System: Accuracy; Interpretability

RISK-19 ICU registry: https://www.risc-19-

Classification Task

Target variable: SOFA variation at day 5

$\Delta_{5,0} = \boldsymbol{Sofa_5} - \boldsymbol{Sofa_0}$

- *worsening:* $\Delta_{5,0} >= +2$
- *improvement:* $\Delta_{5,0} <= -2$

Regression Task

Target variable: SOFA value at day 5

Input/Predictors

Patient characteristics (laboratory exams) at the time of ICU admission

Model

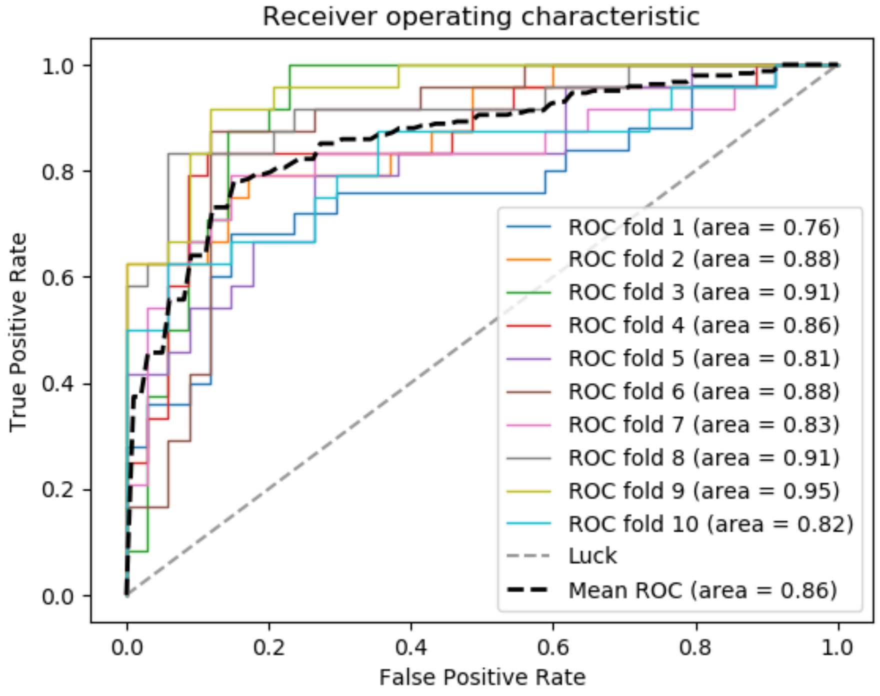
XGBoost (XGB)

Montomoli J., Romeo L., Moccia S., **Bernardini M.**, Migliorelli L., Donati A., Carsetti A., Garcia P., Fumeaux T., Guerci P., Schuepbach R., Frontoni E., RISC-19-ICU Investigators, Hilty M., Predicting 5-day SOFA score at ICU admission in COVID-19 patients: a proof-of-concept study using prospectively collected data from 1613 patients in the RISC-19-ICU registry, *Journal of the American Medical Association*, *2020 [Under Review]*

Covid-19

Experimental results

University of Zurich[UZH]



