

2024 SNUBH Datathon예선

예선 성능 평가 [NARAK]

주최/주관



SNU AI.MED
서울대학교 의료 인공지능 융합연구 양성 사업단



AI NATION

후원



AWS코리아



KHIDI 한국보건산업진흥원



IITP 정보통신기획평가원



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- CITI 이수 여부(이미지첨부)

팀 기본정보

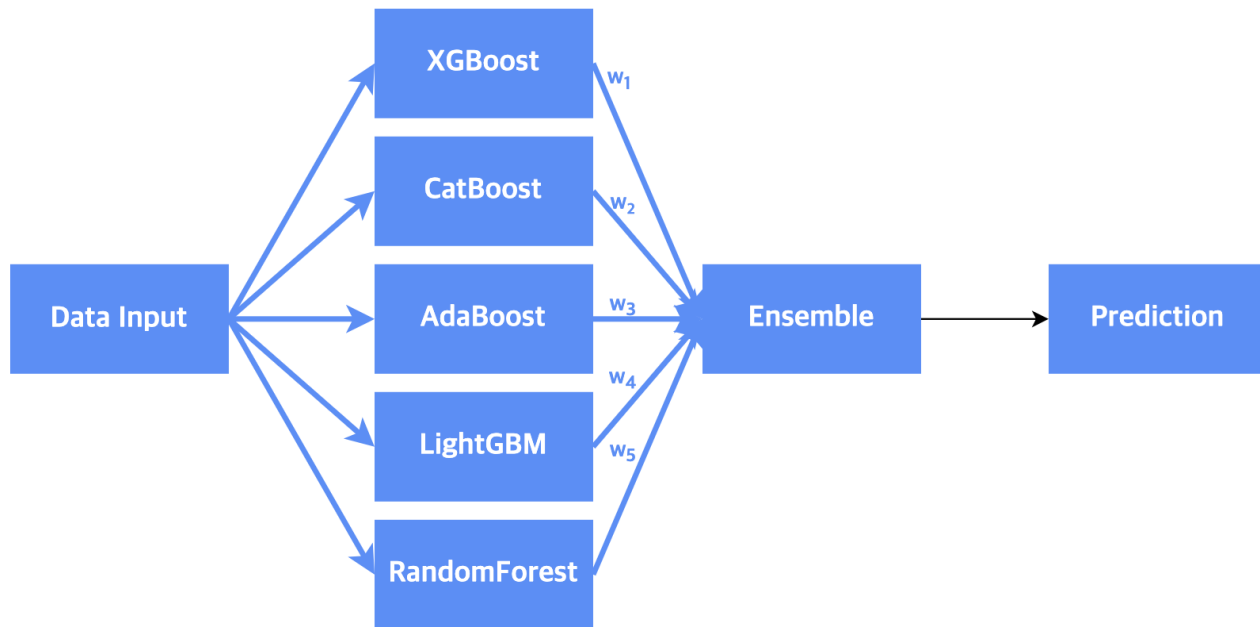
·팀명: NARAK(Nephrology Advanced Research and Analysis in Korea)

· 팀원 설명

- 박준범 (서울대학교 기계공학부 20학번)
- 김시훈 (서울대학교 전기정보공학부 21학번)
- 이윤서 (가톨릭대학교 컴퓨터공학부 20학번)
- 손재혁 (서울대학교 전기정보공학부 24학번)