Regression

MAE	MSE	R2
2.68	12.16	0.41

Classification

Accuracy	F1	Precision	Recall	AUC
0.78	0.78	0.78	0.78	0.86

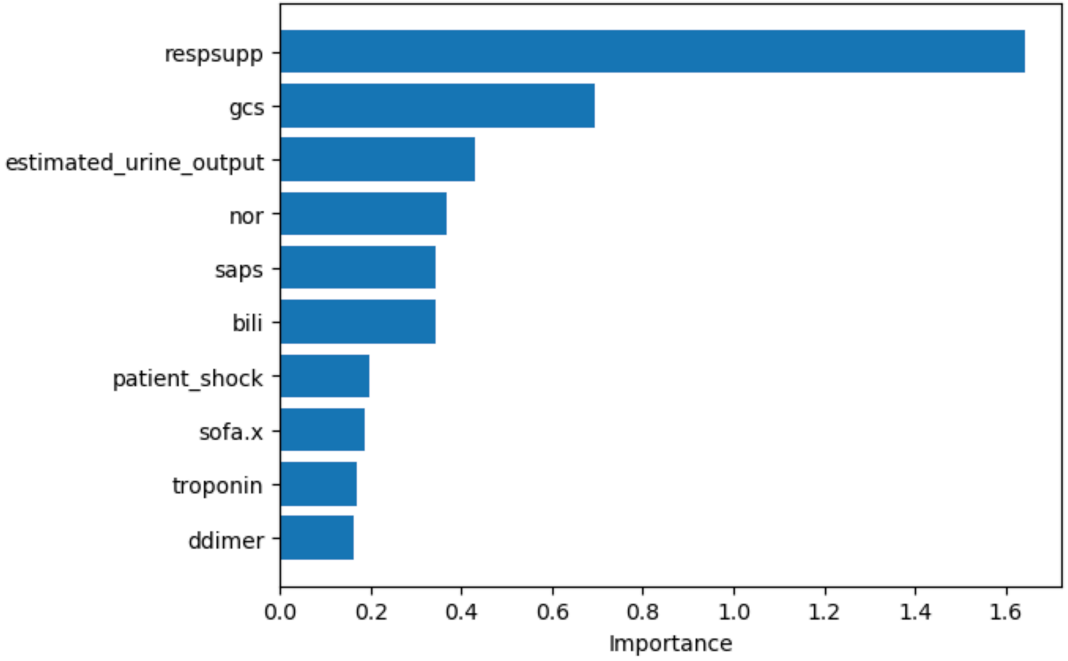
Confusion matrix

Worsening	**83%(320)**	17%(45)
Improvement	28%(80)	**72%(210)**
	Worsening	Improvement

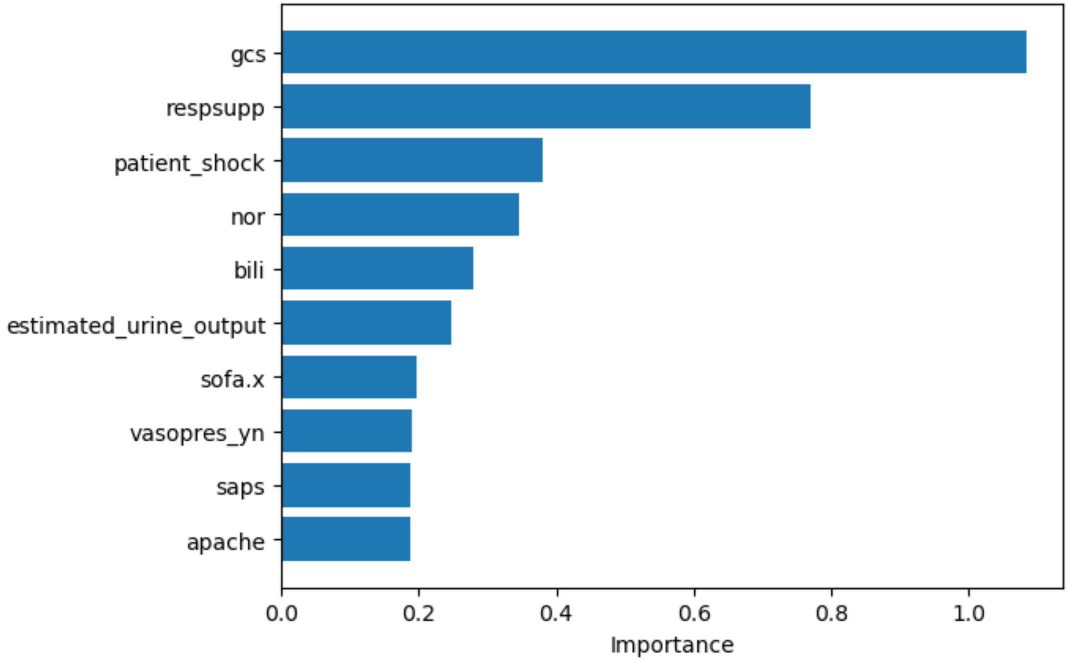
Montomoli J., Romeo L., Moccia S., **Bernardini M.**, Migliorelli L., Donati A., Carsetti A., Garcia P., Fumeaux T., Guerci P., Schuepbach R., Frontoni E., RISC-19-ICU Investigators, Hilty M., Predicting 5-day SOFA score at ICU admission in COVID-19 patients: a proof-of-concept study using prospectively collected data from 1613 patients in the RISC-19-ICU registry, *Journal of the American Medical Association, 2020 [Under Review]*

Covid-19

Experimental results



Regression Task



Classification Task

Montomoli J., Romeo L., Moccia S., **Bernardini M.**, Migliorelli L., Donati A., Carsetti A., Garcia P., Fumeaux T., Guerci P., Schuepbach R., Frontoni E., RISC-19-ICU Investigators, Hilty M., Predicting 5-day SOFA score at ICU admission in COVID-19 patients: a proof-of-concept study using prospectively collected data from 1613 patients in the RISC-19-ICU registry, *Journal of the American Medical Association*, *2020 [Under Review]*

Conclusions

Final considerations

• High-dimensional & heterogeneous data were managed during the preprocessing stage (i.e., features selection, standardization, outliers detection);

• Unbalanced setting was managed by adopting specific optimization metrics and/or optimal thresholds for the posterior probabilities of the decision function;

• Sparse labeling of the predictors was managed with standard static data imputation techniques (i.e, extra-values, mean, median, K-Nearest Neighbors (KNN)), while sparse labeling of the targets was managed by proposing semi-supervised learning (SSL) techniques;

• Temporal ambiguity was managed by proposing different experimental configurations (i.e., time-invariant, stacked-temporal, Multiple Instance Learning (MIL), Multi-Task Learning (MTL) with temporal relatedness/constraints);

• Interpretability/explainability of the results was managed offering always a features importance ranking of the most discriminative predictors to clinically understand the outcome of the ML model;

• Generalization was managed by adopting regularization strategies.