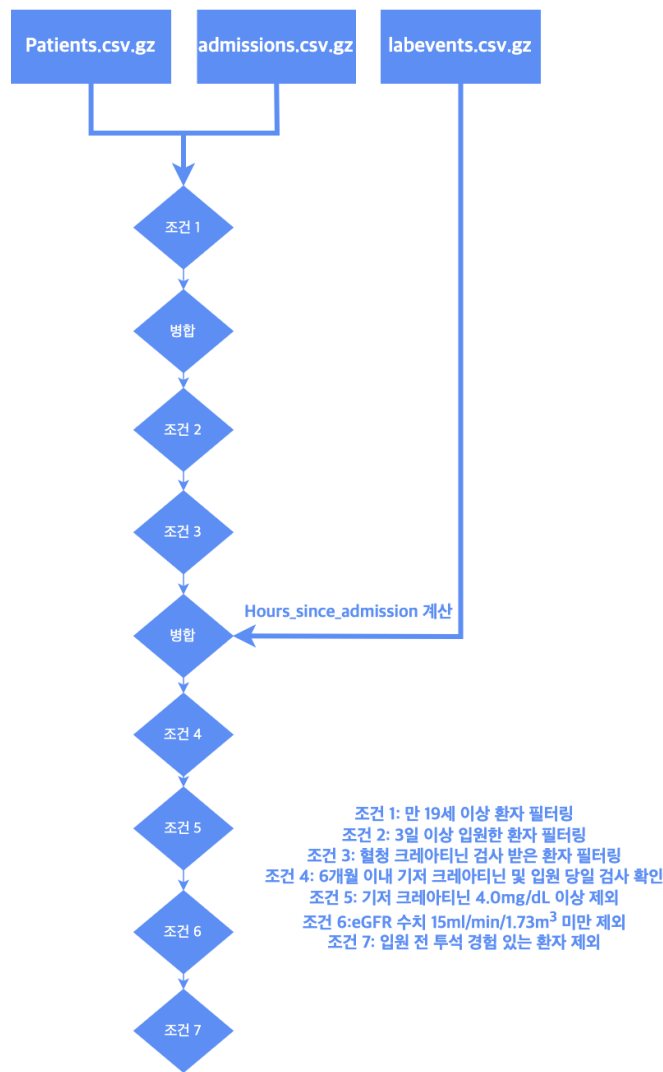
AI 모델명

- AKI 여부를 예측하기 위해서 이진 분류 모델을 사용
- 기본 모델: XGBoost, CatBoost, AdaBoost, LightGBM, RandomForest 를 각 F1-score의 가중치를 사용하여 enser



모델 상세정보

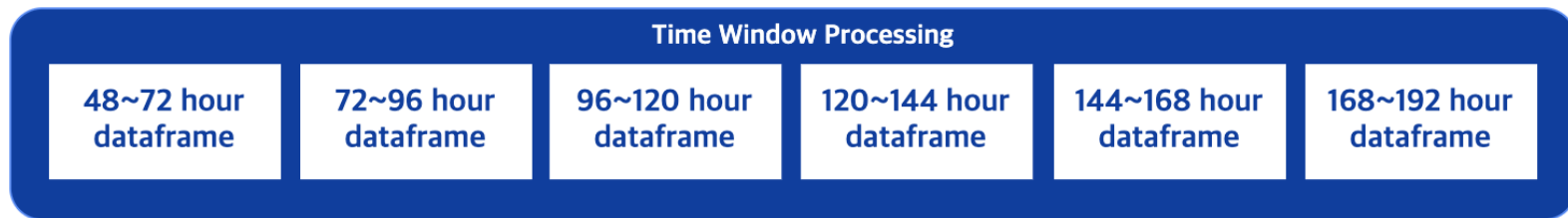
- Dataset의 피쳐들을 추출하여 조건들에 따라 필터링 후 병합
- 결측치가 발생 할 경우 결측치 비율 계산하며 결측치 제거
- 각 피쳐 정보들을 병합 및 정리 실행
- 피쳐들을 Time Window로 나눠 트레이닝 및 결과 추출



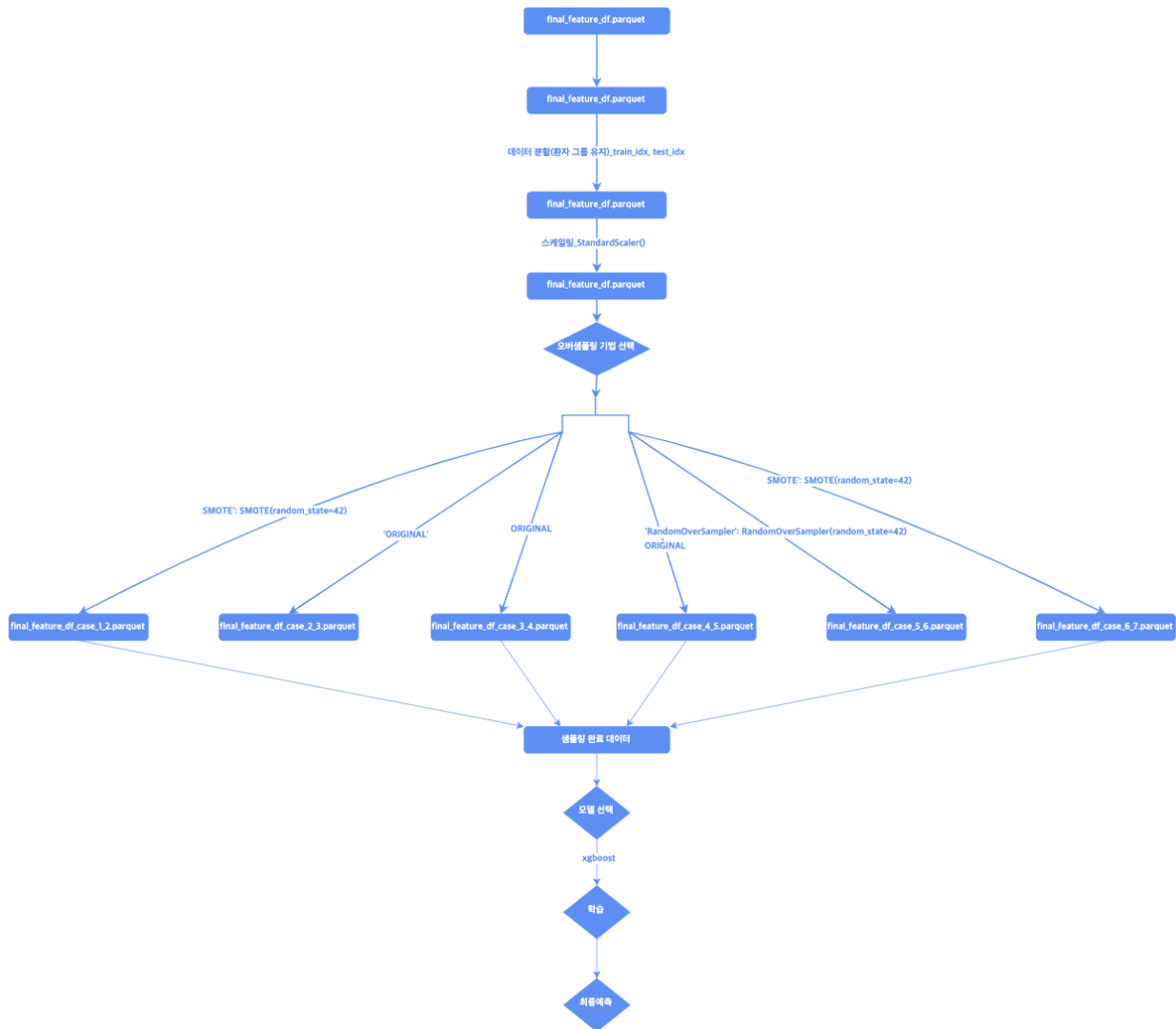
Extracted Features

- Age
- Gender
- Urine Output
- Vasopressor Amount
- Weight
- BMI
- Race
- Admission Time
- Length of Stay
- Baseline Creatinine
- eFGR
- Number of Diagnoses
- Number of Procedures
- Drug severity
- Drug mortality
- Usage of Nephrotoxic
- Renal Replacement Therapy
- Invasive mechanical ventilation
- Lab Measurements(Hemoglobin, Potassium etc.)
- Vital signs(Heart rate, Respiratory rate etc.)