Conclusions

Open challenges

These healthcare ecosystems of predictive precision medicine are not yet being used at a large scale.

The removal of several obstacles could accelerate this transformation process:

1. The first obstacle is the preprocessing stage (i.e., data cleaning, preparation, and standardization);

2. The second obstacle is the ongoing need to build layers of abstraction that permit various users to interact with ML frameworks at their own knowledge level;

3. The third obstacle is the commonization of components.User-friendly ML frameworks should be designed as modular blocks and selected depending on the objective of the clinical task.

Publications

Journal

- Liciotti D., **Bernardini M.**, Romeo L., and Frontoni E., A Sequential Deep Learning Application for Recognising Human Activities in Smart Homes, *Neurocomputing 396 (2020): 501-513*
- **Bernardini M.**, Romeo L., Misericordia P., and Frontoni E., Discovering the Type 2 Diabetes in Electronic Health Records using the Sparse Balanced Support Vector Machine, *IEEE Journal of Biomedical and Health Informatics 24.1 (2019): 235-246*
- **Bernardini M.**, Morettini M., Romeo L., Frontoni E., and Burattini L., TyG-er: An ensemble Regression Forest approach for identification of clinical factors related to insulin resistance condition using Electronic Health Records, *Computers in Biology and Medicine 112 (2019): 103358*
- **Bernardini M.**, Morettini M., Romeo L., Frontoni E., and Burattini L., Early temporal prediction of Type 2 Diabetes Risk Condition from a General Practitioner Electronic Health Record: A Multiple Instance Boosting Approach, *Artificial Intelligence in Medicine (2020): 101847*
- Frontoni E., Romeo L., **Bernardini M.**, Moccia S., Migliorelli L., Paolanti M, Ferri A., Misericordia P., Mancini A., Zingaretti P., A Decision Support System for Diabetes Chronic Care Models Based on General Practitioner Engagement and EHR Data Sharing, *IEEE Journal of Translational Engineering in Health and Medicine 8 (2020): 1-12*
- **Bernardini M.**, Romeo L., Frontoni E., and Amini M. R., A Semi-Supervised Multi-Task Learning Approach for Predicting Short-Term Kidney Disease Evolution, *IEEE Journal of Biomedical and Health Informatics (2021)*

Publications

International Conference

- Calamanti C., Cenci A., **Bernardini M.**, Frontoni E., and Zingaretti P. A Clinical Decision Support System for Chronic Venous Insufficiency. *In ASME International Design Engineering Technical Conferences and Computers and Information in Engineering Conference, 2017*
- Calamanti C., Paolanti M., Romeo L., **Bernardini M.**, and Frontoni E. Machine learning-based approaches to analyse and improve the diagnosis of endothelial dysfunction. *In ASME International Design Engineering Technical Conferences and Computers and Information in Engineering Conference, 2018 [**best paper award**]*
- Frontoni E., Loncarski J., Pierdicca R., **Bernardini M.**, and Sasso M., Cyber physical systems for industry 4.0: Towards real time virtual reality in smart manufacturing. *In International Conference on Augmented Reality, Virtual Reality and Computer Graphics, 2018*
- Paolanti, M., Placidi, V., **Bernardini, M.**, Felicetti, A., Pietrini, R., and Frontoni, E., An agent-based WCET analysis for Top-View Person Re-Identification. *In International Workshop on Real Time compliant Multi-Agent Systems (RTcMAS), IJCAI-ECAI, 2018 [**oral presentation**]*

Publications

International Conference

- **Bernardini M.**, Ferri A., Migliorelli L., Moccia S., Romeo L., Silvestri S., Tiano L., and Mancini A., Augmented Microscopy for DNA Damage Quantification: a Machine Learning Tool for Environmental, Medical and Health Sciences. *In 15th IEEE/ASME International Conference on Mechatronic and Embedded Systems and Applications, 2019*

- Migliorelli L., Cenci A., **Bernardini M.**, Romeo L., Moccia S., and Zingaretti P. A cloud-based healthcare infrastructure for neonatal intensive-care units. *In 15th IEEE/ASME International Conference on Mechatronic and Embedded Systems and Applications, 2019*

- Ferri A., Rosati R., **Bernardini M.**, Gabrielli L., Casaccia S., Romeo L., Monteriù A., and Frontoni E., Towards the Design of a Machine Learning-based Consumer Healthcare Platform powered by Electronic Health Records and measurement of Lifestyle through Smartphone Data. *In IEEE 23rd International Symposium on Consumer Technologies, 2019*

Publications

Under review

- Montomoli J., Romeo L., Moccia S., **Bernardini M.**, Migliorelli L., Donati A., Carsetti A., Garcia P., Fumeaux T., Guerci P., Schuepbach R., Frontoni E., RISC-19-ICU Investigators, Hilty M., Predicting 5-day SOFA score at ICU admission in COVID-19 patients: a proof-of-concept study using prospectively collected data from 1613 patients in the RISC-19-ICU registry, *Journal of the American Medical Association, (2020)*