데이터 정리 및 결측치 처리 & Time Window별 데이터셋 생성



학습



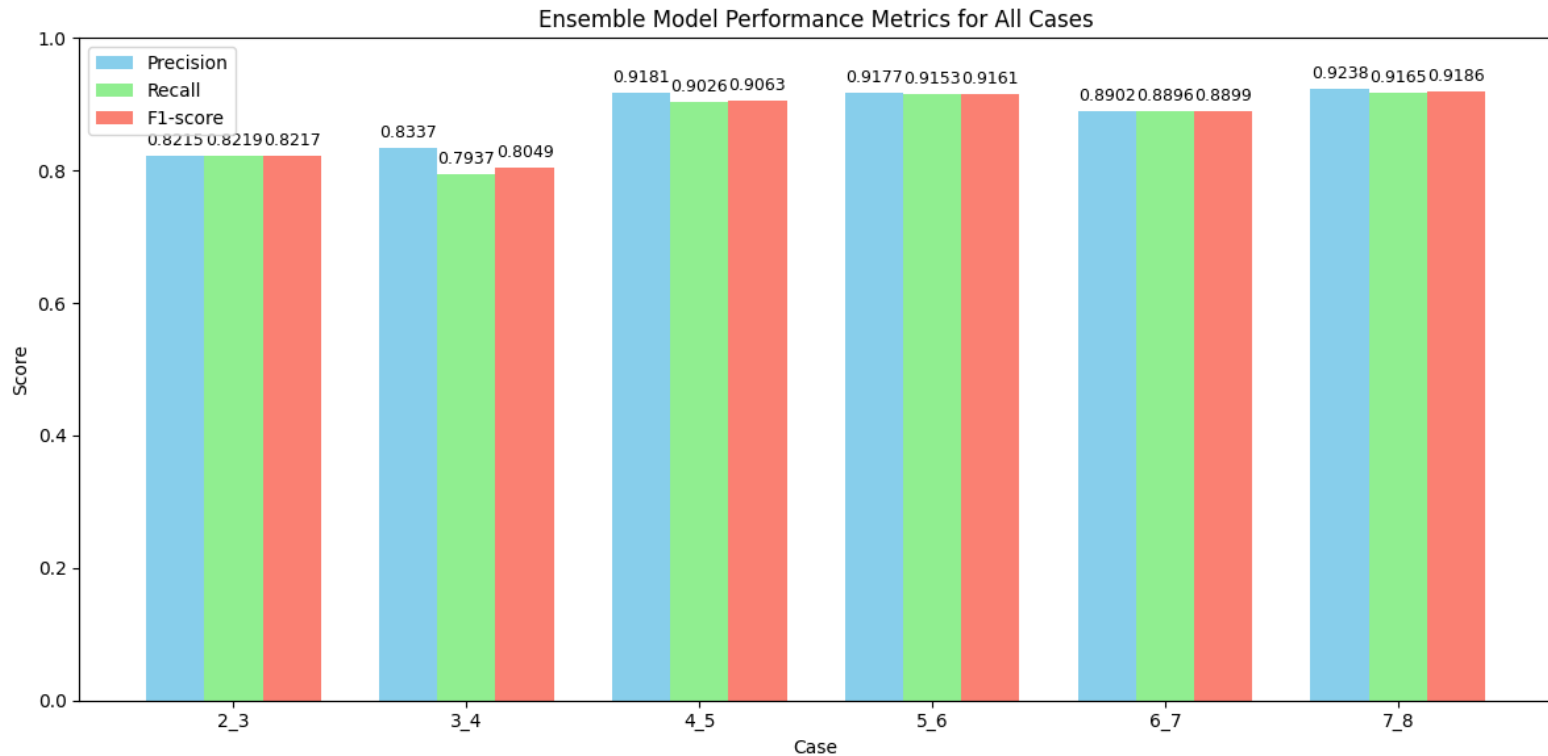
개발환경

Package	Version				

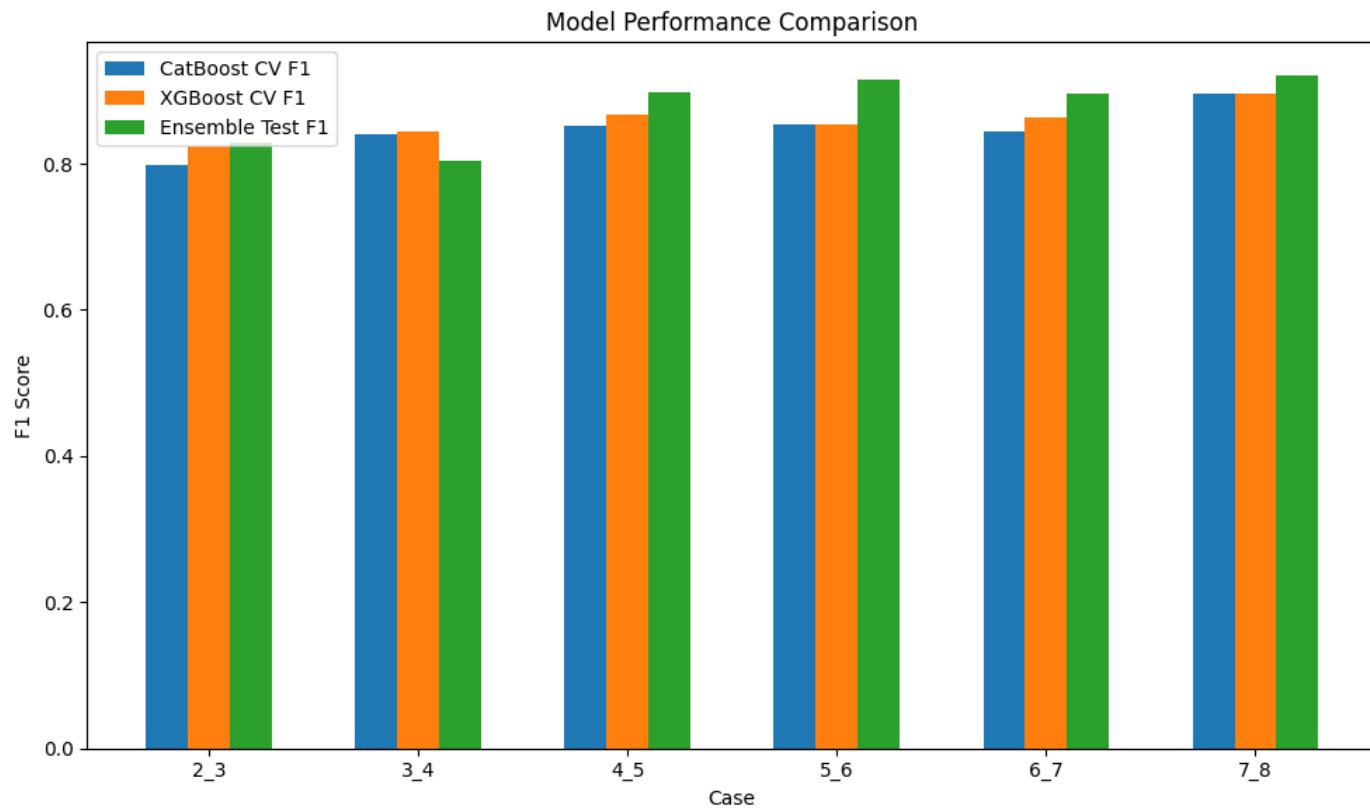
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annotated-types	0.7.0	fastparquet	2024.2.0	mpmath	1.3.0
asttokens	2.4.1	filelock	3.16.1	murmurhash	1.0.10
backcall	0.2.0	fonttools	4.53.1	nest_asyncio	1.6.0
blis	0.7.10	fsspec	2024.9.0	networkx	3.1
Brotli	1.1.0	graphviz	0.20.3	nose	1.3.7
catalogue	2.0.10	h2	4.1.0	numpy	1.24.4
catboost	1.2.7	hpack	4.0.0	osqp	0.6.7.post1
certifi	2024.8.30	hyperframe	6.0.1	packaging	24.1
cffi	1.17.0	idna	3.10	pandas	2.0.3
charset-normalizer	3.3.2	imbalanced-learn	0.12.3	parso	0.8.4
clarabel	0.9.0	imblearn	0.0	partd	1.4.1
click	8.1.7	importlib_metadata	8.5.0	pickleshare	0.7.5
cloudpathlib	0.19.0	importlib_resources	6.4.5	pillow	10.4.0
cloudpickle	3.0.0	iniconfig	2.0.0	pip	24.2
colorama	0.4.6	ipykernel	6.29.5	platformdirs	4.3.6
comm	0.2.2	ipython	8.12.2	plotly	5.24.1
confection	0.1.4	jedi	0.19.1	pluggy	1.5.0
contourpy	1.1.1	Jinja2	3.1.4	preshed	3.0.9
cramjam	2.8.3	joblib	1.4.2	prompt_toolkit	3.0.47
cvxopt	1.3.2	jupyter_client	8.6.3	psutil	6.0.0
cvxpy	1.5.2	jupyter_core	5.7.2	pure_eval	0.2.3
cycler	0.12.1	kiwisolver	1.4.7	pyarrow	17.0.0
cymem	2.0.8	knimpute	0.1.0	pycparser	2.22
dask	2023.5.0	langcodes	3.4.0	pydantic	2.8.2
debugpy	1.8.5	language_data	1.2.0	pydantic_core	2.20.1
decorator	5.1.1	lightgbm	4.5.0	Pygments	2.18.0
ecos	2.0.14	locket	1.0.0	pyparsing	3.1.4
en-core-web-md	3.7.1	marisa-trie	1.1.0	PySocks	1.7.1
exceptiongroup	1.2.2	markdown-it-py	3.0.0	pytest	8.3.3
executing	2.1.0	MarkupSafe	2.1.5	python-dateutil	2.9.0
		matplotlib	3.7.5	pytz	2024.2
		matplotlib-inline	0.1.7	pywin32	306
				PyYAML	6.0.2
				pyzmq	26.2.0
				qlddl	0.1.7.post4
				requests	2.32.3
				rich	13.8.1
				scikit-learn	1.3.2
				scipy	1.10.1
				scs	3.2.7
				seaborn	0.13.2
				setuptools	75.1.0
				shellingham	1.5.4
				six	1.16.0
				smart_open	7.0.4
				spacy	3.7.5
				spacy-legacy	3.0.12
				spacy-loggers	1.0.5
				srsly	2.4.8
				stack-data	0.6.2
				sympy	1.13.3
				tenacity	9.0.0
				thinc	8.2.5
				threadpoolctl	3.5.0
				tomli	2.0.1
				toolz	0.12.1
				torch	2.4.1+cu118
				torchaudio	2.4.1+cu118
				torchvision	0.19.1+cu118
				tornado	6.4.1
				tqdm	4.66.5
				traitlets	5.14.3
				typer	0.12.5
				typer-slim	0.12.5
				typing_extensions	4.12.2
				tzdata	2024.1
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				wasabi	1.1.2
				wcwidth	0.2.13
				weasel	0.4.1
				wheel	0.44.0
				win-inet-pton	1.1.0
				wrapt	1.16.0
				xgboost	2.1.1
				zipp	3.20.2
				zstandard	0.23.0

실행방법

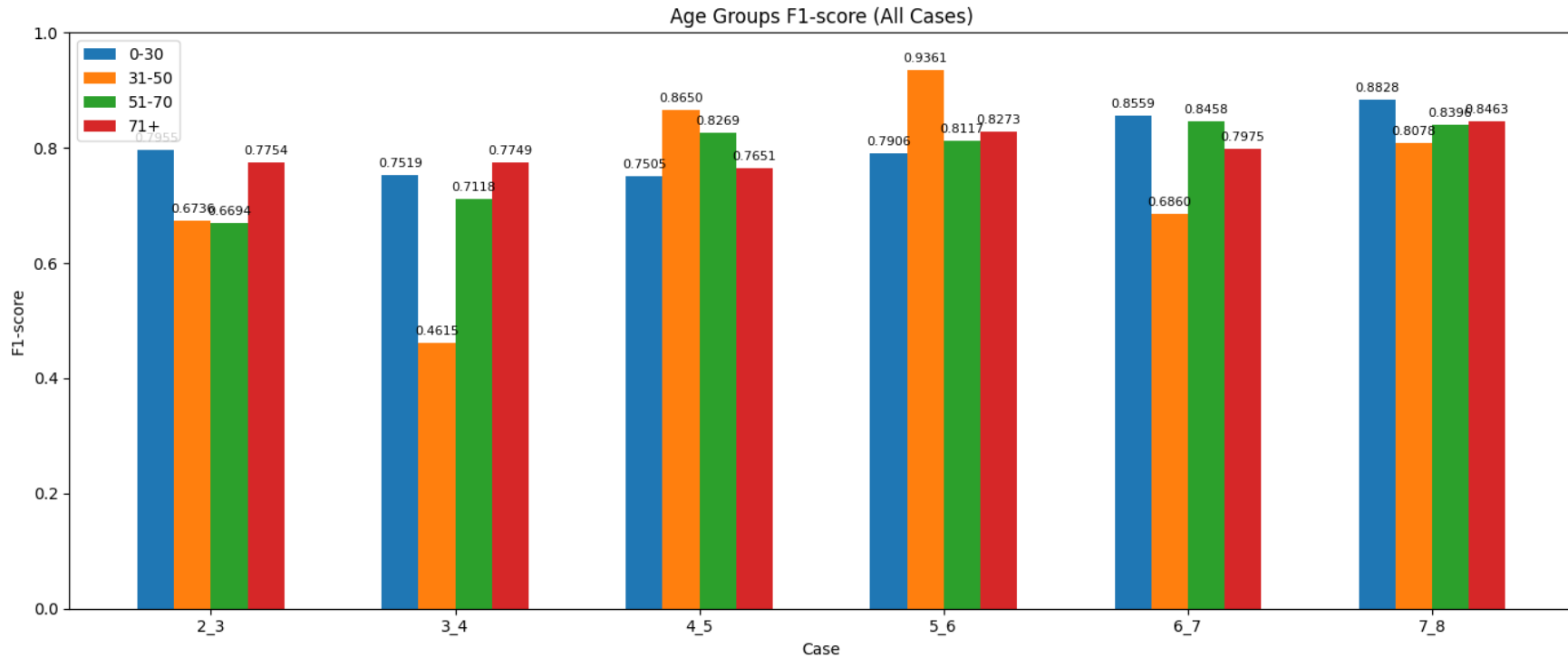
성능평가



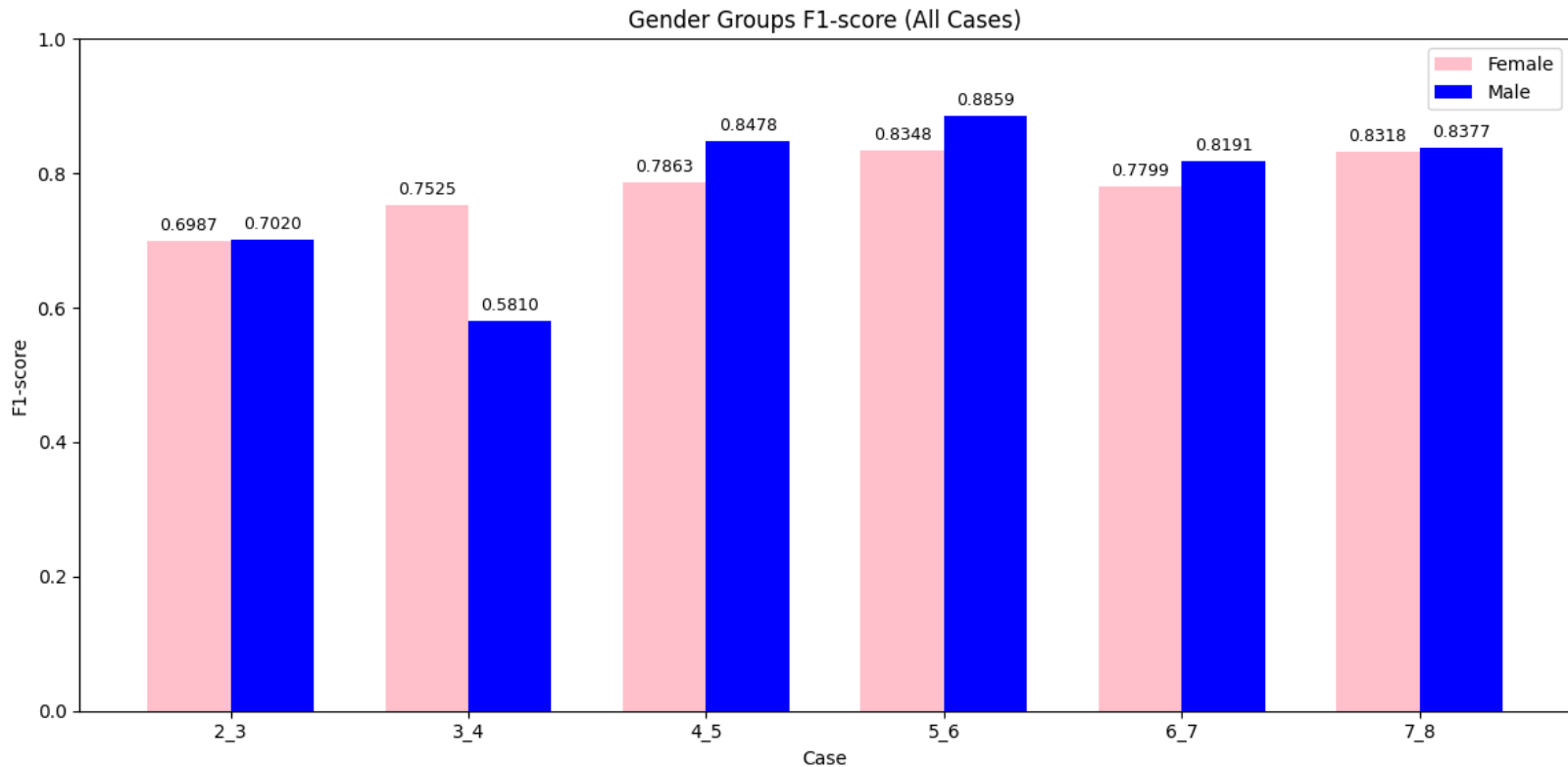
성능평가



공정성평가



공정성평가



본선모델개발방법론

- MIMIC-IV 데이터를 전처리한 방법과 동일하게 서울대 병원 데이터들을 전처리
- 결측값, 이상치, 일관성 없는 데이터 항목 처리 방식 통일
- 대상 데이터셋에 대한 성능을 최적화하기 위해 전이 학습 프로세스 반복 조정
- 또한 MIMIC-IV 데이터들로 계산한 pretrained weight들을 가져와 본선에 사용
- 현재 예선 모델은 회귀만 사용하고 있으나 시계열 특성들을 따로 추출해 시계열 모델 적용
- 추세, 계절성, 주기적 패턴과 같은 시간 기반 특성 추출
- 환자들의 종교, 윤리적 가치관, 혼인여부, 직업 등의 정보들이 존재할 시 모델에 고려

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<https://doi.org/10.1177/2054358118776326